



```

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-19

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Query Match          100.0%; Score 148; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.6e-14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 DROIKIFQNRMRMKKTALDASALQTE 28
Db 1 DROIKIFQNRMRMKKTALDASALQTE 28

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RESULT 3
US-09-847-940B-18
; Sequence 18, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptides
US-09-847-940B-18

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Query Match          90.5%; Score 134; DB 10; Length 28;
Best Local Similarity 92.9%; Pred. No. 6e-12;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 DROIKIFQNRMRMKKTALDASALQTE 28
Db 1 DROIKIFQNRMRMKKTALDASALQTE 28

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RESULT 4
US-09-847-946A-18
; Sequence 18, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard

```

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; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-18

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```

Query Match          90.5%; Score 134; DB 11; Length 28;
Best Local Similarity 92.9%; Pred. No. 6e-12;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 DROIKIFQNRMRMKKTALDASALQTE 28
Db 1 DROIKIFQNRMRMKKTALDASALQTE 28

```

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RESULT 5
US-10-097-175-101
; Sequence 101, Application US/10097175
; Publication No. US20030045680A1
; GENERAL INFORMATION:
; APPLICANT: JOYAL, JOHN L.
; APPLICANT: MUELLER, JOHN
; APPLICANT: OZA, VIBHA B.
; APPLICANT: FINDEIS, MARK A.
; TITLE OF INVENTION: PEPTIDIC MODULATORS OF THE ANDROGEN RECEPTOR
; FILE REFERENCE: PPI-110
; CURRENT APPLICATION NUMBER: US/10/097,175
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/275,240
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/352,399
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Androgen Receptor Binding Polypeptides
US-10-097-175-101

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Query Match          68.2%; Score 101; DB 15; Length 26;
Best Local Similarity 73.9%; Pred. No. 2.4e-07;
Matches 17; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Qy 2 ROIKIFQNRMRMKKTALDASALQTE 24
Db 1 ROIKIFQNRMRMKKTALDASALQTE 23

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```

RESULT 6
US-09-731-023A-12
; Sequence 12, Application US/09731023A
; Patent No. US20020077283A1
; GENERAL INFORMATION:
; APPLICANT: Seese, William
; TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
; FILE REFERENCE: 44574-5076-US
; CURRENT APPLICATION NUMBER: US/09/731,023A
; CURRENT FILING DATE: 2000-12-07

```



PRIOR APPLICATION NUMBER: US 60/231,327  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 12  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: Antennapedia-cav-X fusion peptide  
US-09-731-023A-12

Query Match 67.6%; Score 100; DB 9; Length 36;  
Best Local Similarity 69.2%; Pred. No. 4.5e-07;  
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 ROIKIWFORRMKMKKTALDASALQT 27  
DB 1 ROIKIWFORRMKMKKGIDKAFETT 26

RESULT 7  
US-10-358-365-12  
Sequence 12, Application US/10358365  
Publication No. US20030165510A1  
GENERAL INFORMATION:  
APPLICANT: Seese, William  
TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics  
FILE REFERENCE: 44574-5076-US  
CURRENT APPLICATION NUMBER: US/10/358,365  
CURRENT FILING DATE: 2003-02-04  
PRIOR APPLICATION NUMBER: US 09/731,023  
PRIOR FILING DATE: 2000-12-07  
PRIOR APPLICATION NUMBER: US 60/231,327  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 12  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: Antennapedia-cav-X fusion peptide  
US-10-358-365-12

Query Match 67.6%; Score 100; DB 12; Length 36;  
Best Local Similarity 69.2%; Pred. No. 4.5e-07;  
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 ROIKIWFORRMKMKKTALDASALQT 27  
DB 1 ROIKIWFORRMKMKKGIDKAFETT 26

RESULT 8  
US-10-229-915-1  
Sequence 1, Application US/10229915  
Publication No. US20030083262A1  
GENERAL INFORMATION:  
APPLICANT: Lazarus, Douglas  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING INFLAMMATORY  
FILE REFERENCE: PPI-127  
CURRENT APPLICATION NUMBER: US/10/229,915  
CURRENT FILING DATE: 2002-08-27  
PRIOR APPLICATION NUMBER: US 60/316,328  
PRIOR FILING DATE: 2001-08-30  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1

LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: anti-inflammatory compound  
US-10-229-915-1

Query Match 66.2%; Score 98; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.1e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFORRMKMKKK 17  
DB 1 DRQIKWFORRMKMKKK 17

RESULT 9  
US-08-610-220A-11  
Sequence 11, Application US/08610220A  
Publication No. US2003009638A1  
GENERAL INFORMATION:  
APPLICANT: Troy, Carol M.  
TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL  
TITLE OF INVENTION: DEATH AND USES THEREOF  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/610,220A  
FILING DATE: MAR-04-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 48332/JPM/JML  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-610-220A-11

Query Match 64.2%; Score 95; DB 8; Length 21;  
Best Local Similarity 94.4%; Pred. No. 1.3e-06;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ROIKIWFORRMKMKKTA 19  
DB 1 ROIKIWFORRMKMKKTA 18

RESULT 10  
US-09-150-623-11  
Sequence 11, Application US/09150623  
Patent No. US20020044931A1  
GENERAL INFORMATION:  
APPLICANT: Troy, Carol M.  
TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL

TITLE OF INVENTION: DEATH AND USES THEREOF  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/150,623  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/610,220  
FILING DATE: MAR-04-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 48332/JFW/JML  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-150-623-11

Query Match 64.2%; Score 95; DB 9; Length 21;  
Best Local Similarity 94.4%; Pred. No. 1.3e-06;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RQIKIWPNRRMKWKKA 19  
DB 1 RQIKIWPNRRMKWKKA 18

RESULT 11  
US-10-188-947-11  
Sequence 11, Application US/10188947  
Publication No. US2003002393A1  
GENERAL INFORMATION:  
APPLICANT: MEDHITOV, Ruslan  
APPLICANT: HORNG, Tiffany  
TITLE OF INVENTION: TOLL/INTERLEUKIN-1 RECEPTOR ADAPTER PROTEIN (TIRAP)  
FILE REFERENCE: 044574-5101US  
CURRENT APPLICATION NUMBER: US/10/188,947  
CURRENT FILING DATE: 2002-07-03  
PRIOR APPLICATION NUMBER: 60/289,738  
PRIOR FILING DATE: 2001-05-09  
PRIOR APPLICATION NUMBER: 60/289,815  
PRIOR FILING DATE: 2001-05-09  
PRIOR APPLICATION NUMBER: 60/289,866  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 11  
LENGTH: 30  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: TIRAP/Antennapedia fusion protein  
NAME/KEY: MISC\_FEATURE

OTHER INFORMATION: TIRAP/Antennapedia fusion protein  
US-10-188-947-11

Query Match 64.2%; Score 95; DB 15; Length 30;  
Best Local Similarity 78.3%; Pred. No. 1.9e-06;  
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 RQIKIWPNRRMKWKKTALDASA 24  
DB 1 RQIKIWPNRRMKWKKTALDASA 23

RESULT 12  
US-10-116-275-190  
Sequence 190, Application US/10116275  
Publication No. US20030211476A1  
GENERAL INFORMATION:  
APPLICANT: Elan Pharmaceutical Technology  
APPLICANT: O'Mahony, Daniel J.  
APPLICANT: Brayden, David  
APPLICANT: Byrne, Daragh  
APPLICANT: Lambkin, Imelda  
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and  
FILE REFERENCE: E1067/20087  
CURRENT APPLICATION NUMBER: US/10/116,275  
CURRENT FILING DATE: 2002-10-04  
NUMBER OF SEQ ID NOS: 349  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 190  
LENGTH: 269  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-275-190

Query Match 63.9%; Score 94.5; DB 12; Length 269;  
Best Local Similarity 67.9%; Pred. No. 2e-05;  
Matches 19; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 DRQIKIWPNRRMKWK-K-TALDASALQT 27  
DB 235 ERQIKIWPNRRMKWK-KDKKLSMSLAT 262

RESULT 13  
US-10-161-499-79  
Sequence 79, Application US/10161499  
Publication No. US20030044427A1  
GENERAL INFORMATION:  
APPLICANT: Howley, Peter M.  
APPLICANT: Benson, John  
APPLICANT: Kasukawa, Hiroaki  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING  
TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS  
FILE REFERENCE: HMV-041.01  
CURRENT APPLICATION NUMBER: US/10/161,499  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/347,504  
PRIOR FILING DATE: 1999-07-02  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 79  
LENGTH: 34  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-161-499-79

Query Match 63.5%; Score 94; DB 15; Length 34;  
Best Local Similarity 94.1%; Pred. No. 3e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKIWPNRRMKWK 17

Db 1 EROIKWFONRBMKKKGIMKASFTT 17

Job time : 77.9766 secs

RESULT 14  
US-09-731-023A-11  
; Sequence 11, Application US/09731023A  
; Patent No. US20020077283A1  
; GENERAL INFORMATION:  
; APPLICANT: Seesee, William  
; TITLE OF INVENTION: Caveolin peptides and Their Use as Therapeutics  
; FILE REFERENCE: 44574-5076-US  
; CURRENT APPLICATION NUMBER: US/09/731,023A  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 60/231,327  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Antennapedia-caveolin-1 scaffolding domain fusion  
US-09-731-023A-11

Query Match 63.5%; Score 94; DB 9; Length 36;  
Best Local Similarity 65.4%; Pred. No. 3.1e-06;  
Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 ROIKWFONRBMKKKTALDASALQT 27  
DB 1 ROIKWFONRBMKKKGIMKASFTT 26

RESULT 15  
US-10-358-365-11  
; Sequence 11, Application US/10358365  
; Publication No. US20030165510A1  
; GENERAL INFORMATION:  
; APPLICANT: Seesee, William  
; TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics  
; FILE REFERENCE: 44574-5076-US  
; CURRENT APPLICATION NUMBER: US/10/358,365  
; CURRENT FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: US 09/731,023  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 60/231,327  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Antennapedia-caveolin-1 scaffolding domain fusion  
; OTHER INFORMATION: peptide  
US-10-358-365-11

Query Match 63.5%; Score 94; DB 12; Length 36;  
Best Local Similarity 65.4%; Pred. No. 3.1e-06;  
Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 ROIKWFONRBMKKKTALDASALQT 27  
DB 1 ROIKWFONRBMKKKGIMKASFTT 26

Search completed: February 18, 2004, 15:42:02

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 106.289 Seconds  
(without alignments)  
41.814 Million cell updates/sec

Title: US-09-643-260-19

Perfect score: 148  
Sequence: 1 DRQIKWFMNRKMKKTRALDASALQTE 28

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Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	148	100.0	28	23	ABO8741
2	148	100.0	28	23	AM48524
3	148	100.0	28	24	ABU08435
4	134	90.5	28	23	ABO8740
5	134	90.5	28	23	AM48523
6	134	90.5	28	24	ABU08434
7	101	68.2	26	24	AAE31836
8	100	67.6	36	23	AAU79345
9	98	66.2	20	21	AA13423

10	98	66.2	26	18	AA11630
11	98	66.2	41	22	AA80924
12	98	66.2	41	22	AA80925
13	95	64.2	21	18	AA45976
14	95	64.2	24	19	AA82957
15	95	64.2	30	24	ABP58107
16	95	64.2	36	21	AA178416
17	95	64.2	230	21	AAV58610
18	94	63.5	27	18	AAV27444
19	94	63.5	27	20	AAV27444
20	94	63.5	34	21	AAV79819
21	94	63.5	36	22	AAU79344
22	94	63.5	42	23	ABP53779
23	94	63.5	60	20	AAV42291
24	94	63.5	60	20	AAV27403
25	94	63.5	60	20	AAV04364
26	94	63.5	60	23	ABP84470
27	94	63.5	61	22	AAE00811
28	94	63.5	64	24	AAE32060
29	94	63.5	128	24	ABP97929
30	94	63.5	217	22	AAE10922
31	94	63.5	217	23	ABG96337
32	94	63.5	295	24	AAE32047
33	94	63.5	378	22	ABP72035
34	94	63.5	417	22	ABP57755
35	94	63.5	589	22	ABP56929
36	94	63.5	22	20	AAW91049
37	93	62.8	22	21	AAE27063
38	93	62.8	106	21	AAE21030
39	93	62.8	115	21	AAE53629
40	93	62.8	220	22	AAW41487
41	93	62.8	236	22	AAW39701
42	93	62.8	243	19	AAW48885
43	93	62.8	257	24	AAE32048
44	93	62.8	42	23	ABP53778
45	92.5	62.5			

## ALIGNMENTS

RESULT 1					
ID	ABO8741	standard; peptide; 28 AA.			
XX	ABO8741;				
AC	14-JUN-2002	(first entry)			
DT					
DE	Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 19.				
XX					
XX	IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;				
KW	kinase activation; leukocyte; inflammation; E-selectin; osteoclast;				
KW	autoimmune disease; transplant rejection; osteoporosis; cancer;				
KW	Alzheimer's disease; viral; infection; asthma; anaphylaxis; peritasis;				
KW	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;				
KW	corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;				
KW	osteoporosis; cytostatic; nootropic; neuroprotective; anti-HIV; human;				
KW	antiartherosclerotic; virucide; antiasthmatic; antiallergic;				
KW	dermatological; antibacterial; antiparasitic; antirheumatic;				
KW	antiarthritic; osteopathic; antitumor; mutant; mutagen.				
OS	Homo sapiens.				
OS	Synthetic.				
FT	Key	Location/Qualifiers			
FT	Misc-difference 22	/note= "wildtype Trp substituted by Ala"			
FT	Misc-difference 24	/note= "wildtype Trp substituted by Ala"			
PN	WO200109547-A2.				
XX					

Anti-apoptotic pro  
Mixer SIM peptide.  
Mixer SIM mutant p  
Cysteine protease  
Oestrogen receptor  
Mouse TRAP-antenn  
Drosophila antenna  
Protein regulating  
Anti-apoptotic pro  
Antennapedia inter  
Transduction domai  
Human papillomavir  
Antennapedia-caveo  
Antennapedia helix  
Drosophila antenna  
D. melanogaster PA  
S. cerevisiae Antp  
D. melanogaster an  
Antennapedia C3APL  
Amino acid sequenc  
Human HOXB7 varian  
Human ovarian can  
Clostridium botuli  
Drosophila melanog  
Drosophila melanog  
Internalization se  
Beta-catenin deriv  
Human nucleic acid  
Human colon cancer  
Human polypeptide  
Human polypeptide  
Amino acid sequenc  
Clostridium botuli  
Antennapedia helix

PD 08-NOV-2001.  
 XX  
 XX  
 PF 02-MAY-2001; 2001WO-US40654.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (UYVA ) UNIV YALE.  
 PA  
 PI May MJ, Ghosh S;  
 XX  
 DR WPI; 2002-179356/23.  
 XX  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 binding domain -  
 PS  
 PS Claim 23; Fig 5; 82pp; English.  
 XX  
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprises contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB7313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blocking the interaction of NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of I-kappaB. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polyarthritis, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
 CC binding domain of IKKbeta.  
 XX  
 SQ Sequence 28 AA;  
 Query Match 100.0%; Score 148; DB 23; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 5-6e-15;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DROIKIWFONRRMKKKTALDASALQTE 28  
 DB 1 DROIKIWFONRRMKKKTALDASALQTE 28  
 RESULT 2  
 AAM48524  
 ID AAM48524 standard; Peptide; 28 AA.  
 XX  
 AC AAM48524;  
 XX  
 DT 20-MAR-2002 (first entry)

XX  
 DE NBD peptide SEQ ID NO 19.  
 XX  
 XX  
 KW Antiinflammatory; antiarthritic; cytopathic; antiparasitic; nootropic;  
 KW immunosuppressive; dermatological; osteoporosis; antibacterial; vitruclide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NF-kappaB; I-kappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200183554-A2.  
 PN  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECTIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 PI  
 PI May MJ, Ghosh S, Fandels MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 PS  
 PS Example 5; Fig 5; 86pp; English.  
 XX  
 XX The invention relates to an antiinflammatory compound (especially  
 CC AAM48620-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
 CC cytopathic, antiparasitic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, vitruclide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
 CC activation by blocking interaction of I-kappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of I-kappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 28 AA;  
 Query Match 100.0%; Score 148; DB 23; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 5-6e-15;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DROIKIWFONRRMKKKTALDASALQTE 28  
 DB 1 DROIKIWFONRRMKKKTALDASALQTE 28  
 RESULT 3

ABU08435  
ID ABU08435 standard; peptide, 28 AA.  
XX  
AC ABU08435;  
XX  
DT 12-JUN-2003 (first entry)  
XX  
DE Human mutant NEMO binding site (NBD) peptide.  
XX  
XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;  
XX IKKalpha kinase-beta; IKKalpha kinase-alpha; IKKalpha; NF-kappaB;  
XX nuclear factor-kappaB induction; inflammatory disorder;  
XX autoimmune disease; osteoporosis; cancer; Alzheimer's disease;  
XX atherosclerosis; viral infection; Ataxia telangiectasia;  
XX transplacental detection; immunosuppressive; osteopathic;  
XX cytotoxic; nocrotropic; neuroprotective; antiatherosclerotic; virucide;  
XX vascotropic; antirheumatic; antiautistic; mutant; mutain.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN US2002156000-A1.  
XX  
PD 24-OCT-2002.  
XX  
PF 02-MAY-2001; 2001US-0847940.  
XX  
XX 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
XX  
XX (MAYM/) MAY M J.  
XX (GHOS/) GHOSH S.  
XX  
PI May MJ, Ghosh S;  
XX  
XX WPI; 2003-209142/20.  
DR  
XX Novel antiinflammatory peptide compounds comprising NEMO binding  
PT domain, useful for modulating NF-kappaB induction in a cell and for  
PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,  
PT psoriasis, vasculitis -  
XX  
XX  
PS Claim 22; Fig 5A; 47pp; English.  
XX  
XX The present invention relates to antiinflammatory compounds comprising  
CC NEMO binding domain (NBD) peptides. The NEMO binding domains are  
CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha  
CC (IKKalpha) proteins. The antiinflammatory compounds of the invention  
CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction  
CC in a cell, where the compounds are capable of blocking the interaction  
CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The  
CC antiinflammatory compound further comprises at least one membrane  
CC translocation domain. The compounds are useful for treating  
CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,  
CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia  
CC telangiectasia, and for transplacental detection. The compounds of  
CC the invention block NF-kappaB induction by IKK but do not inhibit  
CC the basal activity of NF-kappaB. The present sequence represents  
CC a human mutant NBD peptide.  
XX  
XX  
SO Sequence 28 AA;  
Query Match 100.0%; Score 148; DB 24; Length 28;  
Best Local Similarity 100.0%; Pred. No. 5, 6e-15;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 DROIKIMFQNRBMKMKKTALDASALQTE 28  
Db 1 DROIKIMFQNRBMKMKKTALDASALQTE 28

ABB08740 standard; peptide, 28 AA.  
XX  
AC ABB08740;  
XX  
DT 14-JUN-2002 (first entry)  
XX  
DE IKKbeta NEMO binding domain SEQ ID NO 18.  
XX  
XX IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
XX kinase activation; leukocyte; inflammation; E-selectin; osteoclast;  
XX autoimmune disease; transplant rejection; osteoporosis; cancer;  
XX Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;  
XX rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
XX corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;  
XX osteopathic; cytotoxic; nocrotropic; neuroprotective; anti-HIV; human;  
XX antiatherosclerotic; virucide; antiaesthetic; antiallergic;  
XX dermatological; antibacterial; antipsoriatic; antirheumatic;  
XX antiautistic; osteopathic; antidiabetic.  
XX  
OS Homo sapiens.  
OS  
XX WO200183547-A2.  
XX  
XX 08-NOV-2001.  
XX  
XX 02-MAY-2001; 2001WO-US40654.  
XX  
XX 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
XX  
XX (UYTA ) UNIV YALE.  
XX  
XX May MJ, Ghosh S;  
XX  
XX WPI; 2002-179350/23.  
DR  
XX Modulating NF-kappaB induction in a cell, useful for treating e.g.  
PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
PT cell with an anti-inflammatory compound comprising at least one NEMO  
PT binding domain -  
XX  
XX  
PS Claim 23; Fig 5; 82pp; English.  
XX  
XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
CC comprises contacting a cell with an anti-inflammatory compound  
CC (ABB08745-ABB08742) comprising at least one NEMO binding domain  
CC (ABB077313). The compound has acts through selective inhibition of  
CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
CC interaction results in inhibition of IKKbeta kinase activation and  
CC subsequent decreased phosphorylation of IkappaB. The compound may also  
CC act (directly or indirectly) by blocking the recruitment of leukocytes  
CC into sites of acute and chronic inflammation, by down-regulating the  
CC expression of E-selectin on leukocytes or by blocking osteoclast  
CC differentiation. The compound is useful in treating NF-kB mediated  
CC conditions, where the condition is an inflammatory disorder, an  
CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
CC telangiectasia. The inflammatory disorder is asthma, allergies,  
CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
CC polyarthritis, scleroderma, Wegner's granulomatosis, temporal arteritis,  
CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
CC diseases include HIV and influenza. The compound may also be useful for  
CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
CC sunburn or aging. The compound may be used to replace corticosteroids in  
CC any application in which corticosteroids are used, including  
CC immunosuppression in transplants and cancer therapy. Also for identifying

CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of the NEMO  
 CC binding domain of IKKbeta.  
 CC  
 XX Sequence 28 AA;  
 Query Match 90.5%; Score 134; DB 23; Length 28;  
 Best Local Similarity 92.9%; Pred. No. 6.7e-13;  
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Db 1 DROIKIWFONRRMKKKTKALDASALQTE 28  
 1 DROIKIWFONRRMKKKTKALDMSWLQTE 28  
 RESULT 5  
 ID AAM48523 standard; Peptide: 28 AA.  
 XX AAM48523;  
 AC  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX NBD peptide SEQ ID NO 18.  
 DE  
 XX Antiinflammatory; antiasthmatic; cytostatic; antiproliferative; neurotrophic;  
 XX antirheumatic; antiarthritic; osteoprotective; antibacterial; virucide;  
 XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 XX autoimmune disorder; multiple sclerosis; transplant rejection;  
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA) UNIV YALE.  
 PI May MJ, Ghosh S, Firdels MA, Phillips K;  
 PI WPI; 2002-121889/16.  
 DR  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 FT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 XX Example 5; Fig 5; 88pp; English.  
 PS  
 XX The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48625-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytostatic, antiproliferative, dermatological, neuroprotective,  
 CC antibacterial, immunosuppressive, cancer, psoriasis, and ataxia  
 CC neurotrophic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The

CC compound are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis, transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 XX Sequence 28 AA;  
 Query Match 90.5%; Score 134; DB 23; Length 28;  
 Best Local Similarity 92.9%; Pred. No. 6.7e-13;  
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Db 1 DROIKIWFONRRMKKKTKALDASALQTE 28  
 1 DROIKIWFONRRMKKKTKALDMSWLQTE 28  
 RESULT 6  
 ID ABU08434 standard; peptide: 28 AA.  
 XX ABU08434;  
 AC  
 XX 12-JUN-2003 (first entry)  
 DT  
 XX Wild-type human NEMO binding site (NBD) peptide.  
 DE  
 XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;  
 XX IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;  
 XX nuclear factor-kappaB induction; inflammatory disorder;  
 XX autoimmune disease; osteoporosis; cancer; Alzheimer's disease;  
 XX atherosclerosis; viral infection; Ataxia telangiectasia;  
 XX transplantation detection; immunosuppressive; osteoprotective;  
 XX cytostatic; neurotrophic; neuroprotective; antiatherosclerotic; virucide;  
 XX vasotropic; antirheumatic; antiarthritic.  
 OS Homo sapiens.  
 XX  
 PN US2002156000-A1.  
 PD 24-OCT-2002.  
 XX  
 PF 02-MAY-2001; 2001US-0847940.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (MAYM/) MAY M J.  
 PA (GHOSH/) GHOSH S.  
 PI May MJ, Ghosh S;  
 PI WPI; 2003-209142/20.  
 DR  
 XX Novel antiinflammatory peptide compounds comprising NEMO binding  
 PT domain, useful for modulating NF-kappaB induction in a cell and for  
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,  
 PT psoriasis, vasculitis -  
 XX  
 XX Claim 35; Page 22; 47pp; English.  
 PS  
 XX The present invention relates to antiinflammatory compounds comprising  
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are  
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha  
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention  
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction  
 CC in a cell, where the compounds are capable of blocking the interaction  
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The

CC antiinflammatory compound further comprises at least one membrane  
 CC translocation domain. The compounds are useful for treating  
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia  
 CC telangiectasia, and for transplantation detection. The compounds of  
 CC the invention block NF-kappaB induction by IKK but do not inhibit  
 CC the basal activity of NF-kappaB. The present sequence represents  
 CC an antiinflammatory compound of the invention.

XX  
 SQ Sequence 28 AA;

Query Match 90.5%; Score 134; DB 24; Length 28;  
 Best Local Similarity 92.9%; Pred. No. 6.7e-13;  
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 DRQIKIWPQNRKMKKKTALDMSALQTE 28  
 1 DRQIKIWPQNRKMKKKTALDMSALQTE 28  
 DB 1 DRQIKIWPQNRKMKKKTALDMSALQTE 28

RESULT 7  
 AAE31836  
 ID AAE31836 standard; peptide; 26 AA.  
 AC AAE31836;  
 XX  
 DT 07-MAR-2003 (first entry)  
 XX  
 DE Androgen receptor binding peptide #87.  
 XX  
 KW Androgen receptor; androgen-associated disorder; prostate cancer; acne;  
 KW benign prostatic hypertrophy; hirsutism; androgen insensitivity syndrome;  
 KW male pattern baldness; Stein-Leventhal syndrome; infertility; cytostatic;  
 KW X-linked spinal bulbar muscular atrophy; antiseborrheic; dermatological;  
 KW depilatory; androgen receptor binding peptide.  
 XX  
 OS Unidentified.  
 OS  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "N-terminal acetyl"  
 FT Modified-site 26  
 FT /note= "C-terminal amide"  
 FT  
 FT WO200272612-A2.  
 XX  
 PN 19-SEP-2002.  
 PD  
 XX 12-MAR-2002; 2002WO-US07487.  
 PF  
 XX 12-MAR-2001; 2001US-275240P.  
 PR 28-JAN-2002; 2002US-352399P.  
 XX  
 PA (PRAE-) PRAECS PHARM INC.  
 XX  
 PI Joyal JL, Mueller J, Oza VB, Findeis MA;  
 PI  
 XX WPI; 2003-067363/06.  
 DR  
 XX  
 XX New peptide modulators of androgen receptor, useful for treating  
 PT androgen-associated disorder, e.g. prostate cancer, particularly  
 PT hormonally refractive prostate cancer, colon cancer, lung cancer, acne,  
 PT or hirsutism -  
 XX  
 PS Example; Page 30; 68pp; English.  
 CC The present invention relates to novel peptide modulators of androgen  
 CC receptor. The peptides of the invention are useful for treating androgen-  
 CC associated disorders such as prostate cancer, particularly hormonally  
 CC refractive prostate cancer, colon cancer, lung cancer, benign prostatic  
 CC hypertrophy, acne, hirsutism, male pattern baldness, Stein-Leventhal  
 CC syndrome, androgen insensitivity syndrome, infertility, endometrial  
 CC cancer and X-linked spinal bulbar muscular atrophy. The present sequence

CC is an androgen receptor binding peptide.  
 XX  
 SQ Sequence 26 AA;

Query Match 68.2%; Score 101; DB 24; Length 26;  
 Best Local Similarity 73.9%; Pred. No. 4.9e-08;  
 Matches 17; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 RQIKIWPQNRKMKKKTALDASA 24  
 1 RQIKIWPQNRKMKKKTALDASSS 23  
 DB 1 RQIKIWPQNRKMKKKTALDASSS 23

RESULT 8  
 AAU79345  
 ID AAU79345 standard; Peptide; 36 AA.  
 AC AAU79345;  
 XX  
 DT 02-JUL-2002 (first entry)  
 XX  
 DE Antennapedia-caveolin-X fusion peptide.  
 XX  
 KW Caveolin; scaffolding domain; endothelial nitric oxide synthase; eNOS;  
 KW vasodilation inhibitor; inflammation inhibitor; tumour cell angiogenesis;  
 KW tumour cell proliferation; osteoporosis; arthritis; atherosclerosis;  
 KW asthma; Alzheimer's disease; allergy; allergic rhinitis; urticaria;  
 KW anaphylaxis; dry sensitivity; food sensitivity; dermatitis; eczema;  
 KW psoriasis; sunburn; aging; osteoarthritis; psoriatic arthritis; lupus;  
 KW sporadic arthritis; chronic obstruction pulmonary disease; cancer; Cav;  
 KW chronic inflammatory bowel disease; tumour growth; malignant neoplasm;  
 KW human; fruit fly; antennapedia internalisation signal.  
 XX  
 OS Drosophila melanogaster.  
 OS Homo sapiens.  
 OS Synthetic.  
 OS  
 FH Key Location/Qualifiers  
 FT Misc-difference 1..16  
 FT /label= "Antennapedia internalisation signal"  
 FT /note= "Specifically claimed in claim 9"  
 FT Misc-difference 17..32  
 FT /label= "Cav-X"  
 FT /note= "Control peptide based on a human caveolin-1  
 FT scaffolding domain shown in AAU79340 residues  
 FT 82-101"  
 FT  
 FT WO200220768-A2.  
 XX  
 PN 14-MAR-2002.  
 PD  
 XX 10-SEP-2001; 2001WO-US42069.  
 PF  
 XX 08-SEP-2000; 2000US-231327P.  
 PR 07-DEC-2000; 2000US-0731023.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI Seesa WC;  
 PI  
 XX WPI; 2002-329877/36.  
 DR  
 XX  
 XX New peptide having caveolin scaffolding domain, useful for modulating  
 PT activity of endothelial nitric oxide synthase and inhibiting  
 PT inflammation and tumour cell angiogenesis proliferation -  
 XX  
 PS Claim 16; Page 72; 73pp; English.  
 CC The invention describes an isolated caveolin scaffolding domain peptide  
 CC (I). A fusion peptide (II) containing (I) and at least a membrane  
 CC translocation sequence is useful for down regulating endothelial nitric  
 CC oxide synthase (eNOS) activity in a cell, resulting in blockage of  
 CC vasodilation. (II) is therefore useful for inhibiting inflammation and



CC tumour cell angiogenesis/proliferation in an animal; and for blocking the  
CC interaction of caveolin with a protein in vivo. (II) may be useful in  
CC treatment of inflammatory conditions such as osteoporosis, rheumatoid  
CC arthritis, atherosclerosis, asthma and Alzheimer's disease. (I) and (II)  
CC are also useful for treating pathological processes associated with a  
CC pro-inflammatory response including allergies such as allergic rhinitis,  
CC urticaria, anaphylaxis, dry sensitivity, food sensitivity, cutaneous  
CC inflammation such as dermatitis, eczema, psoriasis contact dermatitis,  
CC sunburn, aging, arthritis such as osteoarthritis, psoriatic arthritis,  
CC lupus, spondylarthritis, and chronic obstruction pulmonary disease and  
CC chronic inflammatory bowel disease. (I) and (II) are useful for replacing  
CC corticosteroids useful for immunosuppression in transplant and cancer  
CC patients. When administered along with one or more anti-inflammatory  
CC agent (I) and (II) are useful for inhibiting tumour growth or malignant  
CC neoplasm including cellular angiogenesis, proliferation, invasiveness,  
CC and metastasis in biological systems. This sequence represents a fusion  
CC peptide of the invention created from the fruit fly antennapedia  
CC internalisation signal and control sequence Cav-X, based on the human  
CC caveolin-1 scaffolding domain shown in AAU79340, residues 82-101.

CC XX  
SQ Sequence 36 AA;

Query Match 67.6%; Score 100; DB 23; Length 36;  
Best Local Similarity 69.2%; Pred. No. 9.9e-08;  
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 RQIKIWQNRRMKWKTALDASALQT 27  
DB 1 RQIKIWQNRRMKWKTGIDKAFPTT 26

RESULT 9  
AAB13423 standard; peptide; 20 AA.

XX AAB13423;

XX 23-NOV-2000 (first entry)

XX Synthetic alpha smooth muscle actin inhibitor # 3.

XX Alpha smooth muscle actin; alpha-SM; wound contraction;  
XX hypertrophic scar; fibromatosis; Dupuytren disease; fibrotic condition;  
XX lung fibrosis.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note="N-terminal acetyl"

XX MO200038733-A1.

XX 06-JUL-2000.

XX 15-DEC-1999; 99MO-EP09964.

XX 24-DEC-1998; 98EP-0204396.

XX (UNIO ) UCB-BIOPRODUCTS SA.

XX Gabbiani G, Scarso A;

XX WPI; 2000-452308/39.

XX A peptide product for prevention and treatment of a disease related to  
PT alpha-SM actin expression comprises a tetrapeptide associated with a  
PT chemical entity that is able to introduce the tetrapeptide into the  
PT cell -

XX Claim 7; Page 23; 31pp; English.

XX The present invention relates to novel peptides comprising of a specific

CC tetrapeptide associated with an oligopeptide which allows the  
CC introduction of the tetrapeptide into the target cell. The present  
CC sequence is one such peptide. Residues 1 to 4 of the present sequence  
CC correspond to the specific tetrapeptide, while residues 5 to 20  
CC correspond to the oligopeptide. The specific tetrapeptide of the present  
CC sequence interferes with alpha smooth muscle (alpha-SM) actin  
CC organisation in stress fibers. The present sequence may be used in the  
CC prevention and/or treatment of a disease related to alpha-SM actin  
CC expression, e.g. wound contraction, hypertrophic scar, fibromatosis and  
CC fibrotic conditions. The present sequence may also be used to treat  
CC Dupuytren disease and lung fibrosis.

XX SQ Sequence 20 AA;

Query Match 66.2%; Score 98; DB 21; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKIWQNRRMKWKK 17  
DB 4 DRQIKIWQNRRMKWKK 20

RESULT 10  
AAW11630 standard; peptide; 26 AA.

XX AAW11630;

XX 16-OCT-1997 (first entry)

XX Anti-apoptotic protein blocking peptide FP2.

XX Cell permeable; apoptosis; blocking; inhibition; tumour growth;  
XX ex vivo purging; in vivo administration; Bcl-2.

XX Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..17 /label= sig\_peptide

XX DE19526174-A1.

XX 23-JAN-1997.

XX 18-JUL-1995; 95DE-1026174.

XX 18-JUL-1995; 95DE-1026174.

XX (BRAC/) BRACH M.

XX (HERR/) HERMANN F.

XX (KIEH/) KIEHNTOPF M.

XX Brach M, Herrmann F, Kiehnkopf M;

XX WPI; 1997-088160/09.

XX Claim 6; Page 7; 7pp; German.

XX The present sequence is a cell permeable anti-apoptotic protein  
CC blocking peptide, which can be used to inhibit tumour growth, e.g.  
CC by ex vivo purging or (after stabilisation) in vivo  
CC administration. The peptide preferably blocks Bcl-2, and comprises  
CC a signal peptide mediating cell penetration and a functional  
CC sequence corresponding to a Bcl-2 domain.

XX SQ Sequence 26 AA;

Query Match 66.2%; Score 98; DB 18; Length 26;

Best Local Similarity 89.5%; Pred. No. 1.4e-07;  
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 DROIKWPNRRMKWKTA 19  
: |||||  
DB 1 EROIKWPNRRMKWKKA 19

RESULT 11  
AAB80924  
ID AAB80924 standard; Protein; 41 AA.  
XX  
AC AAB80924;  
XX  
DT 04-JUN-2001 (first entry)  
XX  
DE Mixer SIM peptide.  
XX  
KW Smad; Cytostatic; vulnerary; cerebroprotective; immunosuppressive;  
KW Anti-HIV; antidiabetic; ophthalmological; antiinflammatory; SIM;  
KW Smad interaction Motif; tissue repair; fibrotic condition;  
KW immunosuppression; diabetic nephropathy; tumour.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /note="Biotin.Aminohexanoic acid-R"  
XX  
XX MO200114413-A2.  
XX  
PD 01-MAR-2001.  
XX  
PF 25-AUG-2000; 2000WO-GB03265.  
XX  
PR 25-AUG-1999; 99GB-0020000.  
XX  
PI (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
XX  
PI Germain SE, Hill CS, Howell MT;  
XX  
DR WPI; 2001-265836/27.  
XX  
PT Polypeptide capable of interacting with a Smad polypeptide, useful in  
PT the treatment of cancer and for tissue remodelling or healing of a  
PT wound, injury or surgery, comprises a Smad interaction Motif and is  
PT less than 32 amino acids in length -  
XX  
PS Claim 16; Page 140; 179pp; English.  
XX  
CC The present invention relates to peptides capable of interacting with a  
CC Smad protein, comprising a Smad interaction Motif (SIM; amino acid  
CC sequence PP(T/N)K). The present sequence is one such Smad interacting  
CC peptide. Smad proteins are a family of highly conserved, intracellular  
CC proteins that signal cellular responses downstream of Transforming Growth  
CC Factor-beta (TGF-beta) family serine/threonine kinase receptors. The SIM  
CC is thought to be necessary for interaction with the MH2 domain of Smad2.  
CC The peptides of the present invention are useful in the manufacture of a  
CC medicament for the treatment of a patient in need of modulation of  
CC activin or TGF-beta signalling; cancer; a patient in need of reducing  
CC extracellular matrix deposition, encouraging tissue repair and/or  
CC regeneration, tissue remodelling or healing of a wound, injury or  
CC surgery, or reducing scar tissue formation arising from injury to the  
CC brain; a patient with or at risk of end-stage organ failure, pathologic  
CC extracellular matrix accumulation, a fibrotic condition, disease states  
CC associated with immunosuppression (such as different forms of malignancy,  
CC chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour  
CC growth, kidney damage (for e.g. obstructive neuropathy, IGA nephropathy  
CC or non-inflammatory renal disease) or renal fibrosis.  
XX  
SQ Sequence 41 AA;  
Query Match 66.2%; Score 98; DB 22; Length 41;

Best Local Similarity 85.0%; Pred. No. 2.3e-07;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 ROIKWPNRRMKWKALD 21  
: |||||  
DB 1 ROIKWPNRRMKWGLMD 20

RESULT 12  
AAB80925  
ID AAB80925 standard; Protein; 41 AA.  
XX  
AC AAB80925;  
XX  
DT 04-JUN-2001 (first entry)  
XX  
DE Mixer SIM mutant peptide.  
XX  
KW Smad; Cytostatic; vulnerary; cerebroprotective; immunosuppressive;  
KW Anti-HIV; antidiabetic; ophthalmological; antiinflammatory; SIM;  
KW Smad interaction Motif; tissue repair; fibrotic condition;  
KW immunosuppression; diabetic nephropathy; tumour; mucin.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /note="Biotin.Aminohexanoic acid-R"  
FT Misc-difference 25 /note="Wild-type Pro replaced by Ala. Wild-type sequence  
FT given in AAB80924."  
FT Misc-difference 26 /note="Wild-type Pro replaced by Ala"  
XX  
XX MO200114413-A2.  
XX  
PD 01-MAR-2001.  
XX  
PF 25-AUG-2000; 2000WO-GB03265.  
XX  
PR 25-AUG-1999; 99GB-0020000.  
XX  
PI (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
XX  
PI Germain SE, Hill CS, Howell MT;  
XX  
DR WPI; 2001-265836/27.  
XX  
PT Polypeptide capable of interacting with a Smad polypeptide, useful in  
PT the treatment of cancer and for tissue remodelling or healing of a  
PT wound, injury or surgery, comprises a Smad interaction Motif and is  
PT less than 32 amino acids in length -  
XX  
PS Example 2; Page 123; 179pp; English.  
XX  
CC The present invention relates to peptides capable of interacting with a  
CC Smad protein, comprising a Smad interaction Motif (SIM; amino acid  
CC sequence PP(T/N)K). The present sequence is one such Smad interacting  
CC peptide. Smad proteins are a family of highly conserved, intracellular  
CC proteins that signal cellular responses downstream of Transforming Growth  
CC Factor-beta (TGF-beta) family serine/threonine kinase receptors. The SIM  
CC is thought to be necessary for interaction with the MH2 domain of Smad2.  
CC The peptides of the present invention are useful in the manufacture of a  
CC medicament for the treatment of a patient in need of modulation of  
CC activin or TGF-beta signalling; cancer; a patient in need of reducing  
CC extracellular matrix deposition, encouraging tissue repair and/or  
CC regeneration, tissue remodelling or healing of a wound, injury or  
CC surgery, or reducing scar tissue formation arising from injury to the  
CC brain; a patient with or at risk of end-stage organ failure, pathologic  
CC extracellular matrix accumulation, a fibrotic condition, disease states  
CC associated with immunosuppression (such as different forms of malignancy,  
CC chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour  
CC growth, kidney damage (for e.g. obstructive neuropathy, IGA nephropathy

CC or non-inflammatory renal disease) or renal fibrosis.

XX Sequence 41 AA;

Query Match 66.2%; Score 98; DB 22; Length 41;  
Best Local Similarity 85.0%; Pred. No. 2.3e-07;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RQIKIWFOQRNRMKWKKTALD 21  
DB 1 RQIKIWFOQRNRMKWKKTALD 20

## RESULT 13

AAW45976 standard; peptide; 21 AA.

AC AAW45976;

DT 01-JUL-1998 (first entry)

DE Cysteine protease inhibiting peptide for preventing cell death.

XX Neuronal cell death; neurodegenerative disorder; inhibition;

KM cysteine protease; cardiovascular; liver disease.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-3-nitro-2-pyridyl-sulphenyl-Arg"

PN W09735876-A1.

PD 02-OCT-1997.

PF 04-MAR-1997; 97MO-US04158.

PR 04-MAR-1996; 96US-0610220.

PA (UYCO ) UNIV COLUMBIA NEW YORK.

PI Troy CM;

DR WPI; 1997-489561/45.

XX New cysteine protease inhibiting peptide(s) for preventing cell

PT death - in cases of neurodegenerative, cardiovascular and liver

PT identifying enzyme inhibiting peptides

PS Claim 10; Page 68; 112pp; English.

XX This sequence represents a specifically claimed peptide of the formula:

CC V-(AA1)n-Cys(V')-(AA2)m-V' (1), in which n and m = 0-5, totalling 2-5;

CC if n = 1, AA1 = Ala; if n = 2, (AA1)n = Gln-Ala; and if n = 3 or more,

CC (AA1)n = (X)P-Gln-Ala; X = any amino acid; p = 1-3, depending on value

CC of n; if m = 1, AA2 = Arg; if m = 2, (AA2)n = Arg-Gly; if m = 3 or more,

CC (AA2)n = Arg-Gly-(X)q; q = 1-3, depending on value of m; V', V' and V',

CC any or all of which may be absent, = agent able to direct the compound

CC to a specific cell. The peptides are inhibitors of cysteine proteases,

CC specifically interleukin-1 beta converting enzyme (ICE). They inhibit

CC death of cells, particularly in humans, and can be used to treat

CC neurodegenerative diseases (e.g. ageing, Alzheimer's, Machado-Joseph,

CC Parkinson's or Huntington's diseases, multiple sclerosis, muscular

CC dystrophy, stroke), cardiovascular disease and liver disorders.

CC The peptides should be more specific than pseudosubstrate inhibitors.

XX Sequence 21 AA;

Query Match 64.2%; Score 95; DB 18; Length 21;

Best Local Similarity 94.4%; Pred. No. 3e-07;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RQIKIWFOQRNRMKWKKTAA 19  
DB 1 RQIKIWFOQRNRMKWKKTAA 18

## RESULT 14

AAW82957 standard; peptide; 24 AA.

AC AAW82957;

DT 04-FEB-1999 (first entry)

DE Oestrogen receptor activity inhibiting peptide #13.

XX Human; oestrogen receptor activity inhibitor; anti-oestrogen; diagnosis;

KM breast cancer; estrogen; tumour; phosphotyrosyl peptide;

XX malonyltirosyl peptide; steroid receptor co-activator-1.

OS Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 19 /note= "phosphotyrosine"

PN W09846250-A1.

PD 22-OCT-1998.

PF 14-APR-1998; 98MO-US07711.

PR 14-APR-1997; 97US-0043545.

PA (REGC ) UNIV CALIFORNIA.

PI Pietras RJ;

DR WPI; 1998-594522/50.

XX New anti-oestrogen peptide compositions - comprise sequences based

PT on oestrogen receptor and steroid receptor co-activator-1 sequences,

PT used for treating cancers

XX Claim 11; Page 156; 182pp; English.

XX The present invention describes a composition comprising an isolated

CC oestrogen receptor activity inhibiting (anti-oestrogen) peptide. The

CC peptides used in the composition comprise sequences of human oestrogen

CC receptor (OR) surrounding Tyr537 and steroid receptor co-activator-1

CC (SCR-1). The peptide compositions, nucleic acids and vectors of the

CC polypeptide dimerisation in a cell and reduce the binding of SRC-1

CC to a specific cell. The peptides are inhibitors of cysteine proteases,

CC specifically interleukin-1 beta converting enzyme (ICE). They inhibit

CC death of cells, particularly in humans, and can be used to treat

CC neurodegenerative diseases (e.g. ageing, Alzheimer's, Machado-Joseph,

CC Parkinson's or Huntington's diseases, multiple sclerosis, muscular

CC dystrophy, stroke), cardiovascular disease and liver disorders.

CC The peptides should be more specific than pseudosubstrate inhibitors.

XX Sequence 24 AA;

Query Match 64.2%; Score 95; DB 19; Length 24;

Best Local Similarity 85.0%; Pred. No. 3.5e-07;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RQIKIWFOQRNRMKWKKTALD 21  
DB 1 RQIKIWFOQRNRMKWKKTALD 20

## RESULT 15

ABP58107 standard; peptide; 30 AA.

ABP58107

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

XX AC ABP58107;
XX DT 28-MAR-2003 (first entry)
XX DE Mouse TIRAP-Antennapedia fusion protein.
XX KW Toll/interleukin-1 receptor adapter protein; TIRAP; mouse;
XX KW inhibitor; Antennapedia; antiinflammatory.
XX OS Chimeric - Mus sp.
XX OS Chimeric - Drosophila sp.
XX FH Key Location/Qualifiers
XX FT Peptide 1..16
XX FT /note= "Antennapedia peptide"
XX FT 17..30
XX FT /note= "mouse TIRAP inhibitor peptide"
XX PN MO200290520-A2.
XX PD 14-NOV-2002.
XX PF 09-MAY-2002; 2002MO-US14915.
XX PR 09-MAY-2001; 2001US-289738P.
XX PR 09-MAY-2001; 2001US-289815P.
XX PR 29-AUG-2001; 2001US-289866P.
XX PR 19-MAR-2002; 2002US-0101398.
XX PA (UYVA ) UNIV YALE.
XX PI Medzhitov R, Hornig T, Barton G;
XX DR WPI; 2003-120542/11.
XX PT New toll/interleukin-1 receptor adapter protein (TIRAP) polynucleotides
XX PT and polypeptides, useful for treating a disease state associated with
XX PT TIRAP expression, e.g. inflammation, and for inducing and affecting
XX PT immune response
XX PS Disclosure; Page 74; 74pp; English.
XX CC The present sequence is that of a fusion protein comprising an
XX CC Antennapedia peptide and a mouse toll/interleukin-1 receptor
XX CC adapter protein (TIRAP) inhibitor polypeptide (see ABP58106) of
XX CC the invention. Antennapedia, derived from Drosophila, is a
XX CC cellular membrane transport protein and can be used to deliver
XX CC the TIRAP inhibitor across the cell membrane so that it becomes
XX CC therapeutically active within the cell. TIRAP is a component of the
XX CC Toll-like receptor 4 (TLR4) signalling pathway. It mediates MyD88
XX CC independent signalling in response to TLR4 ligation, and controls
XX CC dendritic cell maturation. Characterisation of TIRAP has led to
XX CC the discovery of compounds that inhibit both the MyD88 independent
XX CC pathway as well as the MyD88 dependent pathway of TLR4 by
XX CC inhibiting TIRAP polypeptide mediated signalling. Compounds that
XX CC inhibit TIRAP activity are useful for preventing or reducing in the
XX CC inflammation and septic shock, and especially for assisting in the
XX CC prevention of graft rejection, which occurs, at least in part,
XX CC because of cellular necrosis induced inflammation. The invention
XX CC provides TIRAP inhibitor polynucleotides (see ABY76259-62) and
XX CC polypeptides (see ABP58105-06). The TIRAP inhibitors can inhibit
XX CC both the MyD88 independent response, e.g. activation of NF-kappaB
XX CC and MAP kinases, and the MyD88 dependent response in cells
XX CC expressing TLR4.
XX SQ Sequence 30 AA;

```

DB 1 RQIKIWFOQRMRMKKQLRDAA 23

Search completed: February 18, 2004, 14:26:28  
Job time : 106.269 secs

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OY Query Match 64.2%; Score 95; DB 24; Length 30;
    Best Local Similarity 78.3%; Pred. No. 4.5e-07;
    Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
    2 RQIKIWFOQRMRMKKQLRDAA 24

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 30.7632 Seconds  
(without alignments)  
87.531 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162

Sequence: 1 DRQIKIWFQNRMRKMKKALDMSWLQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR\_76:\*\n2: p1r1:\*\n3: p1r2:\*\n4: p1r3:\*\n5: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	59.9	60	2 PC2399	antennapedia-like
2	97	59.9	60	2 PC2400	antennapedia-like
3	97	59.9	105	2 A27471	homeotic protein R
4	97	59.9	119	2 A03314	homeotic protein m
5	97	59.9	229	2 A28329	homeotic protein H
6	96	58.6	75	2 I51341	homeo box protein
7	95	58.6	66	2 S15536	homeotic protein H
8	95	58.6	81	2 B29585	homeotic protein H
9	95	58.6	96	2 A05266	homeotic protein H
10	95	58.6	97	2 C27176	homeotic protein H
11	95	58.6	224	2 S26400	homeotic protein H
12	95	58.6	224	2 A31324	homeotic protein H
13	94	58.0	33	2 S57235	antennapedia prote
14	94	58.0	42	2 I65241	homeotic protein H
15	94	58.0	45	2 PC1216	homeotic protein D
16	94	58.0	48	2 I51439	homeobox protein
17	94	58.0	66	2 S15538	homeotic protein H
18	94	58.0	71	2 UC1161	homeotic protein 3
19	94	58.0	71	2 A60084	homeotic protein H
20	94	58.0	74	2 D34510	homeotic protein H
21	94	58.0	75	2 S58852	homeotic protein S
22	94	58.0	76	2 C43559	homeotic protein R
23	94	58.0	78	2 I51342	homeo box protein
24	94	58.0	81	2 S47605	homeotic protein H
25	94	58.0	82	2 S08302	homeotic protein H
26	94	58.0	83	2 S47603	homeotic protein H
27	94	58.0	86	2 S50066	homeotic protein H
28	94	58.0	86	2 A34510	homeotic protein H
29	94	58.0	86	2 JT0489	homeotic protein Z

30	94	58.0	86	2 S08303	homeotic protein H
31	94	58.0	87	2 S00589	homeotic protein H
32	94	58.0	88	2 A03317	homeotic protein M
33	94	58.0	96	2 S08639	homeotic protein z
34	94	58.0	97	2 A24779	homeotic protein m
35	94	58.0	103	2 A32167	homeotic protein H
36	94	58.0	105	2 S47602	homeotic protein H
37	94	58.0	106	2 S36448	homeotic protein H
38	94	58.0	107	2 B61045	homeotic protein T
39	94	58.0	113	2 T10775	homeobox protein
40	94	58.0	118	2 A24777	homeotic protein H
41	94	58.0	118	2 UT0273	homeotic protein H
42	94	58.0	118	2 B24777	homeotic protein M
43	94	58.0	138	2 S20087	homeotic protein b
44	94	58.0	148	2 PC4071	homeobox A5 protel
45	94	58.0	153	1 WJHJ3C	homeotic protein H

#### ALIGNMENTS

##### RESULT 1

PC2399 antennapedia-like homeotic protein AHox 2 - sea squirt (Styela clava) (fragment)

C/Species: Styela clava

C/Date: 13-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 21-Jul-2000

C/Accession: PC2399

R/Ge, T./ Lee, H.; Tomlinson, C.R.

Gene 147, 219-222, 1994

A/Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela

A/Reference number: PC2399; PMID:95011617; PMID:7926803

A/Accession: PC2399

A/Molecule type: DNA

A/Residues: 1-60 <GET>

A/Cross-references: GB:S73920; NID:5693714; PIDN:AA833061.2; PID:57387472

A/Note: The authors translated the codon ATT for residue 47 as Glu

C/Superfamily: unassigned homeobox proteins; homeobox homology

C/Keywords: DNA binding; homeobox; nucleus; transcription regulation

F/2-58/Domain: homeobox homology <HOX>

Query Match 59.9%; Score 97; DB 2; Length 60;

Best Local Similarity 94.1%; Pred. No. 1.5e-06;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKIWFQNRMRKMKK 17

DB 42 DRQIKIWFQNRMRKMKK 58

##### RESULT 2

PC2400 antennapedia-like homeotic protein AHox 3 - sea squirt (Styela plicata) (fragment)

C/Species: Styela plicata

C/Date: 26-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 17-Oct-1997

C/Accession: PC2400

R/Ge, T./ Lee, H.; Tomlinson, C.R.

Gene 147, 219-222, 1994

A/Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela

A/Reference number: PC2399; PMID:95011617; PMID:7926803

A/Accession: PC2400

A/Molecule type: DNA

A/Residues: 1-60 <GET>

A/Note: The authors translated the codon ATA for residue 47 as Glu

C/Superfamily: unassigned homeobox proteins; homeobox homology

C/Keywords: DNA binding; homeobox; nucleus; transcription regulation

F/2-58/Domain: homeobox homology <HOX>

Query Match 59.9%; Score 97; DB 2; Length 60;

Best Local Similarity 94.1%; Pred. No. 1.5e-06;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKIWFQNRMRKMKK 17

DB 42 DRQIKIWFQNRMRKMKK 58

Db 42 DRQIKWFORRRMKWKX 58

### RESULT 3

A27471  
 A:Title: homeotic protein R5 - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 23-May-1997  
 C:Accession: A27471  
 R:Palzon, M.; Sanderson, N.; Chung, S.Y.  
 Gene 54, 23-32, 1987  
 A:Title: Cloning and expression of rat homeo-box-containing sequences.  
 A:Reference number: A91576; MUID:87277429; PMID:2886401  
 A:Accession: A27471  
 A:Molecule type: DNA  
 A:Residues: 1-105 <PAL>  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:6-62/Domain: homeobox homology <Hox>

Query Match 59.9%; Score 97; DB 2; Length 105;  
 Best Local Similarity 70.4%; Pred. No. 2.7e-06;  
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWFORRRMKWKXKTALDMSWLT 27  
 :|||||  
 Db 46 ERQIKWFORRRMKWKXKHDESOAPT 72

### RESULT 4

A03314  
 A:Title: homeotic protein m6 - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 24-Jul-1997  
 C:Accession: A03314; S14043  
 R:Colberg-Poley, A.M.; Voss, S.D.; Chowdhury, K.; Gruss, P.  
 Nature 314, 713-718, 1985  
 A:Title: Structural analysis of murine genes containing homeo box sequences and their e  
 A:Reference number: A03314; MUID:85188311; PMID:2886010  
 A:Accession: A03314  
 A:Molecule type: DNA  
 A:Residues: 1-119 <COL>  
 R:Beiler, G.; Bucan, M.; Francke, U.; Colberg-Poley, A.M.; Gruss, P.  
 EMBO J. 5, 2209-2215, 1986  
 A:Title: Sequential expression of murine homeo box genes during F9 EC cell differentiation  
 A:Reference number: S13785; MUID:87053860; PMID:2877873  
 A:Accession: S14043  
 A:Molecule type: DNA  
 A:Residues: 19-48, 'R', 51-87 <BR>  
 C:Genetics:  
 A:Gene: m6  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:20-76/Domain: homeobox homology <Hox>

Query Match 59.9%; Score 97; DB 2; Length 119;  
 Best Local Similarity 70.4%; Pred. No. 3.1e-06;  
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWFORRRMKWKXKTALDMSWLT 27  
 :|||||  
 Db 60 ERQIKWFORRRMKWKXKHDESOAPT 86

### RESULT 5

A28329  
 A:Title: homeotic protein Hox A7 - mouse  
 N:Alternate names: homeotic protein Hox 1.1; m6 homeotic protein  
 C:Species: Mus musculus (house mouse)  
 C>Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 20-Aug-1999  
 C:Accession: A28329; I49131  
 R:Kessel, M.; Schultze, F.; Fildt, M.; Gruss, P.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 5306-5310, 1987

A:Title: Primary structure and nuclear localization of a murine homeodomain protein.  
 A:Reference number: A28329; MUID:87260976; PMID:2885847  
 A:Accession: A28329

A:Molecule type: mRNA  
 A:Residues: 1-229 <KRS>  
 A:Cross-References: GB:M17192; NID:G193906; PIDN:AAA37833.1; PID:G309313  
 R:Patikh, H.; Shah, S.; Hill, D.; Peterkofsky, A.  
 Gene 154, 237-242, 1995  
 A:Title: Organization, sequence and regulation of expression of the murine Hoxa-7 gene.  
 A:Reference number: I49131; MUID:95197009; PMID:7890170  
 A:Accession: I49131  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-42, 'GAG', 46-229 <RES>  
 A:Cross-References: EMBL:U15972; NID:G664757; PIDN:AAC52160.1; PID:G664758  
 C:Genetics:  
 A:Gene: Hoxa7  
 A:Introns: 126/1  
 C:Superfamily: homeotic protein Hox A7; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:130-186/Domain: homeobox homology <Hox>

Query Match 59.9%; Score 97; DB 2; Length 229;  
 Best Local Similarity 70.4%; Pred. No. 6.2e-06;  
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWFORRRMKWKXKTALDMSWLT 27  
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 Db 170 ERQIKWFORRRMKWKXKHDESOAPT 196

### RESULT 6

I51341  
 A:Title: homeo box protein - Atlantic salmon (fragment)  
 C:Species: Salmo salar (Atlantic salmon)  
 C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 24-Sep-1999  
 C:Accession: I51341  
 R:Fjose, A.; Moliven, A.; Eiken, H.G.  
 Gene 62, 141-152, 1988  
 A:Title: Molecular cloning and characterization of homeobox-containing genes from Atlan  
 A:Reference number: I51341; MUID:88226009; PMID:2897318  
 A:Accession: I51341  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-75 <FJO>  
 A:Cross-References: GB:M18903; NID:G213797; PIDN:AAA49559.1; PID:G213798  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:2-58/Domain: homeobox homology <Hox>

Query Match 59.3%; Score 96; DB 2; Length 75;  
 Best Local Similarity 78.3%; Pred. No. 2.6e-06;  
 Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRQIKWFORRRMKWKXKTALDMS 23  
 :|||||  
 Db 42 ERQIKWFORRRMKWKXKHDESD 64

### RESULT 7

S15536  
 A:Title: homeotic protein Hox A7 - human (fragment)  
 N:Alternate names: homeotic protein Hox 1A  
 C:Species: Homo sapiens (man)  
 C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 29-Aug-1997  
 C:Accession: S15536  
 R:Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; S  
 Genome 31, 745-756, 1989  
 A:Title: Organization of human class I homeobox genes.  
 A:Reference number: S15036; MUID:90215256; PMID:2576652  
 A:Accession: S15536  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA

A:Residues: 1-66 <BON>  
C:Genetics:  
A:Gene: GDB:HOXA7  
A:Cross-references: GDB:120647; OMIM:142950  
A:Map position: 7p15.3-7p15.3  
C:Superfamily: unassigned homeobox proteins; homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F:2-58/Domain: homeobox homology <HOX>

Query Match 58.6%; Score 95; DB 2; Length 66;  
Best Local Similarity 81.0%; Pred. No. 3.1e-06;  
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DRQIKWPNRRMKWKKTALD 21  
DB 42 ERQIKWPNRRMKWKKEKHD 62

RESULT 8  
B29585  
homeotic protein Hox 2.2 precursor - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 15-Dec-1988 #sequence\_revision 30-Sep-1991 #text\_change 17-Oct-1997  
C:Accession: B29585  
R:Lomal, P.; Arman, E.; Czosnek, H.; Ruddle, F.H.; Blatt, C.  
DNA 6, 409-418, 1987  
A:Title: New murine homeoboxes: structure, chromosomal assignment, and differential expression  
A:Reference number: A29585; MUID:88054465; PMID:2890503  
A:Accession: B29585  
A:Molecule type: DNA  
A:Residues: 1-81 <LON>  
A:Cross-references: GB:M18167  
A>Note: The authors translated the codon CAG for residue 69 as Glu  
C:Superfamily: unassigned homeobox proteins; homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F:4-60/Domain: homeobox homology <HOX>

Query Match 58.6%; Score 95; DB 2; Length 81;  
Best Local Similarity 66.7%; Pred. No. 3.8e-06;  
Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DRQIKWPNRRMKWKKTALDMSWLQTE 28  
DB 44 ERQIKWPNRRMKWKESKLSASQLSAB 73

RESULT 9  
A05266  
homeotic protein Hox B6 - human (fragment)  
N:Alternate names: homeotic protein Hox 2B; homeotic protein Hu2  
C:Species: Homo sapiens (man)  
C>Date: 03-Jun-1987 #sequence\_revision 30-Sep-1991 #text\_change 17-Oct-1997  
C:Accession: A05266; S15537  
R:Levine, M.; Rudin, G.M.; Tjian, R.  
Cell 38, 667-673, 1984  
A:Title: Human DNA sequences homologous to a protein coding region conserved between hom  
A:Reference number: A05265; MUID:85024858; PMID:6091895  
A:Accession: A05266  
A:Molecule type: DNA  
A:Residues: 1-96 <LEV>  
A:Cross-references: EMBL:K02571  
A>Note: this reading frame extends between two stop codons and does not begin with a str  
A:Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Stc  
Genome 31, 745-756, 1989  
A:Title: Organization of human class I homeobox genes.  
A:Reference number: S15036; MUID:90215256; PMID:2576652  
A:Accession: S15537  
A:Molecule type: DNA  
A:Residues: 18-19, 'R', 21-83 <BON>  
C:Genetics:  
A:Gene: GDB:HOXB6  
A:Cross-references: GDB:120659; OMIM:142961  
A:Map position: 17q21.3-17q21.3

C:Superfamily: unassigned homeobox proteins; homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F:19-75/Domain: homeobox homology <HOX>

Query Match 58.6%; Score 95; DB 2; Length 96;  
Best Local Similarity 66.7%; Pred. No. 4.6e-06;  
Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DRQIKWPNRRMKWKKTALDMSWLQTE 28  
DB 59 ERQIKWPNRRMKWKESKLSASQLSAB 88

RESULT 10  
C27176  
homeotic protein Hox 2.2 - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 24-Sep-1999  
C:Accession: C27176  
R:Hart, C.P.; Fainsod, A.; Ruddle, F.H.  
Genomics 1, 182-195, 1987  
A:Title: Sequence analysis of the murine Hox-2.2, -2.3, and -2.4 homeo boxes: evolution  
A:Reference number: A27176; MUID:88085193; PMID:2891608  
A:Accession: C27176  
A:Molecule type: DNA  
A:Residues: 1-97 <HAR>  
A:Cross-references: GB:M18401; NID:G193936; PID:NAC27130.1; PID:G333522  
C:Genetics:  
A:Gene: Hox-2.2  
C:Superfamily: unassigned homeobox proteins; homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F:20-76/Domain: homeobox homology <HOX>

Query Match 58.6%; Score 95; DB 2; Length 97;  
Best Local Similarity 66.7%; Pred. No. 4.7e-06;  
Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DRQIKWPNRRMKWKKTALDMSWLQTE 28  
DB 60 ERQIKWPNRRMKWKESKLSASQLSAB 89

RESULT 11  
S26400  
homeotic protein Hox 2.2 (variant 1) - human  
C:Species: Homo sapiens (man)  
C>Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 17-Nov-2000  
C:Accession: S26400; S26401  
R:Shen, W.; Derner, K.; Simonitch-Bason, T.A.; Lawrence, H.J.; Largman, C.  
Nucleic Acids Res. 19, 539-545, 1991  
A:Title: Alternative splicing of the Hox 2.2 homeobox gene in human hematopoietic cell.  
A:Reference number: S26400; MUID:91187672; PMID:1672751  
A:Accession: S26400  
A:Molecule type: DNA  
A:Residues: 1-224 <SHB>  
A:Cross-references: EMBL:X58431; NID:G32369; PID:CAA41335.1; PID:G32370  
A:Experimental source: tissue-type placenta  
A>Note: the authors translated the codon ACT for residue 55 as Tyr, CGC for residue 60  
A:Molecule type: DNA  
A:Accession: S26401  
A:Residues: 1-139, 'B', <SH2>  
A:Cross-references: EMBL:X58431; NID:G32369; PID:CAA41336.1; PID:G32371  
A:Experimental source: tissue-type placenta  
A>Note: the authors translated the codon ACT for residue 55 as Tyr, CGC for residue 60  
A>Note: the authors did not translate the codons for residues 139, and 140  
C:Genetics:  
A:Introns: 139/1  
C:Superfamily: unassigned homeobox proteins; homeobox homology  
C:Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regula  
F:147-203/Domain: homeobox homology <HOX>

Query Match 58.6%; Score 95; DB 2; Length 224;  
Best Local Similarity 66.7%; Pred. No. 1.1e-05;

Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;  
 QY 1 DROIKIWFQNRBMKKKTA--LDMSWLTQTE 28  
 :|||||  
 Db 187 EROIKIWFQNRBMKKKESKLSASQLSAE 216

## RESULT 12

A31324  
 homeotic protein Hox 2.2 - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 24-Sep-1999  
 C/Accession: A31324  
 R/Schuhardt, K.; Uteet, M.F.; Awgulawitach, A.; Ruddle, F.H.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 5582-5586, 1988  
 A/Title: Structure and expression of Hox-2.2, a murine homeobox-containing gene.  
 A/Reference number: A31324; MUID:88289762; PMID:2899893  
 A/Accession: A31324  
 A/Molecule type: mRNA  
 A/Residues: 1-224 <SCG>  
 A/Cross-references: GB:U03782; NID:g193929; PIDN:AAA37843.1; PID:g387203  
 C/Superfamily: unassigned homeobox proteins; homeobox homology  
 C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:147-203/Domain: homeobox homology <Hox>

Query Match 58.6%; Score 95; DB 2; Length 224;  
 Best Local Similarity 66.7%; Pred. No. 1.1e-05;  
 Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DROIKIWFQNRBMKKKTA--LDMSWLTQTE 28  
 :|||||  
 Db 187 EROIKIWFQNRBMKKKESKLSASQLSAE 216

## RESULT 13

SS7235  
 antennapedia protein (clone p1105) - fruit fly (Drosophila pseudoobscura) (fragment)  
 C/Species: Drosophila pseudoobscura  
 C/Date: 10-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 15-Oct-1999  
 C/Accession: SS7235  
 R/Randazzo, F.M.; Seeger, M.A.; Hues, C.A.; Sweeney, M.A.; Cecil, J.K.; Kaufman, T.C.  
 Genetics 133, 319-330, 1993  
 A/Title: Structural changes in the antennapedia complex of Drosophila pseudoobscura.  
 A/Reference number: SS7224  
 A/Accession: SS7235  
 A/Molecule type: DNA  
 A/Residues: 1-33 <RAN>  
 A/Cross-references: EMBL:X77711  
 C/Genetics:  
 A/Gene: FLYBase:Antp  
 A/Cross-references: FLYBase:FBgn0012693  
 C/Superfamily: unassigned homeobox proteins; homeobox homology  
 C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:1-22/Domain: homeobox homology (fragment) <Hox>

Query Match 58.0%; Score 94; DB 2; Length 33;  
 Best Local Similarity 94.1%; Pred. No. 2e-06;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRBMKKK 17  
 :|||||  
 Db 6 EROIKIWFQNRBMKKK 22

## RESULT 14

I65241  
 homeotic protein Hox-A - rat (fragment)  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 27-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 15-Oct-1999  
 C/Accession: I65241  
 R/Sakoyama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.  
 Biochem. Genet. 33, 351-360, 1994  
 A/Title: Cloning of rat homeobox genes.

A/Reference number: I52340; MUID:95217128; PMID:7702549  
 A/Accession: I65241  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-42 <RES>  
 A/Cross-references: GB:S76290; NID:g913077  
 C/Genetics:  
 A/Gene: Hox-A; Hox-1  
 C/Superfamily: unassigned homeobox proteins; homeobox homology  
 C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:1-40/Domain: homeobox homology (fragment) <Hox>

Query Match 58.0%; Score 94; DB 2; Length 42;  
 Best Local Similarity 94.1%; Pred. No. 2.6e-06;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRBMKKK 17  
 :|||||  
 Db 24 EROIKIWFQNRBMKKK 40

## RESULT 15

PC1216  
 homeotic protein Dhhx1 - planarian (Dugesia tigritina) (fragment)  
 C/Species: Dugesia tigritina  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Oct-1997  
 C/Accession: PC1216  
 R/Oliver, G.; Vlaspo, M.; Mallhos, A.; Martinez, C.; Sosa-Plinede, B.; Fleitcz, W.; Ehrl.  
 Gene 121, 337-342, 1992  
 A/Title: Homeoboxes in flatworms.  
 A/Reference number: JCI386; MUID:93077050; PMID:1359988  
 A/Accession: PC1216  
 A/Molecule type: DNA  
 A/Residues: 1-45 <OLI>  
 A/Cross-references: EMBL:X66822  
 C/Superfamily: unassigned homeobox proteins; homeobox homology  
 C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:1-45/Domain: homeobox homology (fragment) <Hox>

Query Match 58.0%; Score 94; DB 2; Length 45;  
 Best Local Similarity 94.1%; Pred. No. 2.8e-06;  
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QY 1 DROIKIWFQNRBMKKK 17  
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 Db 29 EROIKIWFQNRBMKKK 45

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 Job time : 31.7632 secs



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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 77.9211 Seconds  
(without alignments)  
75.239 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162

Sequence: 1 DROIKIWFONRRMKKTALDMSWLQTE 28

Scoring table: BLOSUM62  
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Searched: 801455 seqs, 209382283 residues  
Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	162	100.0	28	10 US-09-847-940B-18	Sequence 18, Appl
2	162	100.0	28	11 US-09-847-946A-18	Sequence 18, Appl
3	134	82.7	28	10 US-09-847-940B-19	Sequence 19, Appl
4	134	82.7	28	11 US-09-847-946A-19	Sequence 19, Appl
5	105	64.8	18	11 US-09-847-946A-131	Sequence 131, Appl
6	101	62.3	36	9 US-09-731-023A-12	Sequence 12, Appl
7	101	62.3	36	12 US-10-358-365-12	Sequence 12, Appl
8	98	60.5	17	15 US-10-229-915-1	Sequence 1, Appl
9	97	59.9	34	15 US-10-161-499-79	Sequence 79, Appl
10	96	59.3	26	15 US-10-097-175-101	Sequence 101, Appl
11	95	58.6	21	8 US-08-610-220A-11	Sequence 11, Appl
12	95	58.6	21	9 US-09-150-623-11	Sequence 11, Appl
13	94	58.0	30	15 US-10-188-947-11	Sequence 11, Appl
14	94	58.0	64	15 US-10-118-079-44	Sequence 44, Appl
15	94	58.0	217	15 US-10-097-340-129	Sequence 129, Appl

16	94	58.0	233	12 US-10-420-940-4	Sequence 4, Appl
17	94	58.0	269	12 US-10-116-275-190	Sequence 190, Appl
18	94	58.0	295	15 US-10-118-079-4	Sequence 4, Appl
19	93.5	57.7	36	9 US-09-731-023A-11	Sequence 11, Appl
20	93.5	57.7	36	12 US-10-358-365-11	Sequence 11, Appl
21	93	57.4	22	12 US-10-359-226-50	Sequence 50, Appl
22	93	57.4	28	9 US-09-214-371-9	Sequence 9, Appl
23	93	57.4	115	9 US-09-925-299-1169	Sequence 1169, Appl
24	93	57.4	115	11 US-09-925-299-1169	Sequence 1169, Appl
25	92	56.8	16	8 US-08-610-220A-9	Sequence 9, Appl
26	92	56.8	16	9 US-09-214-371-43	Sequence 43, Appl
27	92	56.8	16	9 US-09-780-070-38	Sequence 38, Appl
28	92	56.8	16	9 US-09-150-623-9	Sequence 9, Appl
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31	92	56.8	16	10 US-09-900-147-8	Sequence 8, Appl
32	92	56.8	16	10 US-09-792-480-29	Sequence 29, Appl
33	92	56.8	16	10 US-09-785-802A-2	Sequence 2, Appl
34	92	56.8	16	10 US-09-785-802A-5	Sequence 5, Appl
35	92	56.8	16	10 US-09-902-432-32	Sequence 32, Appl
36	92	56.8	16	10 US-09-953-031A-10	Sequence 10, Appl
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40	92	56.8	16	11 US-09-775-052-54	Sequence 54, Appl
41	92	56.8	16	11 US-09-295-189-4	Sequence 4, Appl
42	92	56.8	16	11 US-09-965-876A-1	Sequence 1, Appl
43	92	56.8	16	12 US-10-017-672-11	Sequence 11, Appl
44	92	56.8	16	12 US-10-201-389A-14	Sequence 14, Appl
45	92	56.8	16	12 US-10-161-051-1	Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-09-847-940B-18  
; Sequence 18, Application US/09847940B  
; Patent No. US2002015600A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J.  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PRI-117CP  
; CURRENT APPLICATION NUMBER: US/09/847,940B  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: NBD peptides  
US-09-847-940B-18

Query Match 100.0%; Score 162; DB 10; Length 28;  
Best Local Similarity 100.0%; Pred. No. 3e-13;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DROIKIWFONRRMKKTALDMSWLQTE 28  
DB 1 DROIKIWFONRRMKKTALDMSWLQTE 28  
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US-09-847-946A-18  
; Sequence 18, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J

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APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-18
```

```
Query Match      100.0%; Score 162; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 3e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 DROIKIFQNRMRMKKTALDWSWLTQTE 28
DB 1 DROIKIFQNRMRMKKTALDWSWLTQTE 28
```

```
RESULT 3
US-09-847-940B-19
Sequence 19, Application US/9847940B
Patent No. US20020156000A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Sankar
APPLICANT: May, Michael J.
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-117CP
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptides
US-09-847-940B-19
```

```
Query Match      82.7%; Score 134; DB 10; Length 28;
Best Local Similarity 92.9%; Pred. No. 8e-10;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
OY 1 DROIKIFQNRMRMKKTALDWSWLTQTE 28
DB 1 DROIKIFQNRMRMKKTALDWSWLTQTE 28
```

```
RESULT 4
US-09-847-946A-19
Sequence 19, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
```

```
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-19
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```
Query Match      82.7%; Score 134; DB 11; Length 28;
Best Local Similarity 92.9%; Pred. No. 8e-10;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 1 DROIKIFQNRMRMKKTALDWSWLTQTE 28
DB 1 DROIKIFQNRMRMKKTALDWSWLTQTE 28
```

```
RESULT 5
US-09-847-946A-131
Sequence 131, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 131
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence:anti-inflammatory compound
US-09-847-946A-131
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Query Match      64.8%; Score 105; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 11 RRRKKKKKTALDWSWLTQTE 28
DB 1 RRRKKKKKTALDWSWLTQTE 18
```

```
RESULT 6
US-09-731-023A-12
Sequence 12, Application US/09731023A
Patent No. US20020077283A1
GENERAL INFORMATION:
APPLICANT: Seesä, William
APPLICANT: Caveolin Peptides and Their Use as Therapeutics
FILE REFERENCE: 44574-5076-US
```

```
/ CURRENT APPLICATION NUMBER: US/09/731,023A
/ CURRENT FILING DATE: 2000-12-07
/ PRIOR APPLICATION NUMBER: US 60/231,327
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 36
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
US-09-731-023A-12

Query Match          62.3%; Score 101; DB 9; Length 36;
Best Local Similarity 69.2%; Pred. No. 1.1e-05;
Matches 18; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      2 ROIKIWFQNRMRMKKKTALDMSWLOT 27
DB      1 ROIKIWFQNRMRMKKKGIDKAFPTT 26

RESULT 7
US-10-358-365-12
/ Sequence 12, Application US/10358365
/ Publication No. US20030165510A1
/ GENERAL INFORMATION:
/ APPLICANT: Seeger, William
/ TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
/ FILE REFERENCE: 44574-5076-US
/ CURRENT APPLICATION NUMBER: US/10/358,365
/ PRIOR FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: US 09/731,023
/ PRIOR FILING DATE: 2000-12-07
/ PRIOR APPLICATION NUMBER: US 60/231,327
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 36
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
US-10-358-365-12

Query Match          62.3%; Score 101; DB 12; Length 36;
Best Local Similarity 69.2%; Pred. No. 1.1e-05;
Matches 18; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      2 ROIKIWFQNRMRMKKKTALDMSWLOT 27
DB      1 ROIKIWFQNRMRMKKKGIDKAFPTT 26

RESULT 8
US-10-229-915-1
/ Sequence 1, Application US/10229915
/ Publication No. US20030083262A1
/ GENERAL INFORMATION:
/ APPLICANT: Lazarus, Douglas
/ APPLICANT: Hamley, Gerhard
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING INFLAMMATORY
/ TITLE OF INVENTION: DISORDERS
/ FILE REFERENCE: PPI-127
/ CURRENT APPLICATION NUMBER: US/10/229,915
/ CURRENT FILING DATE: 2002-08-27
/ PRIOR APPLICATION NUMBER: US 60/316,328
/ PRIOR FILING DATE: 2001-08-30
/ NUMBER OF SEQ ID NOS: 39
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```
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: anti-inflammatory compound
US-10-229-915-1

Query Match          60.5%; Score 98; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DROIKIWFQNRMRMKK 17
DB      1 DROIKIWFQNRMRMKK 17

RESULT 9
US-10-161-499-79
/ Sequence 79, Application US/10161499
/ Publication No. US20030044427A1
/ GENERAL INFORMATION:
/ APPLICANT: Howley, Peter M.
/ APPLICANT: Benson, John
/ APPLICANT: Kasukawa, Hiroaki
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
/ TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS
/ FILE REFERENCE: HMV-041.01
/ CURRENT APPLICATION NUMBER: US/10/161,499
/ CURRENT FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: US/09/347,504
/ PRIOR FILING DATE: 1999-07-02
/ NUMBER OF SEQ ID NOS: 79
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 79
/ LENGTH: 34
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-161-499-79

Query Match          59.9%; Score 97; DB 15; Length 34;
Best Local Similarity 64.3%; Pred. No. 3.3e-05;
Matches 18; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY      1 DROIKIWFQNRMRMKKKTALDMSWLOT 28
DB      1 EROIKIWFQNRMRMKKKG--WKMKRL 26

RESULT 10
US-10-097-175-101
/ Sequence 101, Application US/10097175
/ Publication No. US20030045680A1
/ GENERAL INFORMATION:
/ APPLICANT: JOYAL, JOHN L.
/ APPLICANT: MUELLER, JOHN
/ APPLICANT: OZA, VIBHA B.
/ APPLICANT: FINDEIS, MARK A.
/ TITLE OF INVENTION: PEPTIDIC MODULATORS OF THE ANDROGEN RECEPTOR
/ FILE REFERENCE: PPI-110
/ CURRENT APPLICATION NUMBER: US/10/097,175
/ CURRENT FILING DATE: 2002-03-12
/ PRIOR APPLICATION NUMBER: 60/275,240
/ PRIOR FILING DATE: 2001-03-12
/ PRIOR APPLICATION NUMBER: 60/352,399
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 102
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 101
/ LENGTH: 26
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
```

```

; FEATURE:
; OTHER INFORMATION: Androgen Receptor Binding Polypeptides
US-10-097-175-101

Query Match      59.3%; Score 96; DB 15; Length 26;
Best Local Similarity 77.3%; Pred. No. 3,4e-05;
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      2 ROIKIWFQNRMRMKKKTALDMS 23
        |||||||
Db      1 ROIKIWFQNRMRMKKKTALDMS 22

RESULT 11
US-08-610-220A-11
; Sequence 11, Application US/08610220A
; Publication No. US2003009963B1
; GENERAL INFORMATION:
; APPLICANT: Troy, Carol M.
; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
; TITLE OF INVENTION: DEATH AND USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/610,220A
; FILING DATE: MAR-04-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 48332/JPW/JML
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-610-220A-11

Query Match      58.6%; Score 95; DB 8; Length 21;
Best Local Similarity 94.4%; Pred. No. 3,7e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 ROIKIWFQNRMRMKKKTAL 19
        |||||||
Db      1 ROIKIWFQNRMRMKKKTAL 18

RESULT 12
US-09-150-623-11
; Sequence 11, Application US/09150623
; Patent No. US20020044931A1
; GENERAL INFORMATION:
; APPLICANT: Troy, Carol M.
; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
; TITLE OF INVENTION: DEATH AND USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/150,623
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/610,220
; FILING DATE: MAR-04-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 48332/JPW/JML
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-150-623-11

Query Match      58.6%; Score 95; DB 9; Length 21;
Best Local Similarity 94.4%; Pred. No. 3,7e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 ROIKIWFQNRMRMKKKTAL 19
        |||||||
Db      1 ROIKIWFQNRMRMKKKTAL 18

RESULT 13
US-10-188-947-11
; Sequence 11, Application US/10188947
; Publication No. US20030023993A1
; GENERAL INFORMATION:
; APPLICANT: MEDHITOV, Ruslan
; APPLICANT: HORNIG, Tiffany
; APPLICANT: BARTON, Gregory
; TITLE OF INVENTION: TOLL/INTERLEUKIN-1 RECEPTOR ADAPTER PROTEIN (TIRAP)
; FILE REFERENCE: 044574-5101US
; CURRENT APPLICATION NUMBER: US/10/188,947
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/289,738
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/289,815
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/289,866
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent version 3.1
; SEQ ID NO 11
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: TIRAP/Antennapedia fusion protein
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: TIRAP/Antennapedia fusion protein
US-10-188-947-11
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Query Match 58.0%; Score 94; DB 15; Length 30;  
Best Local Similarity 89.5%; Pred. No. 6.8e-05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ROIKIWFQNRMRMKKTAL 20  
Db 1 ROIKIWFQNRMRMKKTAL 19

RESULT 14  
US-10-118-079-44  
; Sequence 44, Application US/10118079  
; Publication No. US20030103957A1  
; GENERAL INFORMATION:  
; APPLICANT: MCKERRACHER, LISA  
; TITLE OF INVENTION: FUSION PROTEINS  
; FILE REFERENCE: 06746-004-US-03  
; CURRENT APPLICATION NUMBER: US/10/118,079  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: CA 2,367,636  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: CA 2,362,004  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: CA 2,342,970  
; PRIOR FILING DATE: 2001-04-12  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 44  
; LENGTH: 64  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of Antennapedia from C3APL  
US-10-118-079-44

Query Match 58.0%; Score 94; DB 15; Length 64;  
Best Local Similarity 94.1%; Pred. No. 0.00013;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMRMKWK 17  
Db 46 EROIKIWFQNRMRMKWK 62

RESULT 15  
US-10-097-340-129  
; Sequence 129, Application US/10097340  
; Publication No. US20030087250A1  
; GENERAL INFORMATION:  
; APPLICANT: John MONAHAN  
; APPLICANT: Manjula GANNANAVAPU  
; APPLICANT: Sebaetian HOERSCH  
; APPLICANT: Shubhangi KAMATKAR  
; APPLICANT: Steve G. KOVATS  
; APPLICANT: Rachel E. MEYERS  
; APPLICANT: Michael MORRISSEY  
; APPLICANT: Peter OLANDT  
; APPLICANT: Ami SEN  
; APPLICANT: Peter VEIRBY  
; APPLICANT: Gordon B. MILLS  
; APPLICANT: Robert C. BAST, Jr.  
; APPLICANT: Karen LU  
; APPLICANT: Rosemarie SCHMANDT  
; APPLICANT: Xumei ZHAO  
; APPLICANT: Karen GLATT  
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,  
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer  
; FILE REFERENCE: MRI-030  
; CURRENT APPLICATION NUMBER: US/10/097,340  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: 60/276,025  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/325,149

; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/276,026  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/324,967  
; PRIOR FILING DATE: 2001/09/26  
; PRIOR APPLICATION NUMBER: 60/311,732  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/325,102  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/323,580  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 363  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 129  
; LENGTH: 217  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-097-340-129

Query Match 58.0%; Score 94; DB 15; Length 217;  
Best Local Similarity 94.1%; Pred. No. 0.0004;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMRMKWK 17  
Db 178 EROIKIWFQNRMRMKWK 194

Search completed: February 18, 2004, 15:42:02  
Job time : 78.9766 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 / Search time 106.289 Seconds  
(without alignments)  
41.814 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162  
Sequence: 1 DRQIKWPNRMKMTALDWSLQTE 28

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
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- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*
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- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	100.0	28	23	ABR08740
2	162	100.0	28	23	AA448523
3	162	100.0	28	24	ABU08434
4	134	82.7	28	23	ABR08741
5	134	82.7	28	23	AA448524
6	134	82.7	28	24	ABU08435
7	105	64.8	18	23	AA448628
8	105	64.8	18	23	AA448629
9	101	62.3	36	23	AAU79345

10	100	61.7	41	22	ABR0924
11	100	61.7	41	22	ABR0925
12	98	60.5	20	21	AA113423
13	98	60.5	26	18	AA11630
14	97	59.9	34	21	AA179919
15	96	59.3	26	24	AAE31836
16	95.5	59.0	42	23	ABP53779
17	95	58.6	21	18	AA45976
18	95	58.6	24	19	AA482957
19	95	58.6	36	21	AA178416
20	95	58.6	230	21	AA158610
21	94	58.0	27	18	AA11629
22	94	58.0	27	20	AA127444
23	94	58.0	27	23	ABR83151
24	94	58.0	30	24	ABP58107
25	94	58.0	60	20	AA142291
26	94	58.0	60	20	AA127403
27	94	58.0	60	20	AA104364
28	94	58.0	60	23	ABR84470
29	94	58.0	61	22	AAE00811
30	94	58.0	64	24	AAE32060
31	94	58.0	128	24	ABR99729
32	94	58.0	217	22	AAE10922
33	94	58.0	217	23	ABR95337
34	94	58.0	295	24	AAE32047
35	94	58.0	378	22	ABR72035
36	94	58.0	417	22	ABR57755
37	94	58.0	589	22	ABR58929
38	93.5	57.7	36	23	AAU79344
39	93	57.4	22	20	AA191049
40	93	57.4	22	21	AAE27063
41	93	57.4	106	21	AAE21030
42	93	57.4	115	21	AAE53629
43	93	57.4	220	22	AA41487
44	93	57.4	236	22	AA139701
45	93	57.4	243	19	AA448885

#### ALIGNMENTS

RESULT 1	ABR08740	standard; peptide; 28 AA.
ID	ABR08740	
AC	ABR08740	
XX	14-JUN-2002	(first entry)
DB	IKKbeta NEMO binding domain peptide SEQ ID NO 18.	
XX	IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;	
XX	kinase activation; leukocyte; inflammation; E-selectin; osteoclast;	
XX	autoimmune disease; transplant rejection; osteoporosis; cancer;	
KW	Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;	
KW	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;	
KW	corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;	
KW	osteopathic; cytostatic; neotropic; neuroprotective; anti-HIV; human;	
KW	antiarteriosclerotic; virucide; antiasthmatic; antiallergic;	
KW	dermatological; antibacterial; antipruritic; antirheumatic;	
KW	antiarthritic; osteopathic; antitumor;	
OS	Homo sapiens.	
PN	WO200183547-A2.	
XX	08-NOV-2001.	
PD	02-MAY-2001; 2001WO-USA0654.	
PF	02-MAY-2000; 2000US-201261P.	
XX	22-AUG-2000; 2000US-0643260.	
PR		
XX		

Mixer SIM peptide.  
Mixer SIM mutant p  
Synthetic alpha sm  
Anti-apoptotic pro  
Human papillomavir  
Androgen receptor  
Antennapedia helix  
Antennapedia helix  
Cysteine protease  
Oestrogen receptor  
Drosophila antenna  
Protein regulating  
Anti-apoptotic pro  
Antennapedia inter  
Transduction domai  
Mouse TIRAP-Antenn  
Drosophila antenna  
D. melanogaster PA  
Drosophila antenna  
S. cerevisiae Antp  
D. melanogaster an  
Antennapedia C3APL  
Amino acid sequenc  
Human HOXB7 varian  
Human ovarian canc  
Clostridium botuli  
Drosophila melanog  
Drosophila melanog  
Drosophila melanog  
Antennapedia-caveo  
Internalization be  
Beta-catenin deriv  
Human nucleic acid  
Human colon cancer  
Human polypeptide  
Human polypeptide  
Amino acid sequenc

PA (UYVA ) UNIV YALE.  
 XX May MJ, Ghosh S;  
 XX WPI; 2002-179350/23.  
 DR  
 XX  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 PS Claim 23, Fig 5, 82pp, English.  
 XX  
 XX The invention relates to modulating NF-kappaB (NF-KB) induction in a cell  
 CC comprising contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-KB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of IkbppaB. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-KB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polyarthritis, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of the NEMO  
 CC binding domain of IKKbeta.  
 XX  
 SO Sequence 28 AA;  
 Query Match 100.0%; Score 162; DB 23; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-15;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFONRRMKKTKTALDMSWLQTB 28  
 DB 1 DROIKIWFONRRMKKTKTALDMSWLQTB 28

RESULT 2  
 ID AAM48523 standard; Peptide; 28 AA.  
 XX AAM48523;  
 AC  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DB NBD peptide SEQ ID NO 18.  
 XX  
 XX Antiinflammatory; antiaesthetic; cytostatic; antipsoriatic; nootropic;  
 KW antineumatic; antidiabetic; osteopathic; antibacterial; virocidic;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;

KW cytokine; NFkappaB; IkbppaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 XX MO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRABCTIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 XX May MJ, Ghosh S, Fandels MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 XX  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 PS Example 5, Fig 5, 88pp; English.  
 XX  
 XX The invention relates to an antiinflammatory compound (especially  
 CC AAM48620-AAM48645), comprising a membrane translocation domain  
 CC (AAM48630-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
 CC cytostatic, antipsoriatic, antirheumatic, antidiabetic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virocidic and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkbppaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkbppaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SO Sequence 28 AA;  
 Query Match 100.0%; Score 162; DB 23; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-15;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFONRRMKKTKTALDMSWLQTB 28  
 DB 1 DROIKIWFONRRMKKTKTALDMSWLQTB 28

RESULT 3  
 ID ABU08434 standard; peptide; 28 AA.  
 XX ABU08434;  
 AC  
 XX  
 DT 12-JUN-2003 (first entry)  
 XX

DE Wild-type human NEMO binding site (NBD) peptide.  
 XX  
 XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;  
 KW Ikappab kinase-beta; Ikappab kinase-alpha; IKKalpha; NF-kappab;  
 KW nuclear factor-kappab induction; inflammatory disorder;  
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;  
 KW atherosclerosis; viral infection; Ataxia telangiectasia;  
 KW transplacental detection; immunosuppressive; osteopathic;  
 KW cytostatic; nocotropic; neuroprotective; antiatherosclerotic; virucide;  
 KW vasotropic; antineumatic; antiarthritic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US002156000-A1.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 02-MAY-2001; 2001US-0847940.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (MAYM/) MAY M J.  
 XX (GHOSH/) GHOSH S.  
 XX  
 PI May MJ, Ghosh S;  
 XX  
 DR WPI; 2003-209142/20.  
 XX  
 PT Novel antiinflammatory peptide compounds comprising NEMO binding  
 PT domain, useful for modulating NF-kappab induction in a cell and for  
 PT treating NF-kappab-mediated inflammation disorders e.g., asthma,  
 PT psoriasis, vasculitis -  
 XX  
 PS Claim 35; Page 22; 47pp; English.  
 XX  
 CC The present invention relates to antiinflammatory compounds comprising  
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are  
 CC found on Ikappab kinase-beta (IKKbeta) and Ikappab kinase-alpha  
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention  
 CC are useful for modulating nuclear factor-kappab (NF-kappab) induction  
 CC in a cell, where the compounds are capable of blocking the interaction  
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The  
 CC antiinflammatory compound further comprises at least one membrane  
 CC translocation domain. The compounds are useful for treating  
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia  
 CC telangiectasia, and for transplacental detection. The compounds of  
 CC the invention block NF-kappab induction by IKK but do not inhibit  
 CC the basal activity of NF-kappab. The present sequence represents  
 CC an antiinflammatory compound of the invention.  
 XX  
 SQ Sequence 28 AA;  
 XX  
 Query Match 100.0%; Score 162; DB 24; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-15;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DROIKIPQNRBMKKKTKLADMSGLQTE 28  
 DB 1 DROIKIPQNRBMKKKTKLADMSGLQTE 28  
 AC ABB08741  
 ID ABB08741 standard; peptide; 28 AA.  
 AC ABB08741;  
 XX  
 DT 14-JUN-2002 (first entry)  
 DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 19.

KW IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappab; NF-kB;  
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;  
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;  
 KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;  
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;  
 KW osteopathic; cytostatic; nocotropic; neuroprotective; anti-HIV; human;  
 KW antiarteriosclerotic; virucide; antilesthetic; antiallergic;  
 KW dermatological; antibacterial; antiparasitic; antineumatic;  
 KW antiarthritic; osteopathic; antitumor; mutant; mucin.  
 XX  
 OS Homo sapiens.  
 XX  
 PN Synthetic.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US40654.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S;  
 XX  
 DR WPI; 2002-179350/23.  
 XX  
 PT Modulating NF-kappab induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 XX  
 PS Claim 23; Fig 5; 82pp; English.  
 XX  
 CC The invention relates to modulating NF-kappab (NF-kB) induction in a cell  
 CC comprises contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB077313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of Ikappab. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC polyarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.



CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
 CC binding domain of IKKbeta.

SO Sequence 28 AA:

Query Match 82.7%; Score 134; DB 23; Length 28;  
 Best Local Similarity 92.9%; Pred. No. 4.3e-11;  
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DRQIKIWFQNRRMKWTKTALDMSLTQTE 28  
 1 DRQIKIWFQNRRMKWTKTALDASALTQTE 28

#### RESULT 5

AA048524 standard; Peptide; 28 AA.

AC AA048524;

DT 20-MAR-2002 (first entry)

DE NBD peptide SEQ ID NO 19.

XX Antinflammatory; antiaesthetic; cytoskeletal; antipsoriatic; neurotropic;  
 XX antineumatic; antiaesthetic; osteopathic; antibacterial; virucide;  
 XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 XX autoimmune disorder; multiple sclerosis; transplant rejection;  
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US4346.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

XX (UYTA) UNIV YALE.

XX May MJ, Ghosh S, Finkelstein MA, Phillips K;

XX WPI; 2002-121889/16.

PT Novel antinflammatory compound comprising membrane translocation

PT domain fused to NEMO binding sequence, useful for blocking nuclear

PT factor kappaB activation, and for treating asthma, lung inflammation,

PT psoriasis

XX Example 5; Fig 5; 88pp; English.

XX The invention relates to an antinflammatory compound (especially

CC AA048524-AA048645), comprising a membrane translocation domain

CC (AA048620-AA048627 or AA048646-AA048651) which comprises from 6-15

CC amino acid residues, fused to a NEMO binding sequence

CC (AA048525-AA048619). The antinflammatory compounds have antiaesthetic,

CC cytoskeletal, antipsoriatic, antineumatic, antiaesthetic, osteopathic,

CC antibacterial, immunosuppressive, dermatological, neuroprotective,

CC neurotropic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB

CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at

CC the NEMO binding domain that results in inhibition of IkappaB kinase

CC activation and subsequent decreased phosphorylation of IkappaB. The

CC compounds are useful for treating inflammatory disorders, e.g. asthma,

CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC burns; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.

SO Sequence 28 AA:

Query Match 82.7%; Score 134; DB 23; Length 28;  
 Best Local Similarity 92.9%; Pred. No. 4.3e-11;  
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DRQIKIWFQNRRMKWTKTALDMSLTQTE 28  
 1 DRQIKIWFQNRRMKWTKTALDASALTQTE 28

#### RESULT 6

AB008435 standard; peptide; 28 AA.

AC AB008435;

DT 12-JUN-2003 (first entry)

DE Human mutant NEMO binding site (NBD) peptide.

XX Human; antinflammatory compound; NEMO binding domain; NBD; IKKbeta;  
 XX IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;  
 XX nuclear factor-kappaB induction; inflammatory disorder;  
 XX autoimmune disease; osteoporosis; cancer; Alzheimer's disease;  
 XX atherosclerosis; viral infection; Ataxia telangiectasia;  
 XX transplant rejection; multiple sclerosis; osteopathic;  
 XX cytoskeletal; neurotropic; neuroprotective; antiatherosclerotic; virucide;  
 XX vasotropic; antineumatic; antiaesthetic; mutant; mutein.

OS Homo sapiens.

PN US2002156000-A1.

PD 24-OCT-2002.

PF 02-MAY-2001; 2001US-0847940.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (MAYW/) MAY M J.

XX (GHOS/) GHOSH S.

XX May MJ, Ghosh S;

XX WPI; 2003-209142/20.

PT Novel antinflammatory peptide compounds comprising NEMO binding

PT domain, useful for modulating NF-kappaB induction in a cell and for

PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,

PT psoriasis, vasculitis

XX Claim 22; Fig 5A; 47pp; English.

XX The present invention relates to antinflammatory compounds comprising

CC NEMO binding domain (NBD) peptides. The NEMO binding domains are

CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha

CC (IKKalpha) proteins. The antinflammatory compounds of the invention

CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction

CC in a cell, where the compounds are capable of blocking the interaction

CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The

CC antiinflammatory compound further comprises at least one membrane  
 CC translocation domain. The compounds are useful for treating  
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia  
 CC telangiectasia, and for transplantation detection. The compounds of  
 CC the invention block NF-kappaB induction by IKK but do not inhibit  
 CC the basal activity of NF-kappaB. The present sequence represents  
 CC a human mutant NBD peptide.  
 XX  
 SQ Sequence 28 AA;  
 Query Match 82.7%; Score 134; DB 24; Length 28;  
 Best Local Similarity 92.9%; Pred. No. 4.3e-11;  
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 DRQIKIWFQNRMRMKKKTALDMSWLTQTE 28  
 Db 1 DRQIKIWFQNRMRMKKKTALDMSWLTQTE 28  
 RESULT 7  
 AAM48628 AAM48628 standard; Peptide; 18 AA.  
 XX  
 AC AAM48628;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 131.  
 XX  
 KM Antiinflammatory; antiaesthetic; cyostatic; antipsoriatic; nootropic;  
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 OS Synthetic.  
 XX  
 PN MO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 PI WPI, 2002-121889/16.  
 DR  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 Claim 12; Page 62; 88pp; English.  
 PS  
 XX The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48630-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective, the  
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 18 AA;  
 Query Match 64.8%; Score 105; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 11 RRMKKKKTALDMSWLTQTE 28  
 Db 1 RRMKKKKTALDMSWLTQTE 18  
 RESULT 8  
 AAM48629 AAM48629 standard; Peptide; 18 AA.  
 XX  
 AC AAM48629;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 132.  
 XX  
 KM Antiinflammatory; antiaesthetic; cyostatic; antipsoriatic; nootropic;  
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 OS Synthetic.  
 XX  
 PN MO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 PI WPI, 2002-121889/16.  
 DR  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 Claim 12; Page 63; 88pp; English.  
 PS  
 XX The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM4620-AAM4827 or AAM4846-AAM4851) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,  
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antithrombotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
 CC activation by blocking interaction of I-kappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of I-kappaB kinase  
 CC activation and subsequent decreased phosphorylation of I-kappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 SQ Sequence 18 AA;  
 Query Match 64.8%; Score 105; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 11 RRMKKKTALDMSWLTQTE 28  
 Db 1 RRMKKKTALDMSWLTQTE 18  
 RESULT 9  
 AAV79345  
 ID AAV79345 standard; Peptide: 36 AA.  
 AC AAV79345;  
 XX  
 DT 02-JUN-2002 (first entry)  
 XX  
 DE Antennapedia-caveolin-X fusion peptide.  
 XX  
 KW Caveolin; scaffolding domain; endothelial nitric oxide synthase; eNOS;  
 KW vasodilation inhibitor; inflammation inhibitor; tumour cell angiogenesis;  
 KW tumour cell proliferation; osteoporosis; arthritis; atherosclerosis;  
 KW asthma; Alzheimer's disease; allergy; allergic rhinitis; urticaria;  
 KW anaphylaxis; dry sensitivity; food sensitivity; dermatitis; eczema;  
 KW psoriasis; sunburn; aging; osteoarthritis; psoriatic arthritis; lupus;  
 KW spondylarthritis; chronic obstruction pulmonary disease; cancer; Cav;  
 KW chronic inflammatory bowel disease; tumour growth; malignant neoplasm;  
 KW human; fruit fly; antennapedia internalisation signal.  
 XX  
 OS Drosophila melanogaster.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 1..16  
 FT /label= Antennapedia internalisation signal  
 FT /note= "Specifically claimed in claim 9"  
 FT Misc-difference 17..32  
 FT /label= Cav-X  
 FT /note= "Control peptide based on a human caveolin-1  
 FT scaffolding domain shown in AAV79340 residues  
 FT 82-101"  
 XX  
 XX WO200220768-A2.  
 XX  
 XX 14-MAR-2002.  
 XX  
 XX 10-SEP-2001; 2001WO-US42069.  
 XX  
 XX 08-SEP-2000; 2000US-231327P.

PR 07-DEC-2000; 2000US-0731023.  
 XX  
 XX (UYVA ) UNIV YALE.  
 PA  
 XX  
 XX Sessa WC;  
 PI  
 DR WPI; 2002-329877/36.  
 XX  
 PT New peptide having caveolin scaffolding domain, useful for modulating  
 PT activity of endothelial nitric oxide synthase and inhibiting  
 PT inflammation and tumour cell angiogenesis proliferation -  
 XX  
 PS Claim 16; Page 72; 73pp; English.  
 XX  
 CC The invention describes an isolated caveolin scaffolding domain peptide  
 CC (I). A fusion peptide (II) containing (I) and at least a membrane  
 CC translocation sequence is useful for down regulating endothelial nitric  
 CC oxide synthase (eNOS) activity in a cell, resulting in blockage of  
 CC vasodilation. (II) is therefore useful for inhibiting inflammation and  
 CC tumour cell angiogenesis/proliferation in an animal, and for blocking the  
 CC interaction of caveolin with a protein in vivo. (II) may be useful in  
 CC treatment of inflammatory conditions such as osteoporosis, rheumatoid  
 CC arthritis, atherosclerosis, asthma and Alzheimer's disease. (I) and (II)  
 CC are also useful for treating pathological processes associated with a  
 CC pro-inflammatory response including allergies such as allergic rhinitis,  
 CC urticaria, anaphylaxis, dry sensitivity, food sensitivity, cutaneous  
 CC inflammation such as dermatitis, eczema, psoriasis contact dermatitis,  
 CC sunburn, aging, arthritis such as osteoarthritis, psoriatic arthritis,  
 CC lupus, spondylarthritis, and chronic obstruction pulmonary disease and  
 CC chronic inflammatory bowel disease. (I) and (II) are useful for replacing  
 CC corticosteroids useful for immunosuppression in transplant and cancer  
 CC patients. When administered along with one or more anti-inflammatory  
 CC agent (I) and (II) are useful for inhibiting tumour growth or malignant  
 CC neoplasm including cellular angiogenesis, proliferation, invasiveness,  
 CC and metastasis in biological systems. This sequence represents a fusion  
 CC peptide of the invention created from the fruit fly antennapedia  
 CC internalisation signal and control sequence Cav-X, based on the human  
 CC caveolin-1 scaffolding domain shown in AAV79340, residues 82-101.  
 CC  
 SQ Sequence 36 AA;  
 Query Match 62.3%; Score 101; DB 23; Length 36;  
 Best Local Similarity 69.2%; Pred. No. 1.4e-06;  
 Matches 18; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 QY 2 RQIKIFQNRBMKKKTALDMSWLTQT 27  
 Db 1 RQIKIFQNRBMKKKTALDMSWLTQT 26  
 RESULT 10  
 AAB80924  
 ID AAB80924 standard; Protein: 41 AA.  
 AC AAB80924;  
 XX  
 DT 04-JUN-2001 (first entry)  
 XX  
 DE Mixer SIM peptide.  
 XX  
 KW Smad; Cytostatic; vulnerary; cerebroprotective; immunosuppressive;  
 KW Anti-HIV; antidiabetic; ophthalmological; antiinflammatory; SIM;  
 KW Smad interaction Motif; tissue repair; fibrotic condition;  
 KW immunosuppression; diabetic nephropathy; tumour.  
 XX  
 OS Unidentified.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "Biotin.Aminohexanoic acid-R"  
 FT  
 XX WO200114413-A2.  
 XX

PD 01-MAR-2001.  
 XX  
 PF 25-AUG-2000; 2000WO-GB03265.  
 XX  
 PR 25-AUG-1999; 99GB-0020000.  
 XX  
 PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
 XX  
 PI Germain SE, Hill CS, Howell MT;  
 XX  
 DR MPI; 2001-265836/27.  
 XX  
 PT Polypeptide capable of interacting with a Smad polypeptide, useful in  
 PT the treatment of cancer and for tissue remodeling or healing of a  
 PT wound, injury or surgery, comprises a Smad interaction Motif and is  
 XX less than 32 amino acids in length -  
 XX  
 PS Claim 16; Page 140; 179pp; English.  
 XX  
 CC The present invention relates to peptides capable of interacting with a  
 CC Smad protein, comprising a Smad interaction Motif (SIM; amino acid  
 CC sequence PP(T/N)K). The present sequence is one such Smad interacting  
 CC peptide. Smad proteins are a family of highly conserved, intracellular  
 CC proteins that signal cellular responses downstream of Transforming Growth  
 CC Factor-beta (TGF-beta) family serine/threonine kinase receptors. The SIM  
 CC is thought to be necessary for interaction with the MH2 domain of Smad2.  
 CC The peptides of the present invention are useful in the manufacture of a  
 CC medicament for the treatment of a patient in need of modulation of  
 CC activation or TGF-beta signaling; cancer; a patient in need of reducing  
 CC extracellular matrix deposition, encouraging tissue repair and/or  
 CC regeneration, tissue remodeling or healing of a wound, injury or  
 CC surgery, or reducing scar tissue formation arising from injury to the  
 CC brain; a patient with or at risk of end-stage organ failure, pathologic  
 CC extracellular matrix accumulation, a fibrotic condition, disease states  
 CC associated with immunosuppression (such as different forms of malignancy,  
 CC chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour  
 CC growth, kidney damage (for e.g. obstructive neuropathy, Iga nephropathy  
 CC or non-inflammatory renal disease) or renal fibrosis.  
 XX  
 SQ Sequence 41 AA;  
 Query Match 61.7%; Score 100; DB 22; Length 41;  
 Best Local Similarity 77.3%; Pred. No. 2.2e-06;  
 Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 RQIKWIFQNRMKKTLMDWS 23  
 Db 1 RQIKWIFQNRMKKTLMDFN 22  
 RESULT 11  
 AAB80925  
 ID AAB80925 standard; Protein; 41 AA.  
 XX  
 AC AAB80925;  
 XX  
 DT 04-JUN-2001 (first entry)  
 XX  
 DE Mixer SIM mutant peptide.  
 XX  
 KW Smad; Cytostatic; vulnary; cerebroprotective; immunosuppressive;  
 KW Anti-HIV; antidiabetic; ophthalmological; antiinflammatory; SIM;  
 KW Smad interaction Motif; tissue repair; fibrotic condition;  
 KW immunosuppression; diabetic nephropathy; tumour; mutcin.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "Biotin.Aminohexanoic acid-R"  
 FT Misc-difference 25  
 FT /note= "Wild-type Pro replaced by Ala. Wild-type sequence  
 FT given in AAB80924."

FT Misc-difference 26  
 FT /note= "Wild-type Pro replaced by Ala"  
 FT  
 PN WO200114413-A2.  
 XX  
 PD 01-MAR-2001.  
 XX  
 PF 25-AUG-2000; 2000WO-GB03265.  
 XX  
 PR 25-AUG-1999; 99GB-0020000.  
 XX  
 PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
 XX  
 PI Germain SE, Hill CS, Howell MT;  
 XX  
 DR MPI; 2001-265836/27.  
 XX  
 PT Polypeptide capable of interacting with a Smad polypeptide, useful in  
 PT the treatment of cancer and for tissue remodeling or healing of a  
 PT wound, injury or surgery, comprises a Smad interaction Motif and is  
 XX less than 32 amino acids in length -  
 XX  
 PS Example 2; Page 123; 179pp; English.  
 XX  
 CC The present invention relates to peptides capable of interacting with a  
 CC Smad protein, comprising a Smad interaction Motif (SIM; amino acid  
 CC sequence PP(T/N)K). The present sequence is one such Smad interacting  
 CC peptide. Smad proteins are a family of highly conserved, intracellular  
 CC proteins that signal cellular responses downstream of Transforming Growth  
 CC Factor-beta (TGF-beta) family serine/threonine kinase receptors. The SIM  
 CC is thought to be necessary for interaction with the MH2 domain of Smad2.  
 CC The peptides of the present invention are useful in the manufacture of a  
 CC medicament for the treatment of a patient in need of modulation of  
 CC activation or TGF-beta signaling; cancer; a patient in need of reducing  
 CC extracellular matrix deposition, encouraging tissue repair and/or  
 CC regeneration, tissue remodeling or healing of a wound, injury or  
 CC surgery, or reducing scar tissue formation arising from injury to the  
 CC brain; a patient with or at risk of end-stage organ failure, pathologic  
 CC extracellular matrix accumulation, a fibrotic condition, disease states  
 CC associated with immunosuppression (such as different forms of malignancy,  
 CC chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour  
 CC growth, kidney damage (for e.g. obstructive neuropathy, Iga nephropathy  
 CC or non-inflammatory renal disease) or renal fibrosis.  
 XX  
 SQ Sequence 41 AA;  
 Query Match 61.7%; Score 100; DB 22; Length 41;  
 Best Local Similarity 77.3%; Pred. No. 2.2e-06;  
 Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 RQIKWIFQNRMKKTLMDWS 23  
 Db 1 RQIKWIFQNRMKKTLMDFN 22  
 RESULT 12  
 AAB13423  
 ID AAB13423 standard; peptide; 20 AA.  
 XX  
 AC AAB13423;  
 XX  
 DT 23-NOV-2000 (first entry)  
 XX  
 DE Synthetic alpha smooth muscle actin inhibitor # 3.  
 XX  
 KW Alpha smooth muscle actin; alpha-SM; wound contraction;  
 KW hypertrophic scar; fibromatosis; Dupuytren disease; fibrotic condition;  
 KW lung fibrosis.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1

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FT      /note="N-terminal acetyl"
XX      WO200038733-A1.
XX      06-JUL-2000.
XX      15-DEC-1999; 99WO-EP09964.
XX      24-DEC-1998; 98EP-0204396.
XX      (UNIO ) UCB-BIOPRODUCTS SA.
XX      Gabbiani G, Scarso A;
XX      WPI, 2000-452308/39.
XX      A peptidic product for prevention and treatment of a disease related to
XX      alpha-SM actin expression comprises a tetrapeptide associated with a
XX      chemical entity that is able to introduce the tetrapeptide into the
XX      cell -
XX      Claim 7; Page 23; 31pp; English.
XX      The present invention relates to novel peptides comprising of a specific
XX      tetrapeptide associated with an oligopeptide which allows the
XX      introduction of the tetrapeptide into the target cell. The present
XX      sequence is one such peptide. Residues 1 to 4 of the present sequence
XX      correspond to the specific tetrapeptide, while residues 5 to 20
XX      correspond to the oligopeptide. The specific tetrapeptide of the present
XX      sequence interferes with alpha smooth muscle (alpha-SM) actin
XX      organisation in stress fibres. The present sequence may be used in the
XX      prevention and/or treatment of a disease related to alpha-SM actin
XX      expression, e.g. wound contraction, hypertrophic scars, fibromatosis and
XX      Dupuyren disease and lung fibrosis.
XX      Sequence 20 AA;
SQ      Query Match      60.5%; Score 98; DB 21; Length 20;
        Best Local Similarity 100.0%; Pred. No. 1.9e-06;
        Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 DRQIKWIFQNRBMKMKK 17
        : |||||
        4 DRQIKWIFQNRBMKMKK 20
DB
RESULT 13
AAW11630
ID      AAW11630 standard; peptide; 26 AA.
XX      AAW11630;
XX      16-OCT-1997 (first entry)
XX      Anti-apoptotic protein blocking peptide FP2.
XX      Cell permeable; apoptosis; blocking; inhibition; tumour growth;
XX      ex vivo purging; in vivo administration; Bcl-2.
XX      Synthetic.
XX      Key      Location/Qualifiers
XX      FH      1..17
XX      PT      Peptide      /label= sig_peptide
XX      DB19526174-A1.
XX      23-JAN-1997.
XX      18-JUL-1995; 95DE-1026174.
XX      18-JUL-1995; 95DE-1026174.
XX      18-JUL-1995; 95DE-1026174.

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XX      (BRAC/) BRACH M.
XX      PA      (HERR/) HERRMANN F.
XX      PA      (KIEH/) KIEHNTOFF M.
XX      PI      Brach M, Herrmann F, Kiehnkopf M;
XX      WPI, 1997-088160/09.
XX      Peptide(s) that block anti-apoptotic proteins - useful for
XX      inhibiting tumour growth
XX      Claim 6; Page 7; 7pp; German.
XX      The present sequence is a cell permeable anti-apoptotic protein
XX      blocking peptide, which can be used to inhibit tumour growth, e.g.
XX      by ex vivo purging or (after stabilisation) in vivo
XX      administration. The peptide preferably blocks Bcl-2, and comprises
XX      a signal peptide mediating cell penetration and a functional
XX      sequence corresponding to a Bcl-2 domain.
XX      Sequence 26 AA;
SQ      Query Match      60.5%; Score 98; DB 18; Length 26;
        Best Local Similarity 89.5%; Pred. No. 2.5e-06;
        Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY      1 DRQIKWIFQNRBMKMKKTA 19
        : |||||
        1 BRQIKWIFQNRBMKMKKAA 19
DB
RESULT 14
AAW79919
ID      AAW79919 standard; Peptide; 34 AA.
XX      AAW79919;
XX      10-MAY-2000 (first entry)
XX      Human papillomavirus 16 E2 fusion peptide Ant-WP.
XX      Human papillomavirus 16 E2 fusion peptide Ant-WP.
XX      Papillomavirus; PV; infection; cell proliferation; E2; peptidomimetic;
XX      E1; antiviral; virucide; cytostatic; antiproliferative; dermatological;
XX      premalignant lesion; neoplastic lesion; cutaneous lesion; wart;
XX      epidermodysplasia verruciformis; anorectal carcinoma.
XX      Human papillomavirus.
XX      Synthetic.
XX      WO200001720-A2.
XX      13-JAN-2000.
XX      02-JUL-1999; 99WO-US15144.
XX      02-JUL-1998; 98US-0091661.
XX      (HARD ) HARVARD COLLEGE.
XX      Howley P, Benson J, Kasukawa H;
XX      WPI, 2000-171001/15.
XX      Use of papillomavirus E2 protein peptidomimetics for treating
XX      papillomavirus-infected cells and papillomavirus-induced conditions in
XX      mammals by inhibiting E1-E2 interaction -
XX      Disclosure; Fig 13; 110pp; English.
XX      The present invention describes the use of a small organic compound (A)
XX      which competitively inhibits interaction of a papillomavirus (PV) E2
XX      protein with a PV E1 protein for treating a cell infected with PV or a

```

CC mammal with a PV-induced condition. (A) has antiviral, virucide,  
 CC cytotoxic, antiproliferative and dermatological activities. Methods  
 CC from the present invention can be used to treat PV-induced conditions  
 CC including growth of PV preneoplastic and neoplastic lesions, cutaneous  
 CC lesions chosen from warts and other benign cutaneous lesions, plantar  
 CC warts (verruca plantaris), common warts (verruca plana), Butcher's  
 CC common warts, flat warts, genital warts (condyloma acuminatum) and  
 CC epidermodysplasia verruciformis, laryngeal, oral, pharyngeal,  
 CC esophageal and other upper airway papilloma or vaginal, cervical,  
 CC vulvar, penile and anorectal carcinoma. The B2 inhibitors may also be  
 CC used to treat epithelial and internal fibropapillomas in animals.  
 CC The present sequence represents a peptide sequence used in the  
 CC exemplification of the present invention.

XX Sequence 34 AA;

Query Match 59.9%; Score 97; DB 21; Length 34;

Best Local Similarity 64.3%; Pred. No. 4.5e-06; Mismatches 5; Indels 2; Gaps 1;

Matches 18; Conservative 3; Mismatches 5; Indels 2; Gaps 1;  
 QY 1 DRQIKIWFQNRMRMKKKTALDWSMLQTE 28  
 :|||||:|||||:|:|  
 DB 1 ERQIKIWFQNRMRMKKKG--WKHWRL 26

RESULT 15

AAE31836  
 ID AAE31836 standard; peptide; 26 AA.

XX AAE31836;

XX 07-MAR-2003 (first entry)

XX Androgen receptor binding peptide #87.

XX Androgen receptor; androgen-associated disorder; prostate cancer; acne;  
 KM benign prostatic hypertrophy; hirsutism; androgen insensitivity syndrome;  
 KM male pattern baldness; Stein-Leventhal syndrome; infertility; cytotoxic;  
 KW X-linked spinal bulbar muscular atrophy; antisheborrheic; dermatological;  
 KM depilatory; androgen receptor binding peptide.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 26 /note= "C-terminal amide"

XX WO200272612-A2.

XX 19-SEP-2002.

XX 12-MAR-2002; 2002WO-US07487.

XX 12-MAR-2001; 2001US-275240P.

XX 28-JAN-2002; 2002US-352399P.

XX (PRAE-) PRAECIS PHARM INC.

XX Joyal JL, Mueller J, Oza VB, Findels MA,

XX WPI; 2003-067363/06.

XX New peptide modulators of androgen receptor, useful for treating  
 PT androgen-associated disorder, e.g. prostate cancer, particularly  
 PT hormonally refractive prostate cancer, colon cancer, lung cancer, acne,  
 PT or hirsutism -

XX Example; Page 30; 68pp; English.

XX The present invention relates to novel peptide modulators of androgen  
 CC receptor. The peptides of the invention are useful for treating androgen-

CC associated disorders such as prostate cancer, particularly hormonally  
 CC refractive prostate cancer, colon cancer, lung cancer, benign prostatic  
 CC hypertrophy, acne, hirsutism, male pattern baldness, Stein-Leventhal  
 CC syndrome, androgen insensitivity syndrome, infertility, endometrial  
 CC cancer and X-linked spinal bulbar muscular atrophy. The present sequence  
 CC is an androgen receptor binding peptide.

XX Sequence 26 AA;

Query Match 59.3%; Score 96; DB 24; Length 26;

Best Local Similarity 77.3%; Pred. No. 4.6e-06; Mismatches 3; Indels 0; Gaps 0;

Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 RQIKIWFQNRMRMKKKTALDWS 23  
 :|||||:|||||:|:|  
 DB 1 RQIKIWFQNRMRMKKKTALDWS 22

Search completed: February 18, 2004, 14:26:27  
 Job time : 107.289 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 32.9737 Seconds  
(without alignments)  
35.929 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162  
Sequence: 1 DRQIKIWFQNRMRMKKTALDMSWLQTE 28

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents AA:\*  
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2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
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6: /cgn2\_6/prodata/1/1aa/backfillseq.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	59.9	34	4	US-09-347-504-79
2	95	58.6	24	4	US-09-419-826-34
3	94	58.0	27	4	US-09-040-725A-2
4	94	58.0	61	2	US-08-202-044-3
5	94	58.0	61	3	US-08-751-344B-3
6	94	58.0	61	3	US-08-751-344B-6
7	94	58.0	61	3	US-08-751-344B-9
8	93	57.4	22	4	US-09-057-363C-50
9	93	57.4	27	3	US-09-051-934-51
10	93	57.4	27	3	US-09-051-934-52
11	93	57.4	61	3	US-08-751-344B-7
12	92	56.8	16	2	US-08-928-958-7
13	92	56.8	16	2	US-08-810-540-3
14	92	56.8	16	2	US-08-810-540-6
15	92	56.8	16	2	US-09-072-429-7
16	92	56.8	16	3	US-08-964-302A-6
17	92	56.8	16	3	US-09-116-294-4
18	92	56.8	16	3	US-08-964-614A-4
19	92	56.8	16	3	US-08-849-486-1
20	92	56.8	16	3	US-08-849-486-4
21	92	56.8	16	3	US-09-208-966-54
22	92	56.8	16	3	US-09-308-935-8
23	92	56.8	16	3	US-09-441-416A-6
24	92	56.8	16	4	US-09-296-089-33
25	92	56.8	16	4	US-09-419-826-33
26	92	56.8	16	4	US-09-302-305C-10
27	92	56.8	16	4	US-09-346-847-1

28	92	56.8	16	4	US-09-346-847-25	Sequence 25, Appl
29	92	56.8	16	4	US-09-057-363C-47	Sequence 47, Appl
30	92	56.8	16	4	US-09-043-560B-3	Sequence 3, Appl
31	92	56.8	17	4	US-09-346-847-17	Sequence 17, Appl
32	92	56.8	17	4	US-09-346-847-20	Sequence 20, Appl
33	92	56.8	17	4	US-09-346-847-22	Sequence 22, Appl
34	92	56.8	17	4	US-09-346-847-27	Sequence 27, Appl
35	92	56.8	18	3	US-08-838-545-20	Sequence 20, Appl
36	92	56.8	19	4	US-09-349-533-20	Sequence 20, Appl
37	92	56.8	19	4	US-09-346-847-23	Sequence 23, Appl
38	92	56.8	19	4	US-09-658-517C-7	Sequence 7, Appl
39	92	56.8	20	4	US-09-466-772-3	Sequence 3, Appl
40	92	56.8	20	4	US-09-346-847-16	Sequence 16, Appl
41	92	56.8	20	4	US-09-346-847-18	Sequence 18, Appl
42	92	56.8	20	4	US-09-346-847-30	Sequence 30, Appl
43	92	56.8	20	4	US-09-658-517C-8	Sequence 8, Appl
44	92	56.8	22	4	US-09-346-847-28	Sequence 28, Appl
45	89	54.9	42	3	US-08-751-344B-4	Sequence 4, Appl

#### ALIGNMENTS

RESULT 1  
US-09-347-504-79  
; Sequence 79, Application US/09347504  
; Patent No. 6399075

GENERAL INFORMATION:  
; APPLICANT: Howley, Peter M.

; APPLICANT: Benson, John

; APPLICANT: Kasukawa, Hiroaki

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

FILE REFERENCE: HMV-041.01

; CURRENT APPLICATION NUMBER: US/09/347,504

; CURRENT FILING DATE: 1999-07-02

; NUMBER OF SEQ ID NOS: 79

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 79

LENGTH: 34

TYPE: PRT

ORGANISM: Homo sapiens

US-09-347-504-79

Query Match 59.9%; Score 97; DB 4; Length 34;  
Best Local Similarity 64.3%; Pred. No. 1.9e-06;  
Matches 18; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 1 DRQIKIWFQNRMRMKKTALDMSWLQTE 28  
DB 1 ERQIKIWFQNRMRMKKTG3-WKHMRRLB 26

RESULT 2  
US-09-419-826-34

; Sequence 34, Application US/09419826  
; Patent No. 6306832

GENERAL INFORMATION:  
; APPLICANT:

; TITLE OF INVENTION: PEPTIDE ANTISTROGEN COMPOSITIONS AND METHODS

FOR TREATING BREAST CANCER

NUMBER OF SEQUENCES: 39

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

APPLICATION NUMBER: US/09/419,826

FILING DATE: 14-OCT-1999

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US98/07711

FILING DATE: 14-APR-1998

APPLICATION NUMBER: US 60/043,545  
FILING DATE: 14-APR-1997  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 19  
OTHER INFORMATION: /note= "X = Phosphotyrosine"  
US-09-419-826-34

Query Match 58.6%; Score 95; DB 4; Length 24;  
Best Local Similarity 89.0%; Pred. No. 2,4e-06;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRMRMKKTALD 21  
DB 1 RQIKWIFQNRMRMKKELXD 20

RESULT 3  
US-09-040-725A-2  
Sequence 2, Application US/09040725A  
Patent No. 6399584  
GENERAL INFORMATION:  
APPLICANT: Institut Curie  
APPLICANT: CNRS  
APPLICANT: Arpin, Monique  
APPLICANT: Crepaldi, Tiziana  
APPLICANT: Gautreau, Alexis  
APPLICANT: Louvard, Daniel  
TITLE OF INVENTION: Pharmaceutical composition containing ezrin mutated  
TITLE OF INVENTION: on tyrosine 353  
FILE REFERENCE: 39108200100  
CURRENT APPLICATION NUMBER: US/09/040.725A  
CURRENT FILING DATE: 1998-03-18  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 2  
LENGTH: 27  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: variation  
LOCATION: (22)  
OTHER INFORMATION: Xaa = tyrosine or a phosphorylated tyrosine  
US-09-040-725A-2

Query Match 58.0%; Score 94; DB 4; Length 27;  
Best Local Similarity 89.5%; Pred. No. 3,6e-06;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RQIKWIFQNRMRMKKTAL 20  
DB 1 RQIKWIFQNRMRMKKRL 19

RESULT 4  
US-08-202-044-3  
Sequence 3, Application US/08202044  
Patent No. 5858973  
GENERAL INFORMATION:  
APPLICANT: Habener M.D., Joel F.  
APPLICANT: Miller Ph.D., Christopher P.  
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes  
STREET: Ten Post Office Square

CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,044  
FILING DATE: 23-FEB-1994  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Ph.D., Kathleen A.  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: MGH-124XX  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-2290  
TELEFAX: (617) 451-0313  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
US-08-202-044-3

Query Match 58.0%; Score 94; DB 2; Length 61;  
Best Local Similarity 94.1%; Pred. No. 8,4e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKWIFQNRMRMKK 17  
DB 43 EROIKWIFQNRMRMKK 59

RESULT 5  
US-08-751-344B-3  
Sequence 3, Application US/08751344B  
Patent No. 6210960  
GENERAL INFORMATION:  
APPLICANT: Habener M.D., Joel F.  
APPLICANT: Miller Ph.D., Christopher P.  
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Ltd.  
STREET: One Financial Center  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/751,344B  
FILING DATE: 19-NOV-6210960-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/202,044  
FILING DATE: 23-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Ph.D., Kathleen M.  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)  
TELECOMMUNICATION INFORMATION:



TELEPHONE: (617) 345-9100  
TELEFAX: (617) 345-9111  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
US-08-751-344B-3

Query Match 58.0%; Score 94; DB 3; Length 61;  
Best Local Similarity 94.1%; Pred. No. 8.4e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKIWFQNRKMKKK 17  
:|||||  
DB 43 ERQIKIWFQNRKMKKK 59

RESULT 6  
US-08-751-344B-6  
Sequence 6, Application US/08751344B  
Patent No. 6210960  
GENERAL INFORMATION:  
APPLICANT: Habener M.D., Joel F.  
APPLICANT: Miller Ph.D., Christopher P.  
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES  
TITLE OF INVENTION: THEREFOR  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Ltd.  
STREET: One Financial Center  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/751,344B  
FILING DATE: 19-No. 6210960-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/202,044  
FILING DATE: 23-Feb-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Ph.D., Kathleen M.  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 345-9100  
TELEFAX: (617) 345-9111  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
US-08-751-344B-6

Query Match 58.0%; Score 94; DB 3; Length 61;  
Best Local Similarity 94.1%; Pred. No. 8.4e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRQIKIWFQNRKMKKK 17

DB 43 ERQIKIWFQNRKMKKK 59  
:|||||

RESULT 7  
US-08-751-344B-9  
Sequence 9, Application US/08751344B  
Patent No. 6210960  
GENERAL INFORMATION:  
APPLICANT: Habener M.D., Joel F.  
APPLICANT: Miller Ph.D., Christopher P.  
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES  
TITLE OF INVENTION: THEREFOR  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Ltd.  
STREET: One Financial Center  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/751,344B  
FILING DATE: 19-No. 6210960-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/202,044  
FILING DATE: 23-Feb-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Ph.D., Kathleen M.  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 345-9100  
TELEFAX: (617) 345-9111  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
US-08-751-344B-9

Query Match 58.0%; Score 94; DB 3; Length 61;  
Best Local Similarity 94.1%; Pred. No. 8.4e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKIWFQNRKMKKK 17  
:|||||  
DB 43 ERQIKIWFQNRKMKKK 59

RESULT 8  
US-09-057-363C-50  
Sequence 50, Application US/09057363C  
Patent No. 6551994  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
Gour, Barbara J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE  
INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed Intellectual Property Law Group  
STREET: 701 Fifth Avenue, Suite 6300  
CITY: Seattle

```
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,363C
FILING DATE: 08-Apr-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Christensen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 100086,406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-057-363C-50

Query Match          57.4%; Score 93; DB 3; Length 22;
Best Local Similarity 94.1%; Pred. No. 3,9e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFONRKMKKK 17
Db 6 NRQIKWFONRKMKKK 22

RESULT 9
US-09-051-934-51
Sequence 51, Application US/09051934C
Patent No. 6028053
GENERAL INFORMATION:
APPLICANT: Van der Geer
TITLE OF INVENTION: Peptide Inhibitors of a Phosphotyrosine-Binding Domain
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/051,934C
CURRENT FILING DATE: 1998-04-22
EARLIER APPLICATION NUMBER: 60/011,799
EARLIER FILING DATE: 1996-02-20
EARLIER APPLICATION NUMBER: 60/010,384
EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 60/005,944
EARLIER FILING DATE: 1995-10-27
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51
LENGTH: 27
TYPE: PRT
ORGANISM: phosphotyrosine binding domain
US-09-051-934-51

Query Match          57.4%; Score 93; DB 3; Length 27;
Best Local Similarity 80.0%; Pred. No. 4,9e-06;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ROIKIWFQNRKMKKKTALD 21
Db 1 ROIKIWFQNRKMKKKTALD 20

RESULT 10
US-09-051-934-52
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Sequence 52, Application US/09051934C
Patent No. 6028053
GENERAL INFORMATION:
APPLICANT: Van der Geer
TITLE OF INVENTION: Peptide Inhibitors of a Phosphotyrosine-Binding Domain
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/051,934C
CURRENT FILING DATE: 1998-04-22
EARLIER APPLICATION NUMBER: 60/011,799
EARLIER FILING DATE: 1996-02-20
EARLIER APPLICATION NUMBER: 60/010,384
EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 60/005,944
EARLIER FILING DATE: 1995-10-27
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 52
LENGTH: 27
TYPE: PRT
ORGANISM: phosphotyrosine binding domain
FEATURE:
NAME/KEY: MOD RES
LOCATION: (24)
OTHER INFORMATION: Phosphorylated at Tyr
US-09-051-934-52

Query Match          57.4%; Score 93; DB 3; Length 27;
Best Local Similarity 80.0%; Pred. No. 4,9e-06;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ROIKIWFQNRKMKKKTALD 21
Db 1 ROIKIWFQNRKMKKKTALD 20

RESULT 11
US-08-751-344B-7
Sequence 7, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-NOV-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
```

LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
US-08-751-344B-7

Query Match 57.4%; Score 93; DB 3; Length 61;  
Best Local Similarity 88.2%; Pred. No. 1.1e-05;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ROIKIWFORRRMKKK 17  
DB 43 ERQVKIWFORRRMKKK 59

## RESULT 12

US-08-928-958-7  
Sequence 7, Application US/08928958  
Patent No. 5877282  
GENERAL INFORMATION:  
APPLICANT: NADLER, STEVEN G.  
APPLICANT: CLEVELAND, JEFFREY S.  
APPLICANT: BLAKE, JAMES  
APPLICANT: HAFER, OWAR K.  
TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN  
TITLE OF INVENTION: TRANSLLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND  
TITLE OF INVENTION: METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROBINS & ASSOCIATES  
STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
CITY: MENLO PARK  
STATE: CA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/928,958  
FILING DATE: 12-SEP-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026978  
FILING DATE: 20-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: ROBINS, ROBERTA L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5998-0019  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 345-7812  
TELEFAX: (650) 325-7823  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-928-958-7

Query Match 56.8%; Score 92; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ROIKIWFORRRMKKK 17  
DB 1 ROIKIWFORRRMKKK 16

## RESULT 13

US-08-810-540-3  
Sequence 3, Application US/08810540  
Patent No. 5929042  
GENERAL INFORMATION:  
APPLICANT: TROY, Carol M.  
APPLICANT: Shelanski, Michael L.  
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL  
TITLE OF INVENTION: DEATH AND USES THEREOF  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham, LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/810,540  
FILING DATE: 03-MAR-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq., John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/51247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0526  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-810-540-3

Query Match 56.8%; Score 92; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ROIKIWFORRRMKKK 17  
DB 1 ROIKIWFORRRMKKK 16

## RESULT 14

US-08-810-540-6  
Sequence 6, Application US/08810540  
Patent No. 5929042  
GENERAL INFORMATION:  
APPLICANT: TROY, Carol M.  
APPLICANT: Shelanski, Michael L.  
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL  
TITLE OF INVENTION: DEATH AND USES THEREOF  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham, LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/810,540  
FILING DATE: 03-MAR-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq., John P.  
REGISTRATION NUMBER: 28,678  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0526  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-810-540-6

Query Match 56.8%; Score 92; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RQIKWFOQRNRMKWK 17  
DB 1 RQIKWFOQRNRMKWK 16

RESULT 15  
US-09-072-429-7  
Sequence 7, Application US/09072429  
Patent No. 5962415  
GENERAL INFORMATION:  
APPLICANT: Nadler, Steven G.  
TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE  
TITLE OF INVENTION: INHIBITOR OF NUCLEAR PROTEIN TRANSLOCATION AND AN  
TITLE OF INVENTION: IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bristol-Myers Squibb Company  
STREET: P.O. Box 4000  
CITY: Princeton  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 08543-4000  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/072,429  
FILING DATE: 04-MAY-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Klein, Christopher A.  
REGISTRATION NUMBER: 34,363  
REFERENCE/DOCKET NUMBER: C00141b  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 252-3714  
TELEFAX: (609) 252-4526  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-072-429-7

Query Match 56.8%; Score 92; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RQIKWFOQRNRMKWK 17  
DB 1 RQIKWFOQRNRMKWK 16

Search completed: February 18, 2004, 14:41:52  
Job time : 33.9737 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds

(without alignments)  
41.814 Million cell updates/sec

Title: US-09-643-260-17

Perfect score: 41

Sequence: 1 LDWEVL 6

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	6	23	ABB08739
2	41	100.0	6	23	AAW48522
3	41	100.0	6	23	AAW48542
4	41	100.0	6	23	AAW48614
5	41	100.0	6	24	ABU08432
6	41	100.0	7	23	AAW48618
7	41	100.0	8	23	AAW48611
8	41	100.0	8	23	AAW48619
9	41	100.0	9	23	AAW48610

10	41	100.0	9	23	AAW48613	Anti-inflammatory
11	41	100.0	9	23	AAW48616	Anti-inflammatory
12	41	100.0	9	23	AAW48617	Anti-inflammatory
13	41	100.0	10	23	AAW48612	Anti-inflammatory
14	41	100.0	10	23	AAW48615	Anti-inflammatory
15	41	100.0	11	23	AAW48609	Anti-inflammatory
16	41	100.0	11	23	ABW77307	Human IKKbeta
17	38	92.7	12	21	AAW48529	Human IKKbeta
18	38	92.7	12	21	AAW48529	Human IKKbeta
19	37	90.2	24	23	AAW48529	Human IKKbeta
20	37	90.2	24	23	AAW48529	Human IKKbeta
21	37	90.2	24	23	AAW48529	Human IKKbeta
22	37	90.2	24	23	AAW48529	Human IKKbeta
23	37	90.2	24	23	AAW48529	Human IKKbeta
24	37	90.2	24	23	AAW48529	Human IKKbeta
25	37	90.2	24	23	AAW48529	Human IKKbeta
26	37	90.2	24	23	AAW48529	Human IKKbeta
27	37	90.2	24	23	AAW48529	Human IKKbeta
28	37	90.2	24	23	AAW48529	Human IKKbeta
29	37	90.2	24	23	AAW48529	Human IKKbeta
30	37	90.2	24	23	AAW48529	Human IKKbeta
31	37	90.2	24	23	AAW48529	Human IKKbeta
32	37	90.2	24	23	AAW48529	Human IKKbeta
33	37	90.2	24	23	AAW48529	Human IKKbeta
34	37	90.2	24	23	AAW48529	Human IKKbeta
35	37	90.2	24	23	AAW48529	Human IKKbeta
36	37	90.2	24	23	AAW48529	Human IKKbeta
37	37	90.2	24	23	AAW48529	Human IKKbeta
38	37	90.2	24	23	AAW48529	Human IKKbeta
39	37	90.2	24	23	AAW48529	Human IKKbeta
40	37	90.2	24	23	AAW48529	Human IKKbeta
41	37	90.2	24	23	AAW48529	Human IKKbeta
42	37	90.2	24	23	AAW48529	Human IKKbeta
43	37	90.2	24	23	AAW48529	Human IKKbeta
44	37	90.2	24	23	AAW48529	Human IKKbeta
45	37	90.2	24	23	AAW48529	Human IKKbeta

#### ALIGNMENTS

RESULT 1	ABB08739	standard; peptide; 6 AA.
ID	ABB08739	
AC	ABB08739	
XX	14-JUN-2002	(first entry)
DE	Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 17.	
XX	IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;	
XX	kinase activation; leukocyte; inflammation; B-selectin; osteoclast;	
XX	autoimmune disease; transplant rejection; osteoporosis; cancer;	
XX	Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;	
XX	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;	
XX	corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;	
XX	osteopathic; cyclostatic; nootropic; neuroprotective; anti-HIV; human;	
XX	antiartherosclerotic; virostatic; antiparasitic; antiallergic;	
XX	dermatological; antibacterial; antipneumatic; antirheumatic;	
XX	antiarthritic; osteopathic; antitumor; mutant; mutagen.	
OS	Homo sapiens.	
OS	Synthetic.	
XX	Key	Location/Qualifiers
XX	Misc-difference 4	/note= "Wildtype Ser substituted by Glu"
XX	MO200183547-A2.	
XX	08-NOV-2001.	

PF 02-MAY-2001; 2001WO-US40654.  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (UYTA ) UNITV YALE.  
 PI May MJ, Ghosh S;  
 XX  
 DR WPI; 2002-179350/23.  
 XX  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprising contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 XX  
 PS Claim 23; Page 45; 82pp; English.  
 XX  
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprising contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB077313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of Ikbppa. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC polyarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC spondylarthritis, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
 CC binding domain of IKKbeta.  
 XX  
 SQ Sequence 6 AA;  
 QY 1 LDWEML 6  
 DB 1 LDWEML 6  
 Query Match 100.0%; Score 41; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 2  
 AAM48522  
 ID AAM48522 standard; Peptide; 6 AA.  
 XX  
 AC AAM48522;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DB NBD mutant peptide SEQ ID NO 17.

XX  
 KM Antiinflammatory; antiaesthetic; cytostatic; antipsoriatic; nootropic;  
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; vitruclide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; Ikbppa kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECTIS PHARM INC.  
 PA (UYTA ) UNITV YALE.  
 XX  
 PI May MJ, Ghosh S, Fandels MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Example 6; Page 48; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48620-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, vitruclide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of Ikbppa kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of Ikbppa. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 6 AA;  
 QY 1 LDWEML 6  
 DB 1 LDWEML 6  
 Query Match 100.0%; Score 41; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 3  
 AAM48542  
 ID AAM48542 standard; Peptide; 6 AA.

AC	AAM486542;
XX	
DT	20-MAR-2002 (first entry)
XX	
DE	Anti-inflammatory peptide SEQ ID NO 45.
XX	
KM	Antiinflammatory; antiasthmatic; cycostatic; antiportiatric; nootropic;
KM	antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KM	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KM	antiangiogenic; membrane translocation domain; NEMO binding domain; eczema;
KM	cyclokinic; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;
KM	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KM	autoimmune disorder; multiple sclerosis; transplant rejection;
KM	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KM	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX	
OS	Synthetic.
PN	WO200183554-A2.
XX	
PD	08-NOV-2001.
XX	
PF	02-MAY-2001; 2001WO-US14346.
XX	
PR	02-MAY-2000; 2000US-201261P.
XX	
PR	22-AUG-2000; 2000US-0643260.
XX	
PA	(PRAE-) PRAECIS PHARM INC.
XX	
PA	(UYVA ) UNIV YALE.
XX	
PI	May MJ, Ghosh S, Findeis MA, Phillips K;
DR	WPI; 2002-121889/16.
XX	
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis -
XX	
PS	Claim 6; Page 61; 88pp; English.
CC	The invention relates to an antiinflammatory compound (especially
CC	AAM48628-AAM48645), comprising a membrane translocation domain
CC	(AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AAM48625-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC	cycostatic, antiportiatric, antirheumatic, antiarthritic, osteopathic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	nootropic, antiatherosclerotic, virucide and antiallergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of Ikappab kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of Ikappab. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC	granulomatous, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	prio-inflamatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
SO	Sequence 6 AA:
Query Match	100.0%; Score 41; DB 23; Length 6;
Best Local Similarity	100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
1 LDMEWL 6	

D0 Db  
LDMWTL 6

RESULT 4  
ID AAM48614  
AAM48614 standard; Peptide; 6 AA.  
XX XX  
AC AAM48614;  
XX XX  
DT 20-MAR-2002 (first entry)  
XX XX  
DE Anti-inflammatory peptide SEQ ID NO 117.

Anit-inflammatorty; antiasthmatic; cytostatic; antipsoiatric; noctropic;  
antirheumatic; antiarthritis; osteopathic; antibacterial; virutide;  
immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
anti allergic; membrane translocation domain; NEMO binding domain; eczema  
cytokine; NKkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;  
rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
autoimmune disorder; multiple sclerosis; transplant rejection;  
osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
ataxia telangiectasia; allergy; anaphylaxis; arthritis.

Synthetic.  
XX OS  
XX W0200183554-A2.  
XX PN  
XX 08-NOV-2001.  
XX PD  
PF 02-MAY-2001; 2001MO-US14346.  
XX PP  
PR 02-MAY-2000; 2000US-201261P.  
PP PR 22-AUG-2000; 2000US-0643260.  
XX XX  
PA (PRAE-) PRAECIS PHARM INC.  
PA (UYTA ) UNIV YALE.  
XX PA  
May MJ, Ghosh S, Findeis MA, Phillips K,  
DR WPJ; 2002-121889/16.  
XX DR

Novel antiinflammatory compound comprising membrane translocation  
domain fused to NEMO binding sequence, useful for blocking nuclear  
factor kappaB activation, and for treating asthma, lung inflammation,  
PT PT psoriasis .  
PT PT

Claim 6; Page 62; 88pp; English.

The invention relates to an antiinflammatory compound (especially  
CC CC AAM48628-AA48645), comprising a membrane translocation domain  
CC CC AAM48620-AA48627 or AAM48646-AA48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC CC (AAM48528-AA48619). The antiinflammatory compounds have antiasthmatic,  
CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osepachic,  
CC antibacterial, immunosuppressive, dermatologicl, neuroprotective, The  
CC nootropic, antiatherosclerotic, vitrucide and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
activation by blocking interaction of Ikappab kinase beta (IKKbeta) at  
the NEMO binding domain that results in inhibition of IKKbeta kinase  
activation and subsequent decreased phosphorylation of Ikapap. The  
CC compounds are useful for creating inflammatory disorders, e.g. asthma,  
lung inflammation or cancer, psoriasis, rheumatoicl arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC burstitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis, transplant rejection, osteoporosis;  
Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
telanglectasia. The compounds are also useful for treating  
pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
dring or food sensitivity, eczema, dermatitis, sunburn, aging and  
arthritis.

Sequence 6 AA;

XX XX  
XX Sequence 6 AA;

Query Match 100.0%; Score 41; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDWEML 6  
 |||||  
 Db 1 LDWEML 6

RESULT 5  
 AB008432  
 ID AB008432 standard; peptide: 6 AA.

XX AC AB008432;  
 XX DT 12-JUN-2003 (first entry)  
 XX DE Human NEMO binding site (NBD) mutant peptide #15.

XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;  
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;  
 KW nuclear factor-kappaB induction; inflammatory disorder;  
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;  
 KW atherosclerosis; viral infection; Ataxia telangiectasia;  
 KW translocation detection; immunosuppressive; osteopathic;  
 KW cyostatic; neutrotropic; antiatherosclerotic; virucide;  
 KW vasotrophic; antirheumatic; antiarthritic; mutant; mutcin.

XX OS Homo sapiens.  
 XX OS Synthetic.

XX PN US200215600-A1.

XX PD 24-OCT-2002.

XX PF 02-MAY-2001; 2001US-0847940.

XX PR 02-MAY-2000; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

XX PA (MAYM/) MAY M J.

XX PA (GHOSH/) GHOSH S.

XX PI May MJ, Ghosh S;

XX DR WPI; 2003-209142/20.

XX PT Novel antiinflammatory peptide compounds comprising NEMO binding  
 PT domain, useful for modulating NF-kappaB induction in a cell and for  
 PT creating NF-kappaB-mediated inflammation disorders e.g., asthma,  
 PT psoriasis, vasculitis -

XX PS Claim 22; Page 17; 47pp; English.

XX CC The present invention relates to antiinflammatory compounds comprising  
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are  
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha  
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention  
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction  
 CC in a cell, where the compounds are capable of blocking the interaction  
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The  
 CC antiinflammatory compound further comprises at least one membrane  
 CC translocation domain. The compounds are useful for treating  
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia  
 CC telangiectasia, and for translocation detection. The compounds of  
 CC the invention block NF-kappaB induction by IKK but do not inhibit  
 CC the basal activity of NF-kappaB. AB008418-AB008432 represent human  
 CC NBD mutant peptides.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 41; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDWEML 6  
 |||||  
 Db 1 LDWEML 6

RESULT 6  
 AAM48618  
 ID AAM48618 standard; peptide: 7 AA.

XX AC AAM48618;

XX DT 20-MAR-2002 (first entry)

XX DE Anti-inflammatory peptide SEQ ID NO 121.

XX KW Antiinflammatory; antiaesthetic; cyostatic; antiproliferic; neutrotropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neutrotrophic; antiatherosclerotic;  
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.

XX PN WO200183554-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US14346.

XX PR 02-MAY-2000; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

XX PA (PRAE-) PRAEIS PHARM INC.

XX PA (UYVA) UYVA VAL.

XX PI May MJ, Ghosh S, Finkelstein MA, Phillips K;

XX DR WPI; 2002-121889/16.

XX PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for creating asthma, lung inflammation,  
 PT psoriasis -

XX PS Claim 6; Page 62; 88pp; English.

XX CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48618-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
 CC cyostatic, antiproliferic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC neutrotropic, antiatherosclerotic, virucide and anti-allergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, uterine, anaphylaxis,



CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 100.0%; Score 41; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDWEML 6  
 Db 1 LDWEML 6  
 RESULT 7  
 ID AAM48611 standard; Peptide; 8 AA.  
 XX AAM48611;  
 AC  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 114.  
 KM Anti-inflammatory; antiaesthetic; cytosolic; antiproliferative; nootropic;  
 KM antithrombotic; antiallergic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX WO200183554-A2.  
 PN  
 XX 08-NOV-2001.  
 PD  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findels MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 DR  
 XX  
 XX Novel anti-inflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 PT  
 XX  
 XX Claim 6; Page 62; 88pp; English.  
 PS  
 XX The invention relates to an anti-inflammatory compound (especially  
 CC AAM48628-AAM48651), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiaesthetic,  
 CC cytosolic, antiproliferative, antineuritic, antiallergic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC burns; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 41; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDWEML 6  
 Db 3 LDWEML 8  
 RESULT 8  
 ID AAM48619 standard; Peptide; 8 AA.  
 XX AAM48619;  
 AC  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 122.  
 KM Anti-inflammatory; antiaesthetic; cytosolic; antiproliferative; nootropic;  
 KM antithrombotic; antiallergic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX WO200183554-A2.  
 PN  
 XX 08-NOV-2001.  
 PD  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findels MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 DR  
 XX  
 XX Novel anti-inflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 PT  
 XX  
 XX Claim 6; Page 62; 88pp; English.  
 PS  
 XX The invention relates to an anti-inflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiaesthetic,  
 CC cytosolic, antiproliferative, antineuritic, antiallergic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated Nf-kappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 41; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. NO. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDWEWL 6  
 DB 1 LDWEWL 6  
 RESULT 9  
 ID AAM48610 standard; Peptide; 9 AA.  
 XX AAM48610;  
 AC  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 113.  
 XX  
 KW Antinflammatory; antiasthmatic; cytosolic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virocidic;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; Nf-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 KW  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Flindels MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48658-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytosolic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virocidic and anti-allergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated Nf-kappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 SQ Sequence 9 AA;  
 Query Match 100.0%; Score 41; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. NO. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDWEWL 6  
 DB 1 LDWEWL 6  
 RESULT 10  
 ID AAM48613 standard; Peptide; 9 AA.  
 XX AAM48613;  
 AC  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 116.  
 XX  
 KW Antinflammatory; antiasthmatic; cytosolic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virocidic;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; Nf-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 KW  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Flindels MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis



PR 22-AUG-2000; 2000US-0643260.  
 XX (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
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 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 XX  
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 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 PT  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cycostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
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 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
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 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 SQ Sequence 9 AA;  
 QY  
 Query Match 100.0%; Score 41; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. NO. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 LDWEML 6  
 2 LDWEML 7  
 RESULT 13  
 AAM48612  
 ID AAM48612 standard; Peptide; 10 AA.  
 XX  
 AC AAM48612;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 115.  
 XX  
 KW Antiinflammatory; antiasthmatic; cycostatic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 KW  
 OS Synthetic.  
 XX  
 XX  
 PN WO200183554-A2.

XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 PT  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
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 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cycostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
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 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
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 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 SQ Sequence 10 AA;  
 QY  
 Query Match 100.0%; Score 41; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. NO. 4.4;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 LDWEML 6  
 2 LDWEML 7  
 RESULT 14  
 AAM48615  
 ID AAM48615 standard; Peptide; 10 AA.  
 XX  
 AC AAM48615;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 118.  
 XX  
 KW Antiinflammatory; antiasthmatic; cycostatic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;

KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX Synthetic.  
OS  
XX WO200183554-A2.  
PN  
XX 08-NOV-2001.  
PD  
XX  
PF 02-MAY-2001; 2001WO-US14346.  
XX  
XX 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
XX  
XX (PRAE-) PRACIS PHARM INC.  
PA (UYVA ) UNIV YALE.  
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XX May MJ, Ghosh S, Findels MA, Phillips K;  
PI  
XX WPI; 2002-121889/16.  
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PT factor kappaB activation, and for treating asthma, lung inflammation,  
XX psoriasis  
XX  
PS Claim 6; Page 62; 88pp; English.  
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CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
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CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
CC  
SQ Sequence 10 AA;  
Query Match 100.0%; Score 41; DB 23; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.4;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMEWL 6  
| | | | |  
| | | | |  
DB 3 LDMEWL 8  
| | | | |  
| | | | |  
RESULT 15  
AAM48609  
ID AAM48609 standard; Peptide; 11 AA.  
XX  
XX AAM48609;  
AC  
XX  
XX 20-MAR-2002 (first entry)  
DT  
XX Anti-inflammatory peptide SEQ ID NO 112.  
DE  
XX  
XX Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;  
KM

KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KM autoimmune disorder; multiple sclerosis; transplant rejection;  
KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX Synthetic.  
OS  
XX WO200183554-A2.  
PN  
XX 08-NOV-2001.  
PD  
XX  
PF 02-MAY-2001; 2001WO-US14346.  
XX  
XX 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
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XX May MJ, Ghosh S, Findels MA, Phillips K;  
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XX WPI; 2002-121889/16.  
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CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
CC  
SQ Sequence 11 AA;  
Query Match 100.0%; Score 41; DB 23; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.9;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMEWL 6  
| | | | |  
| | | | |  
DB 3 LDMEWL 8  
| | | | |  
| | | | |

Search completed: February 18, 2004, 14:26:26  
Job time : 22.7763 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds  
(without alignments)  
89.145 Million cell updates/sec

Title: US-09-643-260-16  
Sequence: 1 LDMAML 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	173	16	Q8E5U2
2	40	100.0	173	16	Q8E5U2
3	40	100.0	173	16	Q8E5U2
4	38	95.0	645	2	Q9X6C6
5	37	92.5	740	6	Q9X6C6
6	37	92.5	745	11	Q8CBT3
7	37	92.5	756	6	Q9SKV0
8	36	90.0	27	12	Q9GRU7
9	36	90.0	207	5	Q9GZU3
10	36	90.0	215	17	Q9V227
11	36	90.0	251	16	Q07806
12	36	90.0	304	16	Q91719
13	36	90.0	316	16	Q8UBG8
14	36	90.0	444	2	Q9XBD4
15	36	90.0	516	10	Q42701
16	36	90.0	516	10	Q42701

17	36	90.0	524	10	Q42700	Q42700 catharanthu
18	36	90.0	544	10	Q9FEB1	Q9FEB1 oryza sativ
19	36	90.0	1083	13	Q90W08	Q90W08 oncorhynch
20	36	90.0	1083	13	Q8AXU2	Q8AXU2 oncorhynch
21	36	90.0	1100	13	Q90W09	Q90W09 oncorhynch
22	36	90.0	1127	13	Q9W615	Q9W615 oryza sat
23	36	90.0	1212	16	Q9HX70	Q9HX70 pseudomonas
24	36	90.0	1575	2	P94904	P94904 lyobacter
25	35	87.5	162	16	Q53756	Q53756 mycobacter
26	35	87.5	204	16	Q9KER2	Q9KER2 bacillus ha
27	35	87.5	282	16	Q8D354	Q8D354 wigglewort
28	35	87.5	288	2	Q8VTT4	Q8VTT4 pseudomonas
29	35	87.5	299	16	Q9H218	Q9H218 pseudomonas
30	35	87.5	308	2	Q8KZS2	Q8KZS2 acetobacter
31	35	87.5	311	16	Q92WU7	Q92WU7 rhizobium m
32	35	87.5	313	2	Q8VU06	Q8VU06 pseudomonas
33	35	87.5	318	16	Q8ZC58	Q8ZC58 yersinia pe
34	35	87.5	329	16	Q8XVB4	Q8XVB4 ralsonia s
35	35	87.5	331	16	P94904	P94904 lyobacter
36	35	87.5	337	16	Q8UB44	Q8UB44 agrobacteri
37	35	87.5	341	16	Q8YEH7	Q8YEH7 bruceella su
38	35	87.5	344	16	Q8YEH7	Q8YEH7 bruceella me
39	35	87.5	353	16	Q9A7F0	Q9A7F0 calubacter
40	35	87.5	386	16	Q92U27	Q92U27 rhizobium m
41	35	87.5	393	16	Q87ZL1	Q87ZL1 rhizobium l
42	35	87.5	394	10	Q9M0Y4	Q9M0Y4 arabidopsis
43	35	87.5	418	10	Q944N8	Q944N8 arabidopsis
44	35	87.5	418	10	Q9M0Y3	Q9M0Y3 arabidopsis
45	35	87.5	439	2	Q93Q61	Q93Q61 klebsiella

## ALIGNMENTS

RESULT 1	Q8E5U2	PRELIMINARY	PRT	173 AA
AC	Q8E5U2	01-MAR-2003 (TRENBLREL. 23, Created)		
DT	01-MAR-2003 (TRENBLREL. 23, Last sequence update)			
DT	01-MAR-2003 (TRENBLREL. 23, Last annotation update)			
DE	Hypothetical protein.			
GN	GBS0887.			
OS	Streptococcus agalactiae (serotype III).			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
OX	NCBI_TaxID=216495;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NEW316 / Serotype III;			
RX	MEDLINE=22242508; PubMed=12354221;			
RA	Glaser P., Ruenlokk C., Buchrieser C., Chevalier F., Frangeul L.,			
RA	Madek T., Zouine M., Couve E., Lallou L., Poyart C., Tieu-Cuc P.,			
RA	Kunet P.,			
RT	"Genome sequence of Streptococcus agalactiae, a pathogen causing			
RT	invasive neonatal disease."			
RL	Mol. Microbiol. 45:1499-1513 (2002).			
DR	EMBL; AL766847; CAD46531.1; -			
KW	Sagaliat; gba0887; -			
SO	Hypothetical protein; Complete proteome.			
SO	SEQUENCE 173 AA; 20135 MW; F5F3404F0224CD1 CRC64;			
QY	Query Match	100.0%; Score 40; DB 16; Length 173;		
DB	Best Local Similarity	100.0%; Pred. No. 48;		
	Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
	1 LDMAML 6			
	125 LDMAML 130			
RESULT 2	Q8E065			

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ID Q9E065 PRELIMINARY; PRT; 173 AA.
AC Q9E065;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Acetyltransferase, GNAI family.
GN SAG0870.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCB1_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RC MEDLINE=22222988; PubMed=12200547;
RA Tetteijn H., Maingant I.V., Cieslewicz M.J., Bisen J.A., Peterson S.,
RA Wessels M.R., Pulgen I.T., Nelson K.E., Margalit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beaman M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carey H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Jacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaldo D., Rapunoli R., Telford J.L., Kaaper D.L., Grandi G.,
RA Frazer C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae."
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AE014231; AAM9756.1; -.
DR TIGR; SAG0870; -.
KW Transferrase; Complete proteome.
SQ SEQUENCE 173 AA; 20135 MW; 0081677125975921 CRC64;

Query Match 100.0%; Score 40; DB 16; Length 173;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6
Db 125 LDMAML 130

RESULT 3
Q9X6C6 PRELIMINARY; PRT; 645 AA.
AC Q9X6C6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Beta-galactosidase.
GN BGAT.
OS Thermus brockianus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCB1_TaxID=56956;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IT1360;
RC MEDLINE=99402735; PubMed=10473401;
RA Fridlonsen O., Matzlawick H., Gehweiler A., Rohrhirsch T., Mattes R.;
RT "Cloning of the gene encoding a novel thermostable alpha-galactosidase
RT from Thermus brockianus IT1360."
RL Appl. Environ. Microbiol. 65:3955-3963(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IT1360;
RC MEDLINE=20203878; PubMed=10741834;
RA Fridlonsen O., Matzlawick H., Mattes R.;
RT "The structure of the alpha-galactosidase gene loci in Thermus
RT brockianus IT1360 and Thermus thermophilus TH125."
RL Extremophiles 4:23-33(2000).
DR EMBL; AF135398; AAD33667.1; -.
DR InterPro; IPR001554; Glyco_hydro_14.
DR InterPro; IPR003476; Glyco_hydro_42.

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DR Pfam; PF01373; Glyco_hydro_14; 1.
DR Pfam; PF02449; Glyco_hydro_42; 1.
SQ SEQUENCE 645 AA; 73420 MW; C79A9BIC0020BC40 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 645;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6
Db 48 LDMAML 53

RESULT 4
Q96XZ8 PRELIMINARY; PRT; 396 AA.
AC Q96XZ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative anaerobic glycerol-3-phosphate dehydrogenase subunit C.
GN S72369.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCB1_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RC PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Anka A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kuchida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7."
RL DNA Res. 8:123-140(2001).
DR EMBL; AP000989; BAB67479.1; -.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR004017; DUF224.
DR Pfam; PF02754; DUF224; 2.
DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 396 AA; 45359 MW; 15301A2AF2D0C9F CRC64;

Query Match 95.0%; Score 38; DB 17; Length 396;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6
Db 94 LDMAML 99

RESULT 5
Q95KV1 PRELIMINARY; PRT; 740 AA.
AC Q95KV1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ikb kinase-alpha.
GN BIKKALPHA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCB1_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
DR Rottenberg S., Dobbelaere D.A.E., Heusler V.T.;

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RT "Identification and characterisation of the bovine IKB kinases (IKKs)
RT alpha, beta and gamma."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ414555; CAC93686.1; -.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO0220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
KW SEQUENCE 740 AA; 84343 MW; 01903BE1F44D176 CRC64;

Query Match
Best Local Similarity 92.5%; Score 37; DB 6; Length 740;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMAML 6
Db 733 LDMAML 738

RESULT 6
Q8CBT3 PRELIMINARY; PRT; 745 AA.
ID Q8CBT3;
AC Q8CBT3;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DS Conserved helix-loop-helix ubiquitous kinase.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=urinary bladder;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK035326; BAC29034.1; -.
SQ SEQUENCE 745 AA; 84770 MW; 48C9E01C17A61184 CRC64;

Query Match
Best Local Similarity 92.5%; Score 37; DB 11; Length 745;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMAML 6
Db 738 LDMAML 743

RESULT 7
Q9SKV0 PRELIMINARY; PRT; 756 AA.
ID Q9SKV0;
AC Q9SKV0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DS IKB kinase-beta.
GN BIKKBEA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN [1]

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RP SEQUENCE FROM N.A.
RA Rottenberg S.; Dobbelaere D.A.E.; Heusler V.T.;
RT "Identification and characterisation of the bovine IKB kinases (IKKs)
RT alpha, beta and gamma."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ414556; CAC93687.1; -.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
KW SEQUENCE 756 AA; 86647 MW; A072D15614A176E5 CRC64;

Query Match
Best Local Similarity 92.5%; Score 37; DB 6; Length 756;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMAML 6
Db 737 LDMAML 742

RESULT 8
Q9QRU7 PRELIMINARY; PRT; 27 AA.
ID Q9QRU7;
AC Q9QRU7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DS E2 glycoprotein hypervariable region (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxId=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B-AS;
RA Yeh C.-T.;
RT "Replication of hepatitis C virus in the acetic mononuclear cells and
RT development of distinct quasispecies in the acetic fluid."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF109742; AAD51573.1; -.
DR FT NON_TER 1
DR FT NON_TER 1
SQ SEQUENCE 27 AA; 2964 MW; 8A68DCDC25CE4FAB CRC64;

Query Match
Best Local Similarity 90.0%; Score 36; DB 12; Length 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMAML 6
Db 12 DMAML 16

RESULT 9
Q9QRU6 PRELIMINARY; PRT; 27 AA.
ID Q9QRU6;
AC Q9QRU6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DS E2 glycoprotein hypervariable region (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxId=11103;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=MO;
RA Yeh C.-T.;
RT "Replication of hepatitis C virus in the ascitic mononuclear cells and
RL development of distinct quasispecies in the ascitic fluid.";
DR EMBL: A0109743; AAD51574.1; -.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2964 MW; 8A68DCDC25CE4FAB CRC64;

Query Match          90.0%; Score 36; DB 12; Length 27;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWAML 6
Db 12 DWAML 16

RESULT 10
Q962U3 PRELIMINARY; PRT; 207 AA.
ID Q962U3;
AC Q962U3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cchapsin B-like protease (Fragment).
OS Trypanosoma rangeli.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
CX NCBI_TaxID=5698;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SC 58;
RA Nobrega O.T., Teixeira A.R.L., Campbell D.A., Santana J.M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF400046; AAK65411.1; -.
DR MEROPS; C01.098; -.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR00169; SHPOT_acs1c.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept_C1; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
KM Hydrolyase; Protease; Thiol protease.
FT NON_TER 1
FT NON_TER 207
SQ SEQUENCE 207 AA; 22968 MW; 7AF0D95D5F81C5B CRC64;

Query Match          90.0%; Score 36; DB 5; Length 207;
Best Local Similarity 100.0%; Pred. No. 2,3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWAML 6
Db 71 DWAML 75

RESULT 11
Q9V227 PRELIMINARY; PRT; 215 AA.
ID Q9V227;
AC Q9V227;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Purine phosphoribosyltransferase.
GN GPTA OR PAB2405.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
CX NCBI_TaxID=29292;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GES / Orsay;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RL structure and evolution.";
DR EMBL: AJ246283; CAB49171.1; -.
DR HSSP; Q26997; IOK3.
DR InterPro; IPR000836; PRTtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
KM Glycosyltransferase; Transferase; Complete proteome.
SQ SEQUENCE 215 AA; 24832 MW; A58D71EBB5FD723 CRC64;

Query Match          90.0%; Score 36; DB 17; Length 215;
Best Local Similarity 66.7%; Pred. No. 2,4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAML 6
Db 141 IDWAML 146

RESULT 12
O07806 PRELIMINARY; PRT; 251 AA.
ID O07806;
AC O07806;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Phosphotransferase (Aminoglycoside 3'-phosphotransferase).
GN RV3817 OR MTCY409.13C OR MT3925.1.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
CX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RL MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Bigliamer K., Gas S., Barry C.B. III, Tekela F.,
RA Badcock K., Baaham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Felwell T., Gentile S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagsels K., Krogan A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborn J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RL laboratory strains.";
DR EMBL; Z97186; CAB10016.1; -.
DR EMBL; AE007186; AAK48292.1; -.
DR TIGR; MT3925; -.
DR Tuberculisc; RV3817; -.
DR InterPro; IPR002575; APH.
DR Pfam; PF01636; APH; 1.
KM Transferase; Complete proteome.
SQ SEQUENCE 251 AA; 27241 MW; 52807FDA006A21B3 CRC64;

Query Match          90.0%; Score 36; DB 16; Length 251;
Best Local Similarity 100.0%; Pred. No. 2,8e+02;

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWMAM 6  
86 DWMAM 90

## RESULT 13

ID Q91719 PRELIMINARY; PRT; 304 AA.  
AC Q91719;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Probable cytochrome c oxidase assembly factor.  
GN PA0113.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=287;

RN SEQUENCE FROM N.A.  
RC STRAIN=ATCC 15692 / PA01;  
RX MEDLINE=20437337; PubMed=10984043;  
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
Garber R.L., Goltz L., Tolentino B., Westbrock-Wadman S., Yuan Y.,  
RA Brody L.L., Speller S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
RA Smith K.A., Coulter D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
opportunistic pathogen.";  
RT Nature 406:959-964(2000).  
DR EMBL; AE004449; AAC03503.1; -;  
DR InterPro; IPR006369; Cyoe\_Ctab.  
DR InterPro; IPR000537; UblA-  
DR Pfam; PF01040; UblA; 1.  
DR TIGRPFAM; TIGR01473; Cyoe\_Ctab; 1.  
DR PROSITE; PS00943; UblA; 1.  
KW Complete proteome.  
SQ SEQUENCE 304 AA; 33430 MW; DC278071764B671C CRC64;

Query Match 90.0%; Score 36; DB 16; Length 304;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWAM 5  
259 LDWAM 263

## RESULT 14

ID Q8UBG8 PRELIMINARY; PRT; 316 AA.  
AC Q8UBG8;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE ABC transporter, membrane spanning protein.  
GN ATU3048 OR AGR\_L 3514.  
OS Aerobacterium tumefaciens (strain C58 / ATCC 33970).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Rhizobium.  
OX NCBI\_TaxID=176299;  
RN SEQUENCE FROM N.A.  
RP MEDLINE=21608550; PubMed=11743193;  
RX Wood D.W., Seubert J.C., Kaul R., Monks D.E., Kirejima J.P.,  
RA Okura V.K., Zhou Y., Chen L., Wood G.B., Almeida N.F.Jr., Woo L.,  
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. St.,  
RA Chapman P., Clendenning J., Decherage G., Gillet W., Grant C.,  
RA Kutayavon T., Levy R., Li M.-D., McClelland E., Palmeri A.,  
Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,

RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
RA Chunmley F., Tingey S.V., Tomb S.-F., Gordon M.F., Olson M.V.,  
RA Nester E.W.;  
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
C58.";  
RT Science 294:2317-2323(2001).

RN SEQUENCE FROM N.A.  
RX MEDLINE=21608551; PubMed=11743194;  
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
RA Gurolo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Milln L.,  
RA Houtel K., Gordon J., Vaudin M., Iarchouk O., Epp A., Liu F.,  
RA Wollam C., Allinger M., Doughty D., Scott C., Lappe C., Markelz B.,  
RA Flanagan C., Crowell C., Gursan J., Lomo C., Sear C., Strub G.,  
RA Cielo C., Slater S.;  
RT "Genome sequence of the plant pathogen and biotechnology agent  
Agrobacterium tumefaciens C58.";  
RT Science 294:2323-2328(2001).  
DR EMBL; AE009235; AAL43864.1; -;  
DR InterPro; IPR000515; BPD\_transp.  
DR Pfam; PF00528; BPD\_transp; 1.  
KW Complete proteome.  
SQ SEQUENCE 316 AA; 35079 MW; 7137741D79029267 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 316;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWAM 5  
67 LDWAM 71

## RESULT 15

ID Q9XBD4 PRELIMINARY; PRT; 444 AA.  
AC Q9XBD4;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Putative integral membrane sugar transporter.  
GN CZA382.17C.  
OS Amycolatopsis orientalis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Pseudonocardiaceae; Pseudonocardiaceae; Amycolatopsis.  
OX NCBI\_TaxID=31958;  
RN SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Leonard N., Harris B.;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
RN SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Bentley S.D., Parkhill J., Barrett B.G., Rajandream M.A.;  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
RN SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA van Wageningen A., Kirkpatrick P., Williams D., Harris B., Kershaw J.,  
RA Leonard N., Jones M., Jones S., Solenberg P.;  
RT "Sequencing and analysis of genes involved in the biosynthesis of a  
vancomycin group antibiotic.";  
RT -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC EMBL; AL076635; CAB45038.1; -;  
DR InterPro; IPR007114; MFS.  
DR InterPro; IPR005828; Sub\_transporter.  
DR Pfam; PF00083; sugar\_tr; 1.  
DR PROSITE; PS00850; MFS; 1.  
KW Sugar transport; Transmembrane.

SEQ SEQUENCE 444 AA; 48039 MM; 51ACE2D9EB121EDA CRC64;

Query Match 90.0%; Score 36; DB 2; Length 444;

Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAW 5

DB 194 LDWAW 198

Search completed: February 18, 2004, 14:35:58  
Job time : 18.3684 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds

(without alignments)  
75.239 Million cell updates/sec

Title: US-09-643-260-16

Perfect score: 40

Sequence: 1 LDMAWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	6	10 US-09-847-940B-16	Sequence 16, Appl
2	40	100.0	6	11 US-09-847-946A-16	Sequence 16, Appl
3	40	100.0	6	11 US-09-847-946A-44	Sequence 44, Appl
4	40	100.0	6	11 US-09-847-946A-106	Sequence 106, App
5	40	100.0	7	11 US-09-847-946A-110	Sequence 110, App
6	40	100.0	8	11 US-09-847-946A-103	Sequence 103, App
7	40	100.0	8	11 US-09-847-946A-111	Sequence 111, App
8	40	100.0	9	11 US-09-847-946A-102	Sequence 102, App
9	40	100.0	9	11 US-09-847-946A-105	Sequence 105, App
10	40	100.0	9	11 US-09-847-946A-108	Sequence 108, App
11	40	100.0	9	11 US-09-847-946A-109	Sequence 109, App
12	40	100.0	10	11 US-09-847-946A-104	Sequence 104, App
13	40	100.0	10	11 US-09-847-946A-107	Sequence 107, App
14	40	100.0	11	11 US-09-847-946A-101	Sequence 101, App
15	37	92.5	6	10 US-09-847-940B-2	Sequence 2, Appl

15	37	92.5	6	11 US-09-847-946A-2	Sequence 2, Appl
17	37	92.5	6	11 US-09-847-946A-33	Sequence 33, Appl
18	37	92.5	7	11 US-09-847-946A-37	Sequence 37, Appl
19	37	92.5	8	11 US-09-847-946A-30	Sequence 30, Appl
20	37	92.5	8	11 US-09-847-946A-38	Sequence 38, Appl
21	37	92.5	9	11 US-09-847-946A-32	Sequence 32, Appl
22	37	92.5	9	11 US-09-847-946A-39	Sequence 39, Appl
23	37	92.5	9	11 US-09-847-946A-35	Sequence 35, Appl
24	37	92.5	10	11 US-09-847-946A-36	Sequence 36, Appl
25	37	92.5	10	11 US-09-847-946A-31	Sequence 31, Appl
26	37	92.5	11	11 US-09-847-946A-34	Sequence 34, Appl
27	37	92.5	11	11 US-09-847-946A-28	Sequence 28, Appl
28	37	92.5	11	11 US-09-847-946A-132	Sequence 132, App
29	37	92.5	11	11 US-09-847-946A-140	Sequence 140, App
30	37	92.5	13	11 US-09-847-946A-143	Sequence 143, App
31	37	92.5	13	11 US-09-847-946A-144	Sequence 144, App
32	37	92.5	13	11 US-09-847-946A-145	Sequence 145, App
33	37	92.5	13	11 US-09-847-946A-148	Sequence 148, App
34	37	92.5	17	11 US-09-847-946A-141	Sequence 141, App
35	37	92.5	17	11 US-09-847-946A-142	Sequence 142, App
36	37	92.5	17	11 US-09-847-946A-146	Sequence 146, App
37	37	92.5	17	11 US-09-847-946A-147	Sequence 147, App
38	37	92.5	18	11 US-09-847-946A-131	Sequence 131, App
39	37	92.5	18	11 US-09-847-946A-135	Sequence 135, App
40	37	92.5	18	11 US-09-847-946A-136	Sequence 136, App
41	37	92.5	22	11 US-09-847-946A-133	Sequence 133, App
42	37	92.5	22	11 US-09-847-946A-134	Sequence 134, App
43	37	92.5	22	11 US-09-847-946A-137	Sequence 137, App
44	37	92.5	22	11 US-09-847-946A-138	Sequence 138, App
45	37	92.5	22	11 US-09-847-946A-139	Sequence 139, App

## ALIGNMENTS

RESULT 1  
US-09-847-940B-16  
; Sequence 16, Application US/09847940B  
; Patent No. US20020156000A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J.  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-117CP  
; CURRENT APPLICATION NUMBER: US/09/847,940B  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-16

Query Match 100.0%; Score 40; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LDMAWL 6  
Db 1 LDMAWL 6

RESULT 2  
US-09-847-946A-16  
; Sequence 16, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J

```
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-16
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Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy      1 LDMAWL 6
        |||||
Db      1 LDMAWL 6
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RESULT 3
US-09-847-946A-44
Sequence 44, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-44
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Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy      1 LDMAWL 6
        |||||
Db      1 LDMAWL 6
```

```
RESULT 4
US-09-847-946A-106
Sequence 106, Application US/09847946A
Publication No. US20030054999A1
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GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 106
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-106
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Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy      1 LDMAWL 6
        |||||
Db      1 LDMAWL 6
```

```
RESULT 5
US-09-847-946A-110
Sequence 110, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 110
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-110
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Query Match          100.0%; Score 40; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy      1 LDMAWL 6
        |||||
Db      1 LDMAWL 6
```

```
RESULT 6
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US-09-847-946A-103  
; Sequence 103, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Finkelstein, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 103  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-103  
Query Match 100.0%; Score 40; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDWAWL 6  
Db 3 LDWAWL 8  
RESULT 7  
US-09-847-946A-111  
; Sequence 111, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Finkelstein, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 111  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-111  
Query Match 100.0%; Score 40; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDWAWL 6  
Db 1 LDWAWL 6

RESULT 8  
US-09-847-946A-102  
; Sequence 102, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Finkelstein, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 102  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-102  
Query Match 100.0%; Score 40; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDWAWL 6  
Db 1 LDWAWL 6  
RESULT 9  
US-09-847-946A-105  
; Sequence 105, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Finkelstein, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 105  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-105  
Query Match 100.0%; Score 40; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMAML 6  
Db 1 LDMAML 6

## RESULT 10

US-09-847-946A-108  
; Sequence 108, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847, 946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 108  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-108

Query Match 100.0%; Score 40; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMAML 6  
Db 3 LDMAML 8

## RESULT 11

US-09-847-946A-109  
; Sequence 109, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847, 946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 109  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-109

Query Match 100.0%; Score 40; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMAML 6  
Db 2 LDMAML 7

## RESULT 12

US-09-847-946A-104  
; Sequence 104, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847, 946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 104  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-104

Query Match 100.0%; Score 40; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMAML 6  
Db 2 LDMAML 7

## RESULT 13

US-09-847-946A-107  
; Sequence 107, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847, 946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 107  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-107

US-09-847-946A-107

Query Match 100.0%; Score 40; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAML 6  
DB 3 LDWAML 8

## RESULT 14

US-09-847-946A-101  
; Sequence 101, Application US/09847946A  
; Publication No. US2003054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Flindeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 101  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: NEMO binding  
US-09-847-946A-101

Query Match 100.0%; Score 40; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAML 6  
DB 3 LDWAML 8

## RESULT 15

US-09-847-940B-2  
; Sequence 2, Application US/09847940B  
; Patent No. US20020156000A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J.  
; APPLICANT: Ghosh, Sankar  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-117CP  
; CURRENT APPLICATION NUMBER: US/09/847,940B  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-2

Query Match 92.5%; Score 37; DB 10; Length 6;

Best Local Similarity 83.3%; Pred. No. 7e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAML 6  
DB 1 LDMSWL 6

Search completed: February 18, 2004, 15:42:01  
Job time: 17.7529 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds

(Without alignments)  
41.814 Million cell updates/sec

Title: US-09-643-260-16

Perfect score: 40  
Sequence: 1 LDMAML 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*
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- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	23	ABB08738
2	40	100.0	6	23	AAA48521
3	40	100.0	6	23	AAA48541
4	40	100.0	6	23	AAA48603
5	40	100.0	6	24	ABU08431
6	40	100.0	7	23	AAA48607
7	40	100.0	8	23	AAA48608
8	40	100.0	8	23	AAA48608
9	40	100.0	9	23	AAA48559

10	40	100.0	9	23	AAA48602	Anti-inflammatory
11	40	100.0	9	23	AAA48605	Anti-inflammatory
12	40	100.0	9	23	AAA48606	Anti-inflammatory
13	40	100.0	10	23	AAA48601	Anti-inflammatory
14	40	100.0	10	23	AAA48604	Anti-inflammatory
15	40	100.0	11	23	AAA48598	Anti-inflammatory
16	40	100.0	173	23	ABP30297	Streptococcus poly
17	40	100.0	186	23	ABP27565	Streptococcus poly
18	40	100.0	756	23	ABP77306	Human IKKbeta, muta
19	38	95.0	342	22	AAA40149	Human polyprotein
20	38	95.0	358	22	AAA41935	IKKbeta NEMO bindi
21	37	92.5	6	23	AAA08725	Anti-inflammatory
22	37	92.5	6	23	AAA08530	Anti-inflammatory
23	37	92.5	6	23	AAA48655	NBD mutant peptide
24	37	92.5	6	24	ABU08418	Human NEMO binding
25	37	92.5	7	23	AAA48534	Anti-inflammatory
26	37	92.5	8	23	AAA48527	Anti-inflammatory
27	37	92.5	8	23	AAA48535	Anti-inflammatory
28	37	92.5	9	20	AAA96182	IKK-alpha polypept
29	37	92.5	9	23	AAA48526	Anti-inflammatory
30	37	92.5	9	23	AAA48529	Anti-inflammatory
31	37	92.5	9	23	AAA48532	Anti-inflammatory
32	37	92.5	9	23	AAA48533	Anti-inflammatory
33	37	92.5	10	23	ABB77313	IKKbeta NEMO bindi
34	37	92.5	10	23	AAA48528	Anti-inflammatory
35	37	92.5	10	23	AAA48531	Anti-inflammatory
36	37	92.5	11	23	ABB77311	Human NBD peptide
37	37	92.5	11	23	AAA48506	Human IKKbeta pepc
38	37	92.5	11	23	AAA48525	Anti-inflammatory
39	37	92.5	11	23	AAA48653	NBD peptide, synt
40	37	92.5	13	23	AAA48640	Anti-inflammatory
41	37	92.5	13	23	AAA48641	Anti-inflammatory
42	37	92.5	13	23	AAA48642	Anti-inflammatory
43	37	92.5	13	23	AAA48645	Anti-inflammatory
44	37	92.5	17	23	AAA48638	Anti-inflammatory
45	37	92.5	17	23	AAA48639	Anti-inflammatory

#### ALIGNMENTS

RESULT 1	ABB08738	standard, peptide, 6 AA.
ID	ABB08738	
AC	ABB08738	
XX		
DT	14-JUN-2002	(first entry)
DE	Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 16.	
KW	IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;	
KW	kinase activation; leukocyte; inflammation; E-selectin; osteoclast;	
KW	autoimmune disease; transplant rejection; osteoporosis; cancer;	
KW	Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;	
KW	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;	
KW	corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;	
KW	osteopathic; cytotoxic; neutropenic; neuroprotective; anti-HIV; human;	
KW	antiartherosclerotic; virulence; antidiabetic; antiallergic;	
KW	dermatological; antibacterial; antiparasitic; antirheumatic;	
KW	antiarthritic; osteopathic; antidiabetic; antitumor; mutant; mutain.	
OS	Homo sapiens.	
XX		
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 4	/note="Wildtype Ser substituted by Ala"
XX		
XX	WO200183547-A2.	
XX		
XX	08-NOV-2001.	
XX		

PF 02-MAY-2001; 2001MO-US40654.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S;  
 DR WPI; 2002-179350/23.  
 XX  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 XX  
 PS Claim 23; Page 45; 82pp; English.  
 XX  
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprising contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB077313). The compound has access through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of I-kappaB. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polyarthritis, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
 CC binding domain of IKKbeta.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 40; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMAWL 6  
 DB 1 LDMAWL 6  
 XX  
 RESULT 2  
 ID AAM48521 standard; Peptide; 6 AA.  
 XX  
 AC AAM48521;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE NBD mutant peptide SEQ ID NO 16.

XX  
 KW Antiinflammatory; antiaesthetic; cyostatic; antipsoriatic; nootropic;  
 KW antihemetic; antichratic; osteoprotective; antipariatic; vitruide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001MO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Fandels MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Example 6; Page 48; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
 CC cyostatic, antipsoriatic, antihemetic, antichratic, osteoprotective,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, vitruide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 40; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMAWL 6  
 DB 1 LDMAWL 6  
 XX  
 RESULT 3  
 ID AAM48541 standard; Peptide; 6 AA.



Query Match 100.0%; Score 40; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 LDMAWL 6  
 1 LDMAWL 6

RESULT 5  
 ABU08431  
 ID ABU08431 standard; peptide; 6 AA.

AC ABU08431;  
 DT 12-JUN-2003 (first entry)  
 XX  
 XX Human NEMO binding site (NBD) mutant peptide #14.

XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;  
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;  
 KW nuclear factor-kappaB induction; inflammatory disorder;  
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;  
 KW atherosclerosis; viral infection; Ataxia telangiectasia;  
 KW transplantation detection; immunosuppressive; osteopathic;  
 KW cytostatic; nootropic; neuroprotective; antiatherosclerotic; virucide;  
 KW vasotropic; antirheumatic; antiarthritic; mutant; mutain.

OS Homo sapiens.  
 OS Synthetic.

PN US2002156000-A1.

PD 24-OCT-2002.

PF 02-MAY-2001; 2001US-0847940.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (MAYM/) MAY M J.

PA (GHOS/) GHOSH S.

XX May MJ, Ghosh S;

PI WPI; 2003-209142/20.

PT Novel antiinflammatory peptide compounds comprising NEMO binding  
 PT domain, useful for modulating NF-kappaB induction in a cell and for  
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,  
 PT psoriasis, vasculitis -

PS Claim 22; Page 17; 47pp; English.

XX The present invention relates to antiinflammatory compounds comprising  
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are  
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha  
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention  
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction  
 CC in a cell, where the compounds are capable of blocking the interaction  
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The  
 CC antiinflammatory compound further comprises at least one membrane  
 CC translocation domain. The compounds are useful for treating  
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia  
 CC telangiectasia, and for transplantation detection. The compounds of  
 CC the invention block NF-kappaB induction by IKK but do not inhibit  
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human  
 CC NBD mutant peptides.

XX Sequence 6 AA;  
 Query Match 100.0%; Score 40; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 LDMAWL 6  
 1 LDMAWL 6

RESULT 6  
 AAM48607  
 ID AAM48607 standard; peptide; 7 AA.

AC AAM48607;  
 DT 20-MAR-2002 (first entry)  
 XX  
 XX Anti-inflammatory peptide SEQ ID NO 110.

XX Antiinflammatory; antiaesthetic; cytostatic; antiproliferative; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14346.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

PA (UYVA ) UNIV YALE.

XX May MJ, Ghosh S, Finkels MA, Phillips K;

PI WPI; 2002-121889/16.

PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -

PS Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
 CC cytostatic, antiproliferative, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis, transplant rejection, osteoporosis,  
 CC Alzheimer's disease, atherosclerosis, viral infections, and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 40; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMAWL 6  
Db 1 LDMAWL 6  
RESULT 7  
AAM48600 standard; Peptide; 8 AA.  
XX  
AC AAM48600;  
XX  
DT 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 103.  
XX  
KM Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;  
KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KM cytokine; Ikappab; Ikappab kinase beta; IKKbeta; cancer; psoriasis;  
KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KM autoimmune disorder; multiple sclerosis; transplant rejection;  
KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US14346.  
XX  
PR 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
PA (UYVA ) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Findels MA, Phillips K;  
XX  
DR WPI; 2002-121889/16.  
XX  
PT Novel antiinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappab activation, and for treating asthma, lung inflammation,  
PT psoriasis -  
XX  
PS Claim 6; Page 62; 88pp; English.  
XX  
XX The invention relates to an antiinflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain  
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NFKappab  
CC activation by blocking interaction of Ikappab kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of Ikappab. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, utricaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
XX  
SQ Sequence 8 AA;  
Query Match 100.0%; Score 40; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMAWL 6  
Db 3 LDMAWL 8  
RESULT 8  
AAM48608 standard; Peptide; 8 AA.  
XX  
AC AAM48608;  
XX  
DT 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 111.  
XX  
KM Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;  
KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KM cytokine; NFKappab; Ikappab kinase beta; IKKbeta; cancer; psoriasis;  
KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KM autoimmune disorder; multiple sclerosis; transplant rejection;  
KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US14346.  
XX  
PR 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
PA (UYVA ) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Findels MA, Phillips K;  
XX  
DR WPI; 2002-121889/16.  
XX  
PT Novel antiinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappab activation, and for treating asthma, lung inflammation,  
PT psoriasis -  
XX  
PS Claim 6; Page 62; 88pp; English.  
XX  
XX The invention relates to an antiinflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain  
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The



PT psoriasis -

XX Claim 6; Page 62; 88pp; English.

XX

CC The invention relates to an antiinflammatory compound (especially

CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15

CC amino acid residues, fused to a NEMO binding sequence

CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,

CC cytoskeletal, antiproliferative, antirheumatic, antiarthritic, osteopathic,

CC antibacterial, immunosuppressive, dermatological, neuroprotective,

CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB

CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at

CC the NEMO binding domain that results in inhibition of IKKbeta kinase

CC activation and subsequent decreased phosphorylation of IkappaB. The

CC compounds are useful for treating inflammatory disorders, e.g. asthma,

CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,

CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,

CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;

CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia

CC telangiectasia. The compounds are also useful for treating

CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and

CC arthritis.

XX

XX Sequence 9 AA;

SO

Query Match 100.0%; Score 40; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6

DB 1 LDMAML 6

RESULT 11

AAM48605

ID AAM48605 standard; Peptide; 9 AA.

XX

AC AAM48605;

XX

XX 20-MAR-2002 (first entry)

DT

XX

DE Anti-inflammatory peptide SEQ ID NO 108.

XX

KM Antiinflammatory; antiasthmatic; cytoskeletal; antiproliferative; nootropic;

KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;

KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;

KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;

KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

KM autoimmune disorder; multiple sclerosis; transplant rejection;

KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;

KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX

OS Synthetic.

XX

PN WO200183554-A2.

XX

PD 08-NOV-2001.

XX

PF 02-MAY-2001; 2001WO-US14346.

XX

PR 02-MAY-2000; 2000US-201261P.

XX

PR 22-AUG-2000; 2000US-0643260.

XX

PA (PRAE-) PRAECIS PHARM INC.

PA (UYVA ) UNIV YALE.

XX

XX May MJ, Ghosh S, Flindels MA, Phillips K,

PI

XX

DR WPI; 2002-121889/16.

XX

PT Novel antiinflammatory compound comprising membrane translocation

PT domain fused to NEMO binding sequence, useful for blocking nuclear

PT factor kappaB activation, and for treating asthma, lung inflammation,

PT psoriasis -

XX

XX Claim 6; Page 62; 88pp; English.

XX

CC The invention relates to an antiinflammatory compound (especially

CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15

CC amino acid residues, fused to a NEMO binding sequence

CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,

CC cytoskeletal, antiproliferative, antirheumatic, antiarthritic, osteopathic,

CC antibacterial, immunosuppressive, dermatological, neuroprotective,

CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB

CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at

CC the NEMO binding domain that results in inhibition of IKKbeta kinase

CC activation and subsequent decreased phosphorylation of IkappaB. The

CC compounds are useful for treating inflammatory disorders, e.g. asthma,

CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,

CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,

CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;

CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia

CC telangiectasia. The compounds are also useful for treating

CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and

CC arthritis.

XX

XX Sequence 9 AA;

SO

Query Match 100.0%; Score 40; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6

DB 3 LDMAML 8

RESULT 12

AAM48606

ID AAM48606 standard; Peptide; 9 AA.

XX

AC AAM48606;

XX

XX 20-MAR-2002 (first entry)

DT

XX

DE Anti-inflammatory peptide SEQ ID NO 109.

XX

KM Antiinflammatory; antiasthmatic; cytoskeletal; antiproliferative; nootropic;

KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;

KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;

KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;

KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

KM autoimmune disorder; multiple sclerosis; transplant rejection;

KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;

KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX

OS Synthetic.

XX

PN WO200183554-A2.

XX

PD 08-NOV-2001.

XX

PF 02-MAY-2001; 2001WO-US14346.

XX

PR 02-MAY-2000; 2000US-201261P.

XX

PR	22-AUG-2000; 2000US-0643260.
XX	(PRAE-) PRAECIS PHARM INC.
PA	(UTYA ) UNIV YALE.
XX	
PI	May MJ, Ghosh S, Findels MA, Phillips K;
XX	
DR	WPI; 2002-121889/16.
XX	
PT	Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis -
XX	
PS	Claim 6; Page 62; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AAH48624-AAH48645), comprising a membrane translocation domain
CC	(AAH48620-AAH48627 or AAH48646-AAH48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AAH48525-AAH48619). The antiinflammatory compounds have antiaesthetic,
CC	cytostatic, antiproliferative, immunosuppressive, dermatological, neuroprotective,
CC	antibacterial, immunosuppressive, dermatologic, neuroprotective, The
CC	nootropic, antihypertensive, vitamin D and analgesic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of Ikappab kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of Ikappab. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	gastrointestinal diseases such as lupus, polymyalgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
SQ	Sequence 9 AA;
	Query Match 100.0%; Score 40; DB 23; Length 9;
	Best Local Similarity 100.0%; Pred. No. 9.3e+05;
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 LDMAWL 6 
Db	2 LDMAWL 7
RESULT 13	
AAM48601	
ID	AAM48601 standard; Peptide; 10 AA.
XX	
XX	AAM48601;
XX	
DT	20-MAR-2002 (first entry)
DE	Anti-Inflammatory peptide SEQ ID NO 104.
XX	
KM	Antiinflammatory; antiaesthetic; cytostatic; antiproliferative; nootropic;
KM	antirheumatic; antiarthritic; osteopathic; antibacterial; antiviral;
KM	immunoprotective; dermatological; neuroprotective; antihypertensive;
KM	antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KM	cyclokinase; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;
KM	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KM	autoimmune disorder; multiple sclerosis; transplant rejection;
KM	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KM	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS	Synthetic.
FN	WO200183554-A2.

XX 08-NOV-2001.  
XX  
PD  
XX  
PF 02-MAY-2001; 2001MO-US14346.  
XX  
PP  
PR 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
PA (UYTA ) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Findeis MA, Phillips K;  
XX WPI; 2002-121899/16.  
XX  
DR  
XX Novel antiinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis -  
XX  
PS Claim 6; Page 62; 88pp; English.  
XX  
XX The invention relates to an antiinflammatory compound (especially  
CC AAH48628-AAH48645), comprising a membrane translocation domain  
CC (AAH48620-AAH48627 or AAH48646-AAH48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAH48525-AAH48619). The antiinflammatory compounds have antiasthmatic,  
CC cycostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC nootropic, antihypertensive, virocidic and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
CC activation by blocking interaction of Ikappab kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of Ikappab. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
XX  
SQ Sequence 10 AA;  
  
Query Match 100.0%; Score 40; DB 23; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2,7; Mismatches 0; Gaps 0;  
Matches 6; Conservative 0; Indels 0

OY 1 LDMAWL 6  
|||  
|||  
2 LDMAWL 7

RESULT 14  
AAH48604  
ID AAH48604 standard; Peptide; 10 AA.  
AC AAH48604;  
XX  
XX  
DT 20-MAR-2002 (first entry)  
DE Anti-inflammatory peptide SEQ ID NO 107.  
XX  
XX Antiinflammatory; antiasthmatic; cycostatic; antipsoriatic; nootropic;  
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virocidic;  
KW immunosuppressive; dermatological; neuroprotective; antihypertensive;  
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;



KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX Synthetic.  
 XX WO200183554-A2.  
 PN  
 PD 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 PF  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Finkel MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 CC The invention relates to an antiinflammatory compound (especially  
 CC (AA48628-AA48645), comprising a membrane translocation domain  
 CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,  
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 CC  
 SQ Sequence 10 AA;  
 QY  
 Query Match 100.0%; Score 40; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.7;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMAML 6  
 |||||  
 Db 3 LDMAML 8  
 RESULT 15  
 ID AA48598  
 AA48598 standard; Peptide; 11 AA.  
 AC  
 XX AA48598;  
 XX  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 101.  
 XX  
 KM Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;

KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 XX Synthetic.  
 OS  
 XX WO200183554-A2.  
 PN  
 PD 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 PF  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Finkel MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 CC The invention relates to an antiinflammatory compound (especially  
 CC (AA48628-AA48645), comprising a membrane translocation domain  
 CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,  
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
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 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
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 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
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 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 CC  
 SQ Sequence 11 AA;  
 QY  
 Query Match 100.0%; Score 40; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMAML 6  
 |||||  
 Db 3 LDMAML 8

Search completed: February 18, 2004, 14:26:26  
 Job time : 23.7763 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds  
(without alignments)  
89.145 Million cell updates/sec

Title: US-09-643-260-15

Sequence: 1 LDMSTL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	939	16 Q8YOR3	Q8YOR3 Anabaena sp
2	36	100.0	1466	3 Q42930	Q42930 schizosacch
3	34	94.4	317	16 Q8FMV4	Q8FMV4 corynebacte
4	34	94.4	369	17 Q58160	Q58160 pyrococcus
5	33	91.7	542	3 Q60113	Q60113 schizosacch
6	33	88.9	75	10 Q94HM4	Q94HM4 arabidopsi
7	32	88.9	136	16 P72919	P72919 synecocyst
8	32	88.9	142	6 Q8HYV0	Q8HYV0 sus scrofa
9	32	88.9	153	16 P73698	P73698 synecocyst
10	32	88.9	172	16 Q9RYF2	Q9RYF2 deinococcus
11	32	88.9	221	10 Q9S403	Q9S403 arabidopsi
12	32	88.9	229	17 Q8ZYL1	Q8ZYL1 pyrobaculum
13	32	88.9	262	10 Q9FNJ0	Q9FNJ0 arabidopsi
14	32	88.9	278	10 Q9LUT6	Q9LUT6 arabidopsi
15	32	88.9	308	3 Q12010	Q12010 saccharomyc
16	32	88.9	319	5 Q9NEV3	Q9NEV3 caenorhabdi

17	32	88.9	337	4 Q96RE6	Q96RE6 homo sapien
18	32	88.9	362	5 Q4634	Q4634 caenorhabdi
19	32	88.9	393	16 Q9ZKA8	Q9ZKA8 helicobacte
20	32	88.9	409	4 Q8N6M5	Q8N6M5 homo sapien
21	32	88.9	412	10 Q8RYL7	Q8RYL7 oryza sativ
22	32	88.9	429	12 Q65111	Q65111 adelaide ri
23	32	88.9	438	16 Q8RHMS	Q8RHMS fusobacteri
24	32	88.9	450	16 Q99R10	Q99R10 staphylococ
25	32	88.9	450	16 Q8NUV5	Q8NUV5 staphylococ
26	32	88.9	451	16 Q91151	Q91151 streptomyce
27	32	88.9	455	16 Q8CN46	Q8CN46 staphylococ
28	32	88.9	480	16 Q67595	Q67595 aquifex aeo
29	32	88.9	497	10 Q9LZ84	Q9LZ84 arabidopsi
30	32	88.9	497	10 Q94EY8	Q94EY8 arabidopsi
31	32	88.9	505	16 Q8PAX6	Q8PAX6 xanthomonas
32	32	88.9	542	17 Q30147	Q30147 archaeoglob
33	32	88.9	555	16 Q8PMN9	Q8PMN9 xanthomonas
34	32	88.9	561	16 Q9HTJ2	Q9HTJ2 pseudomonas
35	32	88.9	567	16 Q8ZGM0	Q8ZGM0 yersinia pe
36	32	88.9	573	16 Q8YXB1	Q8YXB1 anabaena sp
37	32	88.9	599	10 Q9FHV3	Q9FHV3 arabidopsi
38	32	88.9	620	11 Q8BQ64	Q8BQ64 mus musculu
39	32	88.9	647	2 Q8YVMS	Q8YVMS staphylococ
40	32	88.9	673	4 Q8RTT9	Q8RTT9 homo sapien
41	32	88.9	708	5 Q9W0D8	Q9W0D8 drosophila
42	32	88.9	738	11 Q8VE80	Q8VE80 mus musculu
43	32	88.9	793	5 Q9VYV0	Q9VYV0 drosophila
44	32	88.9	828	3 Q74240	Q74240 chileavia h
45	32	88.9	839	10 Q9M0G3	Q9M0G3 arabidopsi

## ALIGNMENTS

RESULT 1	Q8YOR3	PRELIMINARY;	PRT;	939 AA.
ID	Q8YOR3			
AC	Q8YOR3			
DT	01-MAR-2002 (TrEMBLrel. 20, Created)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)			
DE	Hypothetical protein AL3756.			
GN	AL3756.			
OS	Anabaena sp. (strain PCC 7120).			
OC	Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.			
OX	NCBI_TaxID=103690;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:2169285; PubMed:11759840;			
RA	Kaneke T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,			
RA	Watanabe A., Iritaguchi M., Ishikawa A., Kawashima K., Kimura T.,			
RA	Kishida Y., Kohara M., Matsumoto M., Matuno A., Muraki A.,			
RA	Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,			
RA	Yasuda M., Tabata S.;			
RT	"Complete genomic sequence of the filamentous nitrogen-fixing			
RT	cyanobacterium Anabaena sp. strain PCC 7120."			
RL	DNA Ref. 8:205-213(2001).			
DR	EMBL; AP003594; BAB75455.1; -			
KW	Hypothetical protein; Complete proteome.			
SO	SEQUENCE 939 AA; 10423 MW; 8FE0AYCAC1759A5 CRC64;			
Query Match	100.0%;	Score 36;	DB 16;	Length 939;
Best Local Similarity	100.0%;	Pred. No. 2.8e+02;		
Matches	6;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;
QY	1 LDMSTL 6			
DB	648 LDMSTL 653			
RESULT 2	Q42930	PRELIMINARY;	PRT;	1466 AA.
ID	Q42930			

No art

AC 042930;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Putative membrane glycoprotein, possible vacuolar protein sorting  
 DE /cargectg.  
 GN SPBC16C6.06.  
 OS Schizosaccharomyces pombe (fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomyces.  
 CX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972h-;  
 RA Rajandream M.A.;  
 RA Rajandream M.A.;  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL021767; CA16914.1; -;  
 DR GeneDB\_Spombe; SPBC16C6.06; -;  
 DR InterPro; IPR002860; GH\_BNR.  
 DR InterPro; IPR006581; VPS10.  
 DR Pfam; PF02012; BNR.12.  
 DR SMART; SM00602; VPS10.2.  
 SQ SEQUENCE 1466 AA; 165061 MW; CB315E0F7688D79 CRC64;

Query Match 100.0%; Score 36; DB 3; Length 1466;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSYL 6  
 Db 1046 LDMSYL 1051

RESULT 3  
 O6PMV4 PRELIMINARY; PRT; 317 AA.  
 ID O6PMV4  
 AC O6PMV4;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Conserved hypothetical protein.  
 GN CB2395.  
 OS Corynebacterium efficiens.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
 CX NCBI\_TaxID=152794;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VS-314 / AJ 12310 / DSM 44549 / JCM 11189;  
 RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,  
 RA Ikeno K., Suzuki M., Maehira J., Itoh T., Yamagishi A., Nishio Y.,  
 RA Ueda Y., Sugimoto S.;  
 RT "The entire genomic sequence of Corynebacterium efficiens VS-314.";  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP005222; BAC19205.1; -;  
 KM Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 317 AA; 33135 MW; 3805BDE05030A81C CRC64;

Query Match 94.4%; Score 34; DB 16; Length 317;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSYL 6  
 Db 114 LDMSYL 119

RESULT 4  
 ID O58160 PRELIMINARY; PRT; 389 AA.  
 AC O58160;

DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Hypothetical protein PH0423.  
 GN PH0423.  
 OS Pyrococcus horikoshii.  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 OC Pyrococcus.  
 CX NCBI\_TaxID=53953;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OT3;  
 RX MEDLINE=98344137; PubMed=9679194;  
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,  
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,  
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,  
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,  
 RA Aoki K.-I., Yoshitawa T., Nakamura Y., Robb F.T., Horikoshi K.,  
 RA Masuichi Y., Shizuya H., Kikuchi H.;  
 RT "Complete sequence and gene organization of the genome of a hyper-  
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";  
 RL DNA Res. 5:55-76(1998).  
 DR EMBL; AP000002; BAA29509.1; -;  
 DR InterPro; IPR002934; NTP\_transf.  
 DR Pfam; PF01909; NTP\_transf\_2; 1.  
 KM Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 389 AA; 46335 MW; 81F32C817B1A53D4 CRC64;

Query Match 94.4%; Score 34; DB 17; Length 389;  
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSYL 6  
 Db 139 LDMSYL 144

RESULT 5  
 O60113 PRELIMINARY; PRT; 542 AA.  
 ID O60113  
 AC O60113;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Amino acid permease.  
 GN SPBC15C4.04C.  
 OS Schizosaccharomyces pombe (fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomyces.  
 CX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972h-;  
 RA Lyne M., Rajandream M.A., Barrell B.G., Xiang Z., Aves S.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL023290; CA18895.1; -;  
 DR GeneDB\_Spombe; SPBC15C4.04C; -;  
 DR InterPro; IPR002293; AA/rel\_permease1.  
 DR InterPro; IPR004840; AAC\_permease.  
 DR InterPro; IPR004756; AA\_permease.  
 DR InterPro; IPR004841; Permease.  
 DR Pfam; PF00324; aa\_permeases; 1.  
 DR TIGRPFAM; TIGR00907; ZA0304; 1.  
 DR PROSITE; PS00218; AMINO\_ACID\_PERMEASE\_1; 1.  
 SQ SEQUENCE 542 AA; 59726 MW; 17D9B15C0429468 CRC64;

Query Match 91.7%; Score 33; DB 3; Length 542;  
 Best Local Similarity 83.3%; Pred. No. 5.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSYL 6  
 Db 1 LDMSYL 6

Db 436 LDMSYV 441

## RESULT 6

Q94HM4 PRELIMINARY; PRT; 75 AA.  
 ID 094HM4  
 AC 094HM4  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 GN Hypothetical 8.8 kDa protein.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC euroside II; Brassicales; Brassicaceae; Arabidopsis.  
 NC NCB1\_Taxid=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Town C.D., Haas B.J., Wu D., Maltl R., Hannick L.I., Chan A.P.,  
 RA Tallon L.J., Rooney T., Utteback T.R., Vanaken S.E., Feldblyum T.V.,  
 RA White O., Fraser C.M.;  
 RT "Arabidopsis thaliana chromosome 1 BAC T4M14 genomic sequence."  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC027036; AAK62781.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 75 AA; 8834 MW; B34EB28B5C41EBB5 CRC64;

Query Match 88.9%; Score 32; DB 10; Length 75;

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSY 5  
 |||||  
 Db 12 LDMSY 16

## RESULT 7

P72919 PRELIMINARY; PRT; 136 AA.  
 ID P72919  
 AC P72919  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 GN Hypothetical protein slr1082.  
 OS Synechocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 NC NCB1\_Taxid=1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; PubMed=8905231;  
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 RA Miyajima N., Hirosewa M., Sugiyura M., Sasegawa S., Kimura T.,  
 RA Hosouchi T., Matsumoto A., Muraki A., Nakazaki N., Nakano K., Okumura S.,  
 RA Shimizu S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,  
 RA Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 RT entire genome and assignment of potential protein-coding regions."  
 RL DNA Res. 3:109-136(1996).  
 DR EMBL: D90901; BAA16936.1; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 136 AA; 15774 MW; E80414D06029605E CRC64;

Query Match 88.9%; Score 32; DB 16; Length 136;

Best Local Similarity 83.3%; Pred. No. 2e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSYL 6  
 |||||  
 Db 42 LDMSYL 47

## RESULT 8

Q8HYV0 PRELIMINARY; PRT; 142 AA.  
 ID Q8HYV0  
 AC Q8HYV0  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 GN Glycogen synthase (Fragment).  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 NC NCB1\_Taxid=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA te Pas M.F., Leenhouters J.I., Knol R.F., Booit M., Pliem J.,  
 RA van der Lende T.;  
 RT "Marker polymorphism in the porcine muscle glycogen synthase (glycogen  
 RT synthase 1)."  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ507152; CAD47844.1; -  
 FT NON\_TER 1 1  
 FT NON\_TER 142 142  
 SQ SEQUENCE 142 AA; 15951 MW; C02BAD285F8A7E CRC64;

Query Match 88.9%; Score 32; DB 6; Length 142;

Best Local Similarity 83.3%; Pred. No. 2.1e+02; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMSYL 6  
 |||||  
 Db 83 LDMSYL 88

## RESULT 9

P73698 PRELIMINARY; PRT; 153 AA.  
 ID P73698  
 AC P73698  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 GN Hypothetical protein slr1813.  
 OS Synechocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 NC NCB1\_Taxid=1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; PubMed=8905231;  
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 RA Miyajima N., Hirosewa M., Sugiyura M., Sasegawa S., Kimura T.,  
 RA Hosouchi T., Matsumoto A., Muraki A., Nakazaki N., Nakano K., Okumura S.,  
 RA Shimizu S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,  
 RA Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 RT entire genome and assignment of potential protein-coding regions."  
 RL DNA Res. 3:109-136(1996).  
 DR EMBL: D90908; BAA17745.1; -  
 DR InterPro: IPR002636; DUF29.  
 DR Pfam: PF01724; DUF29.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 153 AA; 18387 MW; 6B54BB36EDCB9AFL CRC64;

Query Match 88.9%; Score 32; DB 16; Length 153;

Best Local Similarity 83.3%; Pred. No. 2.2e+02; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMSYL 6  
 |||||  
 Db 36 LDMSYL 41



```

RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.
RT Sequence features of the regions of 1,044,062 bp covered by thirteen
RT physically assigned P1 clones."
DL DNA Ref. 4:291-300(1997).
DR EMBL; AB006699; BAB1677.1; -.
DR InterPro; IPR006566; PBD.
DR SMART; SM00579; PBD; 1.
SQ SEQUENCE 262 AA; 30706 MW; CE1SDDB92CD3C6B9 CRC64;

Query Match
Best Local Similarity 88.9%; Score 32; DB 10; Length 262;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSYL 6
DB 46 DMSYL 50

RESULT 14
Q9LUT6 PRELIMINARY; PRT; 278 AA.
AC Q9LUT6;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE Gb|AAD32889.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Sato S.; Nakamura Y.; Kaneko T.; Kato T.; Asamizu E.; Tabata S.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones."
DL DNA Ref. 7:131-135(2000).
DR EMBL; AB022216; BAB02739.1; -.
SQ SEQUENCE 278 AA; 31217 MW; A16AE1B0910484B2 CRC64;

Query Match
Best Local Similarity 88.9%; Score 32; DB 10; Length 278;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSY 5
DB 217 LDMSY 221

RESULT 15
Q12010 PRELIMINARY; PRT; 308 AA.
AC Q12010;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Chromosome XV reading frame ORF YOL092W.
GN YOL092W.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Zumelein E.; Pearson B.M.; Kalogeropoulos A.; Schweitzer M.;

```

```

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=PY1679;
RX MEDLINE=96021609; PubMed=8533473;
RA Zumelein E.; Pearson B.M.; Kalogeropoulos A.; Schweitzer M.;
RT "A 29.425 kb segment on the left arm of yeast chromosome XV contains
RT more than twice as many unknown as known open reading frames."
RL Yeast 11:975-986(1995).
DR EMBL; 274834; CAA99104.1; -.
DR EMBL; X83121; CAA58187.1; -.
DR SGD; S0005452; YOL092W.
DR InterPro; IPR006603; CTNS.
DR SMART; SM00679; CTNS; 2.
SQ SEQUENCE 308 AA; 34872 MW; 38EB1645FA034812 CRC64;

Query Match
Best Local Similarity 88.9%; Score 32; DB 3; Length 308;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSYL 6
DB 267 LDMSYL 272

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Search completed: February 18, 2004, 14:35:57  
Job time : 19.3684 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds  
(without alignments)  
87.531 Million cell updates/sec

Title: US-09-643-260-15

Sequence: 1 LDMSTL 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR.76.\*  
2: PIR.2.\*  
3: PIR.3.\*  
4: PIR.4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	939	2 AE2275	hypothetical prote
2	36	100.0	1466	2 T39557	vacuolar protein s
3	34	94.4	98	2 H64885	YadA protein - Esc
4	34	94.4	389	2 H71152	hypothetical prote
5	33	91.7	330	1 H69798	conserved hypotet
6	33	91.7	542	2 T39474	amino acid permeas
7	32	88.9	136	2 S74785	hypothetical prote
8	32	88.9	153	2 S77187	hypothetical prote
9	32	88.9	172	2 A75592	hypothetical prote
10	32	88.9	221	2 H84781	hypothetical prote
11	32	88.9	265	2 T40878	probable PAD synth
12	32	88.9	308	2 S57377	probable membrane
13	32	88.9	362	2 T32659	hypothetical prote
14	32	88.9	392	2 T45032	hypothetical prote
15	32	88.9	393	2 B71857	probable lipopolys
16	32	88.9	445	2 S27492	hypothetical prote
17	32	88.9	450	2 D90047	hypothetical prote
18	32	88.9	476	2 T43863	cardiolipin syntha
19	32	88.9	480	2 B70446	hypothetical prote
20	32	88.9	497	2 T48367	hypothetical prote
21	32	88.9	542	2 A69261	probable acid-CoA
22	32	88.9	561	2 B82975	cholesterol dehydrog
23	32	88.9	567	2 AC0143	cholesterol dehydrog
24	32	88.9	573	2 AE1569	sulfate permease f
25	32	88.9	707	2 T40070	origin recognition
26	32	88.9	735	2 A33369	glycogen(starch) s
27	32	88.9	737	2 A32156	glycogen(starch) s
28	32	88.9	839	2 F85334	myosin heavy chain
29	32	88.9	1446	2 T04528	myosin heavy chain

30	32	88.9	1556	2 P65587	hypothetical prote
31	32	88.9	1583	2 T00727	myosin heavy chain
32	32	88.9	1611	2 A84743	myosin heavy chain
33	32	88.9	1643	2 T07961	myosin heavy chain
34	32	88.9	1736	2 F86178	hypothetical prote
35	32	88.9	2245	2 T18278	myosin heavy chain
36	32	88.9	2658	2 A86216	protein T23618.2 f
37	31	86.1	223	2 T24188	hypothetical prote
38	31	86.1	231	2 B82644	inositol monophosp
39	31	86.1	237	2 B82644	5-amino-6-(5-phosp
40	31	86.1	264	2 D81971	hypothetical prote
41	31	86.1	506	2 T50211	WD-repeat protein
42	31	86.1	703	2 S45686	glycogen(starch) s
43	31	86.1	703	2 A35362	glycogen(starch) s
44	31	86.1	745	1 I49101	conserved helix-lo
45	31	86.1	757	2 A39283	gamma-glutamyl car

## ALIGNMENTS

RESULT 1  
AE2275  
hypothetical protein alr3756 [imported] - Nostoc sp. (strain PCC 7120)  
C/Spectrum: Nostoc sp. PCC 7120  
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C/Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C/Accession: AE2275  
R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriq;  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,  
DNA Res. 8, 205-213, 2001  
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A  
A/Reference number: AB1807; MUID:21595285; PMID:11759840  
A/Accession: AE2275  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-939 <KUR>  
A/Cross-references: GB:BA000019, PIDN:BA075455.1, PID:G17132890, GSPDB:GN00179  
A/Experimental source: strain PCC 7120  
C/Genetics:  
A/Gene: alr3756

Query Match  
Best Local Similarity 100.0%; Score 36; DB 2; Length 939;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSTL 6  
DB 648 LDMSTL 653

RESULT 2  
T39557  
vacuolar protein sorting - fission yeast (Schizosaccharomyces pombe)  
C/Spectrum: Schizosaccharomyces pombe  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C/Accession: T39557  
R/Purcell, B.; Goffeau, A.; Wood, V.; Lyne, M.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, February 1998  
A/Reference number: Z21863  
A/Accession: T39557  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1466 <PUB>  
A/Cross-references: EMBL:AL021767; PIDN:CA116914.1; GSPDB:GN00067; SPDB:SPBC16C6.06  
C/Genetics:  
A/Experimental source: strain 972h-; cosmid c16C6  
A/Gene: SPDB:SPBC16C6.06  
A/Map position: 2  
A/Introns: 58/3  
Query Match  
Best Local Similarity 100.0%; Score 36; DB 2; Length 1466;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





DNA Ref. 3, 109-136, 1996  
A>Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* B.  
A/Reference number: S74322; MUID:97061201; PMID:8905231  
A/Accession: S74785  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-136 <KAN>  
A/Cross-references: EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAAL6936.1; PID:g165201  
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C/Superfamily: *Synechocystis* hypothetical protein slr0489

Query Match 88.9%; Score 32; DB 2; Length 136;  
Best Local Similarity 83.3%; Pred. No. 59;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSYL 6  
Db 42 LDMSFL 47

RESULT 8  
S77187  
hypothetical protein slr1813 - *Synechocystis* sp. (strain PCC 6803)  
C/Species: *Synechocystis* sp.  
A/Variety: PCC 6803  
C/Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
C/Accession: S77187  
R/Kanehisa, T.; Sato, S.; Kanehisa, H.; Tanaka, A.; Asami, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimizu, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Ref. 3, 109-136, 1996  
A>Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* B.  
A/Reference number: S74322; MUID:97061201; PMID:8905231  
A/Accession: S77187  
A/Status: nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-153 <KAN>  
A/Cross-references: EMBL:D90908; GB:AB001339; NID:g1652725; PIDN:BAAL7745.1; PID:g165282  
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C/Superfamily: hypothetical protein slr1203

Query Match 88.9%; Score 32; DB 2; Length 153;  
Best Local Similarity 83.3%; Pred. No. 67;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMSYL 6  
Db 36 LDMSYL 41

RESULT 9  
A75592  
hypothetical protein - *Deinococcus radiodurans* (strain R1)  
C/Species: *Deinococcus radiodurans*  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 28-Jul-2000  
C/Accession: A75592  
R/White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Usterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A>Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.  
A/Reference number: A75250; MUID:20036896; PMID:10567266  
A/Accession: A75592  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-172 <MT>  
A/Cross-references: GB:AB001863; GB:AE001825; NID:g6460670; PIDN:AAFI3501.1; PID:g646079  
A/Experimental source: strain R1  
C/Genetics:  
A/Map position: 2  
C/Superfamily: *Deinococcus radiodurans* hypothetical protein DRA0366

Query Match 88.9%; Score 32; DB 2; Length 172;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSY 5  
Db 96 LDMSY 100

RESULT 10  
H84781  
hypothetical protein At2g36550 (imported) - *Arabidopsis thaliana*  
C/Species: *Arabidopsis thaliana* (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C/Accession: H84781  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bent, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon, eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999  
A>Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: H84781  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-221 <STO>  
A/Cross-references: GB:AE002093; NID:g4581153; PIDN:AAD24637.1; GSPDB:GN00139  
C/Genetics:  
A/Map position: 2

Query Match 88.9%; Score 32; DB 2; Length 221;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSY 5  
Db 208 LDMSY 212

RESULT 11  
T40878  
probable FAD synthetase - fission yeast (*Schizosaccharomyces pombe*)  
C/Species: *Schizosaccharomyces pombe*  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C/Accession: T40878  
R/Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.  
submitted to the EMBL Data Library, September 1998  
A/Reference number: Z21954  
A/Accession: T40878  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-265 <WOO>  
A/Cross-references: EMBL:AL031764; PIDN:CA21108.1; GSPDB:GN00068; SPDB:SPCC1235.04C  
A/Experimental source: strain 972h-; cosmid c1235  
C/Genetics:  
A/Map position: 3  
A/Map position: 46/2; 182/3

Query Match 88.9%; Score 32; DB 2; Length 265;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSY 5  
Db 173 LDMSY 177

RESULT 12  
S57377  
probable membrane protein YOL092w - Yeast (*Saccharomyces cerevisiae*)  
N/Alternate names: hypothetical protein O0929; protein YBR17w homolog

C/Species: Saccharomyces cerevisiae  
 C/Date: 28-Oct-1999 #sequence\_revision 03-Nov-1995 #text\_change 19-Apr-2002  
 C/Accession: S57377; S6786; S50413  
 R/Zumstede, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.  
 Yeast 11, 975-986, 1995  
 A/Title: A 29.425 kb segment on the left arm of yeast chromosome XV contains more than 6  
 A/Reference number: S57374; MUID:96021609; PMID:8533473  
 A/Accession: S57377  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: DNA  
 A/Residues: 1-308 <ZMW>  
 A/Cross-references: EMBL:X83121, NID:G600461, PIDN:CA58187.1, PID:G600466  
 R/Zumstede, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.  
 submitted to the Protein Sequence Database, July 1996  
 A/Reference number: S66775  
 A/Accession: S66786  
 A/Molecule type: DNA  
 A/Residues: 1-308 <ZMW>  
 A/Cross-references: EMBL:Z74834, NID:G141937, PID:G141938; MIPS:YOL092W  
 A/Experimental source: strain S288C  
 C/Genetics:  
 A/Cross-references: SGD:S0005452  
 A/Map position: 15L  
 C/Superfamily: Saccharomyces probable membrane protein YBR147W  
 C/Keywords: transmembrane protein  
 F/14-30/Domain: transmembrane #status predicted <TM1>  
 F/45-61/Domain: transmembrane #status predicted <TM2>  
 F/73-89/Domain: transmembrane #status predicted <TM3>  
 F/168-184/Domain: transmembrane #status predicted <TM4>  
 F/248-265/Domain: transmembrane #status predicted <TM5>  
 F/278-294/Domain: transmembrane #status predicted <TM6>

Query Match 88.9%; Score 32; DB 2; Length 308;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LDMSYL 6  
 DB 267 LDMSYL 272

RESULT 13  
 132659  
 hypothetical protein F16B4.2 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 R/Davidson, S.; Wohlmann, P.; Bauer, C.; O'Neal, D.  
 submitted to the EMBL Data Library, December 1997  
 A/Description: The sequence of C. elegans cosmid F16B4.  
 A/Reference number: Z21208  
 A/Accession: T32659  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-362 <DNA>  
 A/Cross-references: EMBL:AF039048, PIDN:AAB94233.1; GSPDB:GN00023; CESP:F16B4.2  
 A/Experimental source: strain Bristol N2; clone F16B4  
 C/Genetics:  
 A/Map position: 5  
 A/Introns: 48/2; 112/2; 160/3; 255/3; 291/2; 333/3

Query Match 88.9%; Score 32; DB 2; Length 362;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSYL 6  
 DB 26 LDMSYL 31

RESULT 14  
 T45032

hypothetical protein Y39B6B.f [imported] - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
 C/Accession: T45032  
 R/Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berke, M.; Bonfield, J.; Burton  
 Raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Jon  
 B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifkin, L.; Roopre, A.; Saunders, D.  
 Nature 368, 32-38, 1994  
 A/Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonhammer, E.;  
 Lock, L.; Wilkinson-Spratt, J.; Wohlmann, P.  
 A/Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.  
 A/Reference number: S43531; MUID:94150718; PMID:7906398  
 A/Accession: T45032  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-392 <NTL>  
 A/Cross-references: EMBL:AL138965, NID:G6434440; PIDN:CAB60911.1; PID:G6434446  
 A/Experimental source: clone Y39B6B  
 C/Genetics:  
 A/Map position: 3  
 A/Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3  
 A/Note: Y39B6B.f

Query Match 88.9%; Score 32; DB 2; Length 392;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSYL 6  
 DB 289 DMSYL 293

RESULT 15  
 B71857  
 Probable lipopolysaccharide biosynthesis protein - Helicobacter pylori (strain J99)  
 C/Species: Helicobacter pylori  
 A/Variety: strain J99  
 C/Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 08-Oct-1999  
 C/Accession: B71857  
 R/Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.  
 ; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.  
 Nature 397, 176-180, 1999  
 A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric pa  
 A/Reference number: A71800; MUID:99120557; PMID:9923682  
 A/Accession: B71857  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-393 <ARN>  
 A/Cross-references: GB:AE001531; GB:AE001439, NID:G4155617; PIDN:AAD06611.1; PID:G4155  
 A/Experimental source: strain J99  
 C/Genetics:  
 A/Map position: 3  
 A/Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3  
 A/Note: Y39B6B.f

Query Match 88.9%; Score 32; DB 2; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSYL 6  
 DB 284 DMSYL 288

Search completed: February 18, 2004, 14:38:51  
 Job time : 7.5921 secs

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds  
(Without alignment)  
35.929 Million cell updates/sec

Title: US-09-643-260-15

Perfect score: 36

Sequence: 1 LDMSYL 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 4231088 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database:

Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/prodata/1/1aa/PCUS\_COMB.pep.\*
- 6: /cgn2\_6/prodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	829	US-09-252-991A-27150	Sequence 27150, A
2	32	88.9	462	US-09-134-001C-4300	Sequence 4300, Ap
3	32	88.9	597	US-09-252-991A-17139	Sequence 17139, A
4	32	88.9	651	US-09-107-532A-4902	Sequence 4902, Ap
5	32	88.9	706	US-08-484-105-16	Sequence 16, Appl
6	32	88.9	706	US-08-484-106-16	Sequence 16, Appl
7	32	88.9	911	US-08-596-985-2	Sequence 2, Appl
8	31	86.1	745	US-08-887-518-3	Sequence 3, Appl
9	31	86.1	745	US-09-023-321-3	Sequence 3, Appl
10	31	86.1	745	US-08-890-853-4	Sequence 4, Appl
11	31	86.1	745	US-09-032-475-3	Sequence 3, Appl
12	31	86.1	745	US-09-032-475-3	Sequence 3, Appl
13	31	86.1	745	US-09-099-125A-4	Sequence 4, Appl
14	31	86.1	745	US-09-099-125A-4	Sequence 4, Appl
15	31	86.1	745	US-08-890-854-4	Sequence 4, Appl
16	31	86.1	745	US-09-023-324-4	Sequence 4, Appl
17	31	86.1	745	US-09-168-629-2	Sequence 2, Appl
18	31	86.1	745	US-08-910-820-10	Sequence 10, Appl
19	31	86.1	745	US-08-810-131A-2	Sequence 2, Appl
20	31	86.1	745	US-09-109-986-4	Sequence 4, Appl
21	31	86.1	745	US-09-844-908-10	Sequence 10, Appl
22	31	86.1	745	US-09-868-758-3	Sequence 3, Appl
23	31	86.1	756	US-08-867-518-4	Sequence 4, Appl
24	31	86.1	756	US-09-023-321-4	Sequence 4, Appl
25	31	86.1	756	US-08-890-853-2	Sequence 2, Appl
26	31	86.1	756	US-09-032-475-4	Sequence 4, Appl
27	31	86.1	756	US-09-099-125A-2	Sequence 2, Appl

28	31	86.1	756	2	US-09-099-124A-2	Sequence 2, Appl
29	31	86.1	756	3	US-09-032-476-2	Sequence 2, Appl
30	31	86.1	756	3	US-08-890-854-2	Sequence 2, Appl
31	31	86.1	756	3	US-09-023-324-2	Sequence 2, Appl
32	31	86.1	756	3	US-09-168-629-15	Sequence 15, Appl
33	31	86.1	756	3	US-08-910-820-9	Sequence 9, Appl
34	31	86.1	756	4	US-09-109-986-2	Sequence 2, Appl
35	31	86.1	756	4	US-09-844-908-9	Sequence 9, Appl
36	31	86.1	756	4	US-09-868-758-4	Sequence 4, Appl
37	31	86.1	758	4	US-07-756-250-16	Sequence 16, Appl
38	31	86.1	996	4	US-09-417-197-123	Sequence 123, App
39	31	86.1	997	4	US-09-417-197-123	Sequence 121, App
40	30	83.3	122	4	US-08-936-165A-397	Sequence 397, App
41	30	83.3	363	1	US-07-681-704A-2	Sequence 2, Appl
42	30	83.3	417	3	US-08-640-906-4	Sequence 4, Appl
43	30	83.3	417	3	US-08-640-906-4	Sequence 18, Appl
44	30	83.3	417	4	US-09-395-936-4	Sequence 4, Appl
45	30	83.3	417	4	US-09-395-936-18	Sequence 18, Appl

## ALIGNMENTS

RESULT 1  
US-09-252-991A-27150  
Sequence 27150, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US-60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US-60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 27150  
LENGTH: 829  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-27150

Query Match 100.0%; Score 36; DB 4; Length 829;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSYL 6  
|||||  
Db 486 LDMSYL 491

RESULT 2  
US-09-134-001C-4300  
Sequence 4300, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US-60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US-60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 4300  
LENGTH: 462  
TYPE: PRT

ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4300  
Query Match 88.9%; Score 32; DB 4; Length 462;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSY 5  
DB 159 LDMSY 163  
RESULT 3  
US-09-252-991A-17139  
Sequence 17139, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 17139  
LENGTH: 597  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-17139  
Query Match 88.9%; Score 32; DB 4; Length 597;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 DMSYL 6  
DB 153 DMSYL 157  
RESULT 4  
US-09-107-532A-4902  
Sequence 4902, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSER: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER READABLE FORM:  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 4902:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 651 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1..651  
SEQUENCE DESCRIPTION: SEQ ID NO: 4902:  
US-09-107-532A-4902  
Query Match 88.9%; Score 32; DB 4; Length 651;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSY 5  
DB 360 LDMSY 364  
RESULT 5  
US-08-484-105-16  
Sequence 16, Application US/08484105  
Patent No. 5589341  
GENERAL INFORMATION:  
APPLICANT: STILLMAN, Bruce  
APPLICANT: BELL, Stephen P  
APPLICANT: KOBAYASHI, Ryuji  
APPLICANT: RINE, Jasper  
APPLICANT: FOSS, Margit  
APPLICANT: McNALLY, Francis J  
APPLICANT: LAURENSEN, Patricia  
APPLICANT: HERSKOWITZ, Ira  
APPLICANT: Li, Joachim J  
APPLICANT: GAVIN, Kimberly  
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSER: FLHER, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,105  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman Ph.D., Richard Atton  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: A-59032/DJB/BAO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 494-8700  
TELEFAX: (415) 494-8771  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:

LENGTH: 706 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-484-105-16

Query Match 88.9%; Score 32; DB 1; Length 706;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSY 5  
Db 193 LDMSY 197

RESULT 6  
US-08-484-106-16  
Sequence 16, Application US/08484106  
Patent No. 5614618  
GENERAL INFORMATION:  
APPLICANT: STILLMAN, Bruce  
APPLICANT: BELL, Stephen P  
APPLICANT: KOBAYASHI, Ryuji  
APPLICANT: RINE, Jasper  
APPLICANT: FOSS, Margit  
APPLICANT: MCNALLY, Francis J  
APPLICANT: LAURENSEN, Patricia  
APPLICANT: HERSKOWITZ, Ira  
APPLICANT: LI, Joachim J  
APPLICANT: GAVIN, Kimberly  
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHER, HOHACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
City: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,106  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman Ph.D., Richard Aron  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: A-59032/DVB/RAO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 494-8700  
TELEFAX: (415) 494-8771  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 706 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-484-106-16

Query Match 88.9%; Score 32; DB 1; Length 706;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSY 5  
Db 193 LDMSY 197

RESULT 7  
US-08-596-985-2  
Sequence 2, Application US/08596985  
Patent No. 5736374  
GENERAL INFORMATION:  
APPLICANT: Berka, Randy M.  
APPLICANT: Hucul, John A.  
APPLICANT: Ward, Michael  
TITLE OF INVENTION: Increased Production of  
BETA-galactosidase in Aspergillus oryzae  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genencor International, Inc  
STREET: 180 Kimball Way  
CITY: South San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/596,985  
FILING DATE: 05-FEB-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/267,631  
FILING DATE: 29-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Horn, Margaret A  
REGISTRATION NUMBER: 33,401  
REFERENCE/DOCKET NUMBER: GC250  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 742-7536  
TELEFAX: (415) 742-7217  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 911 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-596-985-2

Query Match 88.9%; Score 32; DB 1; Length 911;  
Best Local Similarity 83.3%; Pred. No. 6.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMSYL 6  
Db 675 LDMSYL 680

RESULT 8  
US-08-887-518-3  
Sequence 3, Application US/08887518  
Patent No. 5843721  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
APPLICANT: Wu, Lin  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-887-518-3

Query Match 86.1%; Score 31; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDMSYL 6  
Db 738 LDMSWL 743

RESULT 9  
US-09-023-321-3  
Sequence 3, Application US/0902321  
Patent No. 5844073  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
APPLICANT: Wu, Lin  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,321  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-321-3

Query Match 86.1%; Score 31; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDMSYL 6  
Db 738 LDMSWL 743

RESULT 10  
US-08-890-853-4  
Sequence 4, Application US/08890853  
Patent No. 5851812  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Moroncz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-853-4

Query Match 86.1%; Score 31; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDMSYL 6  
Db 738 LDMSWL 743

RESULT 11  
US-09-032-475-3  
Sequence 3, Application US/09032475  
Patent No. 5854003  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
APPLICANT: Wu, Lin  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP  
;; STREET: 268 BUSH STREET, SUITE 3200  
;; CITY: SAN FRANCISCO  
;; STATE: CALIFORNIA  
;; COUNTRY: USA  
;; ZIP: 94104  
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;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
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;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/032,475  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/887,518  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: OSMAN, RICHARD A  
;; REGISTRATION NUMBER: 36,627  
;; REFERENCE/DOCKET NUMBER: T97-008  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 343-4341  
;; TELEFAX: (415) 343-4342  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 745 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
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;; US-09-032-475-3  
;;  
Query Match 86.1%; Score 31; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSTL 6  
Db 738 LDMSTL 743  
;;  
RESULT 12  
US-09-099-125A-4  
;; Sequence 4, Application US/09099125A  
;; Patent No. 5916760  
;; GENERAL INFORMATION:  
;; APPLICANT: Goeddel, David V.  
;; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
;; NUMBER OF SEQUENCES: 4  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP  
;; STREET: 268 BUSH STREET, SUITE 3200  
;; CITY: SAN FRANCISCO  
;; STATE: CALIFORNIA  
;; COUNTRY: USA  
;; ZIP: 94104  
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;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
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;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/099,125A  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/890,853  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: OSMAN, RICHARD A  
;; REGISTRATION NUMBER: 36,627  
;; REFERENCE/DOCKET NUMBER: T97-006-1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 343-4341  
;; TELEFAX: (415) 343-4342  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 745 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;;  
;; US-09-099-124A-4  
;;  
Query Match 86.1%; Score 31; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSTL 6  
Db 738 LDMSTL 743  
;;  
RESULT 13  
US-09-099-124A-4  
;; Sequence 4, Application US/09099124A  
;; Patent No. 5939302  
;; GENERAL INFORMATION:  
;; APPLICANT: Goeddel, David V.  
;; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
;; NUMBER OF SEQUENCES: 4  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP  
;; STREET: 268 BUSH STREET, SUITE 3200  
;; CITY: SAN FRANCISCO  
;; STATE: CALIFORNIA  
;; COUNTRY: USA  
;; ZIP: 94104  
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;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/099,124A  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/890,853  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: OSMAN, RICHARD A  
;; REGISTRATION NUMBER: 36,627  
;; REFERENCE/DOCKET NUMBER: T97-006-1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 343-4341  
;; TELEFAX: (415) 343-4342  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 745 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
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;; US-09-099-124A-4  
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Query Match 86.1%; Score 31; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSTL 6  
Db 738 LDMSTL 743

;; NAME: OSMAN, RICHARD A  
;; REGISTRATION NUMBER: 36,627  
;; REFERENCE/DOCKET NUMBER: T97-006-1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 343-4341  
;; TELEFAX: (415) 343-4342  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 745 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
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;; US-09-099-125A-4  
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Query Match 86.1%; Score 31; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSTL 6  
Db 738 LDMSTL 743  
;;  
RESULT 13  
US-09-099-124A-4  
;; Sequence 4, Application US/09099124A  
;; Patent No. 5939302  
;; GENERAL INFORMATION:  
;; APPLICANT: Goeddel, David V.  
;; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
;; NUMBER OF SEQUENCES: 4  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP  
;; STREET: 268 BUSH STREET, SUITE 3200  
;; CITY: SAN FRANCISCO  
;; STATE: CALIFORNIA  
;; COUNTRY: USA  
;; ZIP: 94104  
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;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/099,124A  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/890,853  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: OSMAN, RICHARD A  
;; REGISTRATION NUMBER: 36,627  
;; REFERENCE/DOCKET NUMBER: T97-006-1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 343-4341  
;; TELEFAX: (415) 343-4342  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 745 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;;  
;; US-09-099-124A-4  
;;  
Query Match 86.1%; Score 31; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSTL 6  
Db 738 LDMSTL 743

Db 738 LDWSWL 743

## RESULT 14

US-09-032-476-4  
Sequence 4, Application US/09032476  
Patent No. 6235492  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Cao, Zhaoan  
APPLICANT: R. gnier, Catherine  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,476  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/890,854  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-032-476-4

Query Match 86.1%; Score 31; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWSYL 6  
Db 738 LDWSWL 743

RESULT 15  
US-08-890-854-4  
Sequence 4, Application US/08890854  
Patent No. 6235512  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Cao, Zhaoan  
APPLICANT: R. gnier, Catherine  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA

COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,854  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-854-4

Query Match 86.1%; Score 31; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWSYL 6  
Db 738 LDWSWL 743

Search completed: February 18, 2004, 14:41:51  
Job time : 8.06579 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds  
(without alignments)  
75.239 Million cell updates/sec

Title: US-09-643-260-15

Perfect score: 36  
Sequence: 1 LDMSYL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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12: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	6	10 US-09-847-940B-15	Sequence 15, Appl
2	36	100.0	6	11 US-09-847-946A-15	Sequence 15, Appl
3	34	94.4	98	12 US-10-287-274-432	Sequence 432, App
4	32	88.9	6	10 US-09-847-940B-14	Sequence 14, Appl
5	32	88.9	6	11 US-09-847-946A-14	Sequence 14, Appl
6	32	88.9	27	11 US-09-974-879-385	Sequence 385, App
7	32	88.9	27	11 US-09-305-735-385	Sequence 385, App
8	32	88.9	27	12 US-09-818-683-385	Sequence 385, App
9	32	88.9	376	12 US-10-369-493-12565	Sequence 12565, A
10	32	88.9	412	12 US-10-374-780A-1378	Sequence 1378, App
11	32	88.9	445	15 US-10-156-761-8567	Sequence 8567, App
12	32	88.9	525	12 US-10-369-493-267	Sequence 267, App
13	32	88.9	542	12 US-10-369-493-913	Sequence 913, App
14	32	88.9	560	12 US-10-369-493-13768	Sequence 13768, A
15	32	88.9	561	9 US-09-815-242-12101	Sequence 12101, A

16	32	88.9	562	12 US-10-032-585-7639	Sequence 7639, App
17	32	88.9	583	12 US-10-369-493-15366	Sequence 15366, A
18	32	88.9	724	12 US-10-369-493-2523	Sequence 2523, App
19	32	88.9	1024	15 US-10-213-990-10	Sequence 30, Appl
20	32	88.9	1689	15 US-10-080-943-2	Sequence 2, Appl1
21	31	86.1	6	10 US-09-847-940B-2	Sequence 2, Appl1
22	31	86.1	6	11 US-09-847-946A-2	Sequence 2, Appl1
23	31	86.1	6	11 US-09-847-946A-3	Sequence 3, Appl1
24	31	86.1	7	11 US-09-847-946A-37	Sequence 37, Appl1
25	31	86.1	8	11 US-09-847-946A-30	Sequence 30, Appl1
26	31	86.1	8	11 US-09-847-946A-38	Sequence 38, Appl1
27	31	86.1	9	11 US-09-847-946A-29	Sequence 29, Appl1
28	31	86.1	9	11 US-09-847-946A-32	Sequence 32, Appl1
29	31	86.1	9	11 US-09-847-946A-35	Sequence 35, Appl1
30	31	86.1	9	11 US-09-847-946A-36	Sequence 36, Appl1
31	31	86.1	10	11 US-09-847-946A-31	Sequence 31, Appl1
32	31	86.1	10	11 US-09-847-946A-34	Sequence 34, Appl1
33	31	86.1	11	11 US-09-847-946A-28	Sequence 28, Appl1
34	31	86.1	11	11 US-09-847-946A-132	Sequence 132, App
35	31	86.1	11	11 US-09-847-946A-140	Sequence 140, App
36	31	86.1	13	11 US-09-847-946A-143	Sequence 143, App
37	31	86.1	13	11 US-09-847-946A-144	Sequence 144, App
38	31	86.1	13	11 US-09-847-946A-145	Sequence 145, App
39	31	86.1	13	11 US-09-847-946A-148	Sequence 148, App
40	31	86.1	17	11 US-09-847-946A-141	Sequence 141, App
41	31	86.1	17	11 US-09-847-946A-142	Sequence 142, App
42	31	86.1	17	11 US-09-847-946A-146	Sequence 146, App
43	31	86.1	17	11 US-09-847-946A-147	Sequence 147, App
44	31	86.1	18	11 US-09-847-946A-131	Sequence 131, App
45	31	86.1	18	11 US-09-847-946A-135	Sequence 135, App

## ALIGNMENTS

RESULT 1  
US-09-847-940B-15  
; Sequence 15, Application US/09847940B  
; Patent No. US20020156000A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J.  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-117CP  
; CURRENT APPLICATION NUMBER: US/09/847.940B  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIORITY FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-15

Query Match 100.0%; Score 36; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSYL 6  
DB 1 LDMSYL 6  
RESULT 2  
US-09-847-946A-15  
; Sequence 15, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J

```
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hamnig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-15
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Query Match          100.0%; Score 36; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LDMSYL 6
Db 1 LDMSYL 6
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RESULT 3
US-10-287-274-432
Sequence 432, Application US/10287274
Publication No. US20030181408A1
GENERAL INFORMATION:
APPLICANT: Foreysth, R. Allym
APPLICANT: Ohlsen, Karl
APPLICANT: Zykkind, Judith
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THEREOF
FILE REFERENCE: EITRA.008DVI
CURRENT APPLICATION NUMBER: US/10/287,274
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US 60/164415
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: US 09/711164
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 469
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 432
LENGTH: 98
TYPE: PRT
ORGANISM: Escherichia coli
US-10-287-274-432
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Query Match          94.4%; Score 34; DB 12; Length 98;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LDMSYL 6
Db 67 LDMSYL 72
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RESULT 4
US-09-847-940B-14
Sequence 14, Application US/09847940B
Patent No. US2002015600A1
GENERAL INFORMATION:
APPLICANT: May, Michael J.
APPLICANT: Ghosh, Sankar
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-117CP
```

```
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-14
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Query Match          88.9%; Score 32; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LDMSYL 6
Db 1 LDMSFL 6
```

```
RESULT 5
US-09-847-946A-14
Sequence 14, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hamnig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-14
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Query Match          88.9%; Score 32; DB 11; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LDMSYL 6
Db 1 LDMSFL 6
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RESULT 6
US-09-974-879-385
Sequence 385, Application US/09974879
Publication No. US20030028003A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 125 Human Secreted Proteins
FILE REFERENCE: P2020P2
CURRENT APPLICATION NUMBER: US/09/974,879
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/239,893
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 09/818,663
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; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,900
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,908
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,908
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,984
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,985
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/066,094
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,100
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,089
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,095
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,090
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 385
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-974-879-385

Query Match      88.9%; Score 32; DB 11; Length 27;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSY 5
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Db      8 LDMSY 12

RESULT 7
US-09-305-736-385
; Sequence 385, Application US/09305736
; Publication No. US20030088078A1
; GENERAL INFORMATION:
; APPLICANT: Peng et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P1
; CURRENT APPLICATION NUMBER: US/09/305,736
; PRIOR FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: PCT/US98/23435
; EARLIER FILING DATE: 1998-11-04
; EARLIER APPLICATION NUMBER: 60/064,911
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,912
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,983
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,900
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,988
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,987
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; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,908
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,984
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,985
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/066,094
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,100
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,089
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,095
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,090
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 612
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 385
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-305-736-385

Query Match      88.9%; Score 32; DB 11; Length 27;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSY 5
      |||||
Db      8 LDMSY 12

RESULT 8
US-09-818-683-385
; Sequence 385, Application US/09818683
; Publication No. US20030211472A1
; GENERAL INFORMATION:
; APPLICANT: Peng et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P1
; CURRENT APPLICATION NUMBER: US/09/818,683
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 612
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 385
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-818-683-385

Query Match      88.9%; Score 32; DB 12; Length 27;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSY 5
      |||||
Db      8 LDMSY 12

RESULT 9
US-10-369-493-12565
; Sequence 12565, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
```

```

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12565
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(376)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-12565

Query Match          88.9%; Score 32; DB 12; Length 376;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DMSYL 5
Db      372 LDMSY 376

RESULT 10
US-10-374-780A-1378
; Sequence 1378, Application US/10374780A
; Publication No. US2004001927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James
; APPLICANT: Brown, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: Patent version 3.2
; SEQ ID NO 1378
; LENGTH: 412
; TYPE: PRT
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; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Orthologous to G1062
US-10-374-780A-1378

Query Match          88.9%; Score 32; DB 12; Length 412;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DMSYL 6
Db      57 DMSYL 61

RESULT 11
US-10-156-761-8567
; Sequence 8567, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8567
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8567

Query Match          88.9%; Score 32; DB 15; Length 445;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DMSYL 6
Db      394 DMSYL 398

RESULT 12
US-10-369-493-267
; Sequence 267, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 267
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Xenorhabdus nematophilus
US-10-369-493-267
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Query Match 88.9%; Score 32; DB 12; Length 525;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 DMSYL 6  
Db 87 DMSYL 91

RESULT 13  
US-10-369-493-913  
; Sequence 913, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; PRIOR FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 913  
; LENGTH: 542  
; TYPE: PRT  
; ORGANISM: Archaeoglobus fulgidus  
US-10-369-493-913

Query Match 88.9%; Score 32; DB 12; Length 542;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSYL 6  
Db 292 DMSYL 296

RESULT 14  
US-10-369-493-13768  
; Sequence 13768, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; PRIOR FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 13768  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Pseudomonas fluorescens  
US-10-369-493-13768

Query Match 88.9%; Score 32; DB 12; Length 560;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 DMSYL 6  
Db 117 DMSYL 121

Db 117 DMSYL 121

RESULT 15  
US-09-815-242-12101  
; Sequence 12101, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA, 011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12101  
; LENGTH: 561  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-815-242-12101

Query Match 88.9%; Score 32; DB 9; Length 561;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 DMSYL 6  
Db 117 DMSYL 121

Search completed: February 18, 2004, 15:42:00  
Job time : 16.7529 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds  
(without alignments)  
41.814 Million cell updates/sec

Title: US-09-643-260-15  
Perfect score: 36  
Sequence: 1 LDMSYL 6

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /SIDSI/gcgdata/geneseq/emb1/AA1980.DAT:\*  
2: /SIDSI/gcgdata/geneseq/emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/geneseq/emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/geneseq/emb1/AA1983.DAT:\*  
5: /SIDSI/gcgdata/geneseq/emb1/AA1984.DAT:\*  
6: /SIDSI/gcgdata/geneseq/emb1/AA1985.DAT:\*  
7: /SIDSI/gcgdata/geneseq/emb1/AA1986.DAT:\*  
8: /SIDSI/gcgdata/geneseq/emb1/AA1987.DAT:\*  
9: /SIDSI/gcgdata/geneseq/emb1/AA1988.DAT:\*  
10: /SIDSI/gcgdata/geneseq/emb1/AA1989.DAT:\*  
11: /SIDSI/gcgdata/geneseq/emb1/AA1990.DAT:\*  
12: /SIDSI/gcgdata/geneseq/emb1/AA1991.DAT:\*  
13: /SIDSI/gcgdata/geneseq/emb1/AA1992.DAT:\*  
14: /SIDSI/gcgdata/geneseq/emb1/AA1993.DAT:\*  
15: /SIDSI/gcgdata/geneseq/emb1/AA1994.DAT:\*  
16: /SIDSI/gcgdata/geneseq/emb1/AA1995.DAT:\*  
17: /SIDSI/gcgdata/geneseq/emb1/AA1996.DAT:\*  
18: /SIDSI/gcgdata/geneseq/emb1/AA1997.DAT:\*  
19: /SIDSI/gcgdata/geneseq/emb1/AA1998.DAT:\*  
20: /SIDSI/gcgdata/geneseq/emb1/AA1999.DAT:\*  
21: /SIDSI/gcgdata/geneseq/emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/geneseq/emb1/AA2001.DAT:\*  
23: /SIDSI/gcgdata/geneseq/emb1/AA2002.DAT:\*  
24: /SIDSI/gcgdata/geneseq/emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	6	23	ABB08737	Mutated IKKbeta NE
2	100.0	6	23	AAW48520	NBD mutant peptide
3	100.0	6	24	ABU08430	Human NEMO binding
4	100.0	756	23	ABB77301	Human IKKbeta muta
5	94.4	98	22	AAAG8962	E. coli growth and
6	91.7	193	22	AAU04899	Microsomepoxa eve
7	88.9	6	23	ABB08736	Mutated IKKbeta NE
8	88.9	6	23	AAW48519	NBD mutant peptide
9	88.9	6	24	ABU08429	Human NEMO binding

10	32	88.9	320	22	ABG13516
11	32	88.9	320	22	ABG27654
12	32	88.9	393	19	AAV11025
13	32	88.9	393	23	AAU76667
14	32	88.9	455	22	AAAG8777
15	32	88.9	462	23	ABP39455
16	32	88.9	465	22	ABG18718
17	32	88.9	561	22	AAU36508
18	32	88.9	562	23	ABP78802
19	32	88.9	706	18	AAW22231
20	32	88.9	707	18	AAW14137
21	32	88.9	708	22	ABBS6811
22	32	88.9	737	23	ABP65156
23	32	88.9	756	23	ABP77300
24	32	88.9	793	22	ABBS6973
25	32	88.9	911	17	AAK92508
26	32	88.9	937	22	ABBS6195
27	32	88.9	952	22	ABG22297
28	32	88.9	1005	18	AAW11238
29	32	88.9	1317	22	ABG18723
30	32	88.9	1483	21	AAAG4640
31	32	88.9	1493	21	AAAG4639
32	32	88.9	1495	21	AAAG30440
33	32	88.9	1505	21	AAAG30439
34	32	88.9	1544	21	AAAG4638
35	32	88.9	1556	21	AAAG30438
36	32	88.9	1675	22	AAU00418
37	32	88.9	1689	22	AAU00415
38	32	88.9	1894	22	ABG18725
39	32	88.9	5464	22	ABG11810
40	31	86.1	6	23	ABBS08725
41	31	86.1	6	23	AAW48530
42	31	86.1	6	23	AAW48555
43	31	86.1	6	24	ABU08418
44	31	86.1	7	23	AAW48534
45	31	86.1	8	23	AAW48527

ALIGNMENTS

RESULT 1  
ID ABB08737 standard; peptide; 6 AA.  
AC ABB08737;  
XX  
XX  
DE 14-JUN-2002 (first entry)  
XX  
XX  
DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 15.  
XX  
XX  
XX IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
XX kinase activation; leukocyte; inflammation; E-selectin; osteoclast;  
XX autoimmune disease; transplant rejection; osteoporosis; cancer;  
XX Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;  
XX rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
XX corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;  
XX osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;  
XX dermatological; antibacterial; antiparasitic; antineoplastic;  
XX antiarthritic; osteopathic; antitumor; mutant; mutain.  
XX  
XX Homo sapiens.  
OS  
OS Synthetic.  
FH Key Location/Qualifiers  
FT Misc-difference 5 /note="Wildtype Trp substituted by Tyr"  
FT  
PN WO200183547-A2.  
XX  
XX 08-NOV-2001.  
PD  
XX

PF 02-MAY-2001; 2001WO-US40654.  
XX  
XX 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
XX  
PA (UYVA ) UNIV YALE.  
XX  
XX May MJ, Ghosh S;  
XX  
XX WPI; 2002-179350/23.  
XX  
XX Modulating NF-kappaB induction in a cell, useful for treating e.g.  
PT inflammatory disorders; osteoporosis and cancer, comprises contacting a  
PT cell with an anti-inflammatory compound comprising at least one NEMO  
PT binding domain -  
XX  
XX Claim 23; Page 45; 82pp; English.  
XX  
XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
CC comprising contacting a cell with an anti-inflammatory compound  
CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
CC (ABB77313). The compound has acts through selective inhibition of  
CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
CC interaction results in inhibition of IKKbeta kinase activation and  
CC subsequent decreased phosphorylation of Ikbppa. The compound may also  
CC act (directly or indirectly) by blocking the recruitment of leukocytes  
CC into sites of acute and chronic inflammation, by down-regulating the  
CC expression of E-selectin on leukocytes or by blocking osteoclast  
CC differentiation. The compound is useful in treating NF-kB mediated  
CC conditions, where the condition is an inflammatory disorder, an  
CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
CC telangiectasia. The inflammatory disorder is asthma, allergies,  
CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
CC sporadic arthritis. Also for Crohn's disease, ulcerative colitis,  
CC polyarthritis, scleroderma, Wegner's granulomatosis, temporal arteritis,  
CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
CC diseases include HIV and influenza. The compound may also be useful for  
CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
CC sunburn or aging. The compound may be used to replace corticosteroids in  
CC an application in which corticosteroids are used, including  
CC immunosuppression in transplants and cancer therapy. Also for identifying  
CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
CC The compound may be administered alone or in combination with other known  
CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
CC binding domain of IKKbeta.  
XX  
XX Sequence 6 AA;  
SO  
Query Match 100.0%; Score 36; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 LDMSTYL 6  
DB 1 LDMSTYL 6  
RESULT 2  
ID AAM48520  
AA AAM48520 standard; Peptide; 6 AA.  
XX  
XX AAM48520;  
AC  
XX  
XX 20-MAR-2002 (first entry)  
DT  
XX  
XX NBD mutant peptide SEQ ID NO 15.

XX  
XX Antiinflammatory; antiaesthetic; cytotoxic; antipsoriatic; neurotropic;  
XX antineumatic; antiaesthetic; osteopathic; antipsoriatic; virucide;  
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
XX cytokine; NF-kappaB; Ikbppa kinase beta; IKKbeta; cancer; psoriasis;  
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX autoimmune disorder; multiple sclerosis; transplant rejection;  
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
XX Synthetic.  
XX  
XX WO200183554-A2.  
XX  
XX 08-NOV-2001.  
XX  
XX  
XX 02-MAY-2001; 2001WO-US14346.  
XX  
XX 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
XX  
XX (PRAE-) PRAECIS PHARM INC.  
XX (UYVA ) UNIV YALE.  
XX  
XX May MJ, Ghosh S, Fandels MA, Phillips K;  
XX  
XX WPI; 2002-121889/16.  
XX  
XX Novel antiinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis -  
XX  
XX Example 6; Page 48; 88pp; English.  
XX  
XX The invention relates to an antiinflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain  
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
CC cytotoxic, antipsoriatic, antineumatic, antiaesthetic, osteopathic,  
CC antiatherosclerotic, immunosuppressive, dermatological, neuroprotective,  
CC neurotropic, antiatherosclerotic, virucide and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
CC activation by blocking interaction of Ikbppa kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of Ikbppa. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
XX  
XX Sequence 6 AA;  
SO  
Query Match 100.0%; Score 36; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 LDMSTYL 6  
DB 1 LDMSTYL 6  
RESULT 3  
ID ABU08430  
AA ABU08430 standard; peptide; 6 AA.

```

XX AC ABB08430;
XX DT 12-JUN-2003 (first entry)
XX DE Human NEMO binding site (NBD) mutant peptide #13.
XX
XX KM Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
XX KM Ikappab kinase-beta; Ikappab kinase-alpha; IKKalpha; NF-kappab;
XX KM nuclear factor-kappab induction; inflammatory disorder;
XX KM autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
XX KM atherosclerosis; viral infection; Ataxia telangiectasia;
XX KM transplantation detection; immunosuppressive; osteopathic;
XX KM cytostatic; neurotropic; neuroprotective; antiatherosclerotic; virucide;
XX KM vasotropic; antirheumatic; antiarthritic; mutant; mutein.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN US2002156000-A1.
XX PD 24-OCT-2002.
XX PF 02-MAY-2001; 2001US-0847940.
XX PR 02-MAY-2000; 2000US-201261P.
XX PR 22-AUG-2000; 2000US-0643260.
XX PA (MAYM/) MAY M J.
XX PA (GHOS/) GHOSH S.
XX PI May MJ, Ghosh S;
XX DR WPI; 2003-209142/20.
XX DR N-PSDB; ABX94271, ABX94272.
XX
XX PT Novel antiinflammatory peptide compounds comprising NEMO binding
XX PT domain, useful for modulating NF-kappab induction in a cell and for
XX PT treating NF-kappab-mediated inflammation disorders e.g., asthma,
XX PT psoriasis, vasculitis -
XX
XX PS Claim 22; Page 17; 47pp; English.
XX
XX CC The present invention relates to antiinflammatory compounds comprising
XX CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
XX CC found on Ikappab kinase-beta (IKKbeta) and Ikappab kinase-alpha
XX CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
XX CC are useful for modulating nuclear factor-kappab (NF-kappab) induction
XX CC in a cell, where the compounds are capable of blocking the interaction
XX CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
XX CC antiinflammatory compound further comprises at least one membrane
XX CC translocation domain. The compounds are useful for treating
XX CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
XX CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
XX CC telangiectasia, and for transplantation detection. The compounds of
XX CC the invention block NF-kappab induction by IKK but do not inhibit
XX CC the basal activity of NF-kappab. ABB08418-ABB08432 represent human
XX CC NBD mutant peptides.
XX
XX SQ Sequence 6 AA;

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Query Match 100.0%; Score 36; DB 24; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LDMSYL 6
   |||||
DB 1 LDMSYL 6

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RESULT 4
ABB77301
ID ABB77301 standard; protein; 756 AA.

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XX AC ABB77301;
XX DT 14-JUN-2002 (first entry)
XX DE Human IKKbeta mutant W741Y.
XX
XX KM IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappab; NF-kB;
XX KM kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
XX KM autoimmune disease; transplant rejection; osteoporosis; cancer;
XX KM Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;
XX KM rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
XX KM corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
XX KM osteopathic; cytostatic; neurotropic; neuroprotective; anti-HIV; human;
XX KM antiatherosclerotic; virucide; antialexic; antiallergic;
XX KM dermatological; antibacterial; antipneumonic; antirheumatic;
XX KM antiarthritic; osteopathic; antitumor; mutant; mutein.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200183547-A2.
XX PD 08-NOV-2001.
XX PF 02-MAY-2001; 2001WO-US40654.
XX PR 02-MAY-2000; 2000US-201261P.
XX PR 22-AUG-2000; 2000US-0643260.
XX PA (UYVA ) UNIV YALE.
XX PI May MJ, Ghosh S;
XX DR WPI; 2002-179350/23.
XX
XX PT Modulating NF-kappab induction in a cell, useful for treating e.g.
XX PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
XX PT cell with an anti-inflammatory compound comprising at least one NEMO
XX PT binding domain -
XX
XX PS Example 11; Page -; 82pp; English.
XX
XX CC The invention relates to modulating NF-kappab (NF-kB) induction in a cell
XX CC comprises contacting a cell with an anti-inflammatory compound
XX CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
XX CC (ABB77313). The compound has acts through selective inhibition of
XX CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
XX CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
XX CC interaction results in inhibition of IKKbeta kinase activation and
XX CC subsequent decreased phosphorylation of Ikappab. The compound may also
XX CC act (directly or indirectly) by blocking the recruitment of leukocytes
XX CC into sites of acute and chronic inflammation, by down-regulating the
XX CC expression of E-selectin on leukocytes or by blocking osteoclast
XX CC differentiation. The compound is useful in treating NF-kB mediated
XX CC conditions, where the condition is an inflammatory disorder, an
XX CC autoimmune disease, transplant rejection, osteoporosis, cancer,
XX CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
XX CC telangiectasia. The inflammatory disorder is asthma, allergies,
XX CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
XX CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
XX CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
XX CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
XX CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
XX CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
XX CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
XX CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
XX CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
XX CC diseases include HIV and influenza. The compound may also be useful for

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CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta  
 CC mutant, useful in examples of the invention.  
 CC Note: The present sequence is not given in the specification but is  
 CC derived from GenBank Accession No. 014920 (AB077294).

SO Sequence 756 AA;

Query Match 100.0%; Score 36; DB 23; Length 756;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSYL 6  
 DB 737 LDMSYL 742

#### RESULT 5

AAG98962 ID AAG98962 standard; Protein; 98 AA.

AC AAG98962;

DT 26-SEP-2001 (first entry)

DE E. coli growth and proliferation related protein sequence SEQ ID NO:432.

KM Escherichia coli; growth; proliferation; microbial; antimicrobial;

OS Bacterial infection; microorganism.

OS Escherichia coli.

PN WO200134810-A2.

PD 17-MAY-2001.

PF 09-NOV-2000; 2000WO-US30950.

PR 09-NOV-1999; 99US-0164415.

PA (ELIT-) ELITRA PHARM INC.

PI Forsyth RA, Ohlsen K, Zyskind J,

WPI; 2001-335933/35.

DR N-PSDB; AAH84633.

PT Novel nucleic acids that inhibit Escherichia coli proliferation, useful  
 PT for screening for homologous genes and for designing expression vectors

PS Claim 19; Page 490-491; 522pp; English.

CC AAH84373 to AAH84499 represent Escherichia coli growth and proliferation  
 CC related DNA sequences (I). AAH84500 to AAH84670 encode the E. coli  
 CC growth and proliferation related proteins given in AAG99078 and AAG98830  
 CC to AAG98999. (I) can be used as potential targets for the generation of  
 CC new antimicrobial agents, and for identification of compounds which  
 CC interact with the gene products of (I). In addition the expression of  
 CC (I) and the purification of the proteins, the purified proteins can be  
 CC used to generate reagents and screen small molecule libraries or other  
 CC candidate compound libraries for compounds that can be further developed  
 CC to yield novel antimicrobial compounds. In addition, nucleic acid probes  
 CC complementary to (I) that are specific for particular species of  
 CC microorganisms can be used to identify particular microorganism species  
 CC in clinical specimens, therefore, providing a rapid and dependable  
 CC method by which to identify the causative agents of a bacterial  
 CC infection. Also, antibodies generated against proteins translated from

CC mRNA transcribed from proliferation-required sequences can also be used  
 CC to screen for specific microorganisms that produce such proteins in a  
 CC species-specific manner. AAH84371 and AAH84670 represent sequencing  
 CC primers used in the isolation of E. coli growth and proliferation  
 CC related sequence, which are used in an example from the present  
 CC invention.

SO Sequence 98 AA;

Query Match 94.4%; Score 34; DB 22; Length 98;  
 Best Local Similarity 83.3%; Pred. No. 67;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSYL 6  
 DB 67 LDMSYL 72

#### RESULT 6

AAU04899 ID AAU04899 standard; Protein; 193 AA.

AC AAU04899;

DT 26-SEP-2001 (first entry)

DE Micromonospora evernimycin biosynthetic enzyme evyMR2.

KM Evernimycin; antibiotic; bottle-neck gene; orthomycin;

OS fermentation; resistance mechanism gene; evyMR2.

OS Micromonospora carbonacea var. africana.

PN WO200151639-A2.

PD 19-JUL-2001.

PF 12-JAN-2001; 2001WO-US01187.

PR 12-JAN-2000; 2000US-0175751.

PA (SCHE) SCHERING CORP.

PI Hosted TJ, Horan AC, Wang TX;

WPI; 2001-442147/47.

DR N-PSDB; AAS08693.

PT New nucleic acid molecules encoding evernimycin pathway gene  
 PT products, useful for improving yields of evernimycin, to produce new  
 PT evernimycin and as probes to identify homologous sequences -

PS Claim 19; Fig 11; 109pp; English.

CC The sequence is a protein, evyMR2, encoded by a resistance mechanism  
 CC gene. The protein comprises one of 98 enzymes of the  
 CC evernimycin antibiotic biosynthetic pathway. A vector comprising a  
 CC M. carbonacea evernimycin biosynthetic pathway resistance gene  
 CC product is useful for selecting for a transfected or transformed host  
 CC cell. An integrative version of the vector is useful for introducing a  
 CC the genus Micromonospora. The DNA encoding the biosynthetic proteins is  
 CC useful for synthesizing novel evernimycin-related compounds, arising  
 CC from modifications of the DNA sequence designed to change glycosyl and  
 CC modified oxetane acid groups contained in evernimycin, for  
 CC expressing functional or mutant evernimycin biosynthetic enzyme for  
 CC evaluation, diagnosis and preferably biosynthesis of evernimycin or  
 CC other secondary metabolic products, improving the yield of evernimycin  
 CC and to produce novel evernimycin and also as a hybridization probe to  
 CC identify homologous sequences. The encoded polypeptides are useful for  
 CC combinatorial biosynthesis to generate libraries of orthomycin, e.g.  
 CC evernimycin analogues/homologues and drug discovery. The  
 CC DNA encoding the integrase allows for increasing a given gene dosage. The

CC Integrative vector can be used to permanently integrate copies of a  
 CC heterologous gene of choice into chromosomes of different hosts and to  
 CC integrate genes which increase the yield of known products or to generate  
 CC novel products such as hybrid antibiotics or other novel secondary  
 CC metabolites. The vector can also be used to integrate antibiotic  
 CC resistance genes in order to carry out bioconversions with compounds to  
 CC which the strain is normally sensitive and is thus useful in fermentation  
 CC processes involving e.g. Streptomyces antibiotics.

XX Sequence 193 AA;

CC Query Match 91.7%; Score 33; DB 22; Length 193;

CC Best Local Similarity 83.3%; Pred. No. 2e+02;

CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSYL 6

DB 139 LDMSYL 144

RESULT 7

AB08736

AC ABB08736;

DT 14-JUN-2002 (first entry)

DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 14.

XX IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
 XX kinase activation; leukocyte; inflammation; E-selectin; osteoclast;  
 XX autoimmune disease; transplant rejection; osteoporosis; cancer;  
 XX Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;  
 XX rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 XX corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;  
 XX osteopathic; cytotoxic; nocotropic; neuroprotective; anti-HIV; human;  
 XX antiarteriosclerotic; vinuclide; antiaesthetic; antiallergic;  
 XX dermatological; antibacterial; antipsoriatic; antineumatic;  
 XX antiarthritic; osteopathic; antitumor; mutant; mutain.

XX Homo sapiens.  
 XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 5 /note= "Wildtype Trp substituted by Phe"

XX WO200183547-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US40654.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (UYTA) UNIV YALE.

XX May MJ, Ghosh S;

XX WPI; 2002-179350/23.

XX Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 XX inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 XX cell with an anti-inflammatory compound comprising at least one NEMO  
 XX binding domain

XX Claim 23; Page 45; 82pp; English.

XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 XX comprises contacting a cell with an anti-inflammatory compound  
 XX (ABB08725-ABB08742) comprising at least one NEMO binding domain

CC (ABB7213). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of I-kappaB. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
 CC binding domain of IKKbeta.

XX Sequence 6 AA;

CC Query Match 88.9%; Score 32; DB 23; Length 6;

CC Best Local Similarity 83.3%; Pred. No. 9.3e+05;

CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSYL 6

DB 1 LDMSYL 6

RESULT 8

AA048519

AC AA048519;

DT 20-MAR-2002 (first entry)

DE NBD mutant peptide SEQ ID NO 14.

XX Anti-inflammatory; antiarthritic; cytosolic; antipsoriatic; nocotropic;  
 XX antineumatic; antiarthritic; osteopathic; antibacterial; vinuclide;  
 XX immunosuppressive; dermatological; neuroprotective; antineuroleptic;  
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 XX cytokine; NF-kappaB; I-kappaB kinase beta; IKKbeta; cancer; psoriasis;  
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 XX autoimmune disorder; multiple sclerosis; transplant rejection;  
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA) UNIV YALE.  
 XX  
 XX  
 PI May MJ, Ghosh S, Finkelstein MA, Phillips K,  
 XX WPI, 2002-121889/16.  
 XX  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 XX Example 6; Page 48; 86pp; English.  
 XX  
 XX The invention relates to an antiinflammatory compound (especially  
 CC AAM4628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytoactive, antiproliferative, antineoplastic, antitumor, osteoprotective,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC neurotropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g., asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis, transplant rejection, osteoporosis,  
 CC Alzheimer's disease, atherosclerosis, viral infections, and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX Sequence 6 AA;  
 XX  
 SQ  
 Query Match 88.9%; Score 32; DB 23; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSYL 6  
 |||||  
 Db 1 LDMSFL 6  
 |||||  
 RESULT 9  
 ABU08429  
 ID ABU08429 standard; peptide; 6 AA.  
 XX  
 AC ABU08429;  
 XX  
 DT 12-JUN-2003 (first entry)  
 XX  
 DE Human NEMO binding site (NBD) mutant peptide #12.  
 XX  
 XX Human; antiinflammatory compound; NEMO binding domain; NBD: IKKbeta;  
 KM IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;  
 KM nuclear factor-kappaB induction; inflammatory disorder;  
 KM autoimmune disease; osteoporosis; cancer; Alzheimer's disease;  
 KM atherosclerosis; viral infection; Ataxia telangiectasia;  
 KM transplant rejection; immunosuppressive; osteopathic;  
 KM cytoactive; neurotropic; neuroprotective; antiatherosclerotic; virucide;  
 KM vasotropic; antineoplastic; antitumor; mutant; mutcin.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 XX US2002156000-A1.  
 XX

PD 24-OCT-2002.  
 XX  
 XX 02-MAY-2001; 2001US-0847940.  
 PF  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR  
 XX 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (MAYM/) MAY M J.  
 PA (GHOS/) GHOSH S.  
 XX  
 XX May MJ, Ghosh S;  
 PI  
 XX WPI, 2003-209142/20.  
 DR  
 XX  
 XX Novel antiinflammatory peptide compounds comprising NEMO binding  
 PT domain, useful for modulating NF-kappaB induction in a cell and for  
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,  
 PT psoriasis, vasculitis -  
 XX  
 XX Claim 22; Page 17; 47pp; English.  
 XX  
 XX The present invention relates to antiinflammatory compounds comprising  
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are  
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha  
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention  
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction  
 CC in a cell, where the compounds are capable of blocking the interaction  
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The  
 CC antiinflammatory compound further comprises at least one membrane  
 CC translocation domain. The compounds are useful for treating  
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia  
 CC telangiectasia, and for transplantation detection. The compounds of  
 CC the invention block NF-kappaB induction by IKK but do not inhibit  
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human  
 CC NBD mutant peptides.  
 CC  
 XX Sequence 6 AA;  
 XX  
 SQ  
 Query Match 88.9%; Score 32; DB 24; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSYL 6  
 |||||  
 Db 1 LDMSFL 6  
 |||||  
 RESULT 10  
 ABG13516  
 ID ABG13516 standard; Protein; 320 AA.  
 XX  
 XX ABG13516;  
 AC  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #13507.  
 XX  
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KM food supplement; medical imaging; diagnostic; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US08631.  
 XX  
 XX 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 XX (HYSR-) HYSRQ INC.  
 PA

XX Drmanac RT, Liu C, Tang YT;  
XX WPI, 2001-639362/73.  
DR N-PSDB; AAS77703.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX  
PS Claim 20; SEQ ID No 43875; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 320 AA;  
XX  
Query Match 88.9%; Score 32; DB 22; Length 320;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2 DMSYL 6  
Db 240 DMSYL 244

RESULT 11  
ABG27654  
ID ABG27654 standard; Protein; 320 AA.  
XX  
AC ABG27654;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #27645.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US08631.  
XX  
PR 31-MAR-2000; 2000US-0540217.  
PR 23-AUG-2000; 2000US-0649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;

XX WPI, 2001-639362/73.  
DR N-PSDB; AAS91841.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX  
PS Claim 20; SEQ ID No 58013; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 320 AA;  
XX  
Query Match 88.9%; Score 32; DB 22; Length 320;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2 DMSYL 6  
Db 240 DMSYL 244

RESULT 12  
AAV11025  
ID AAV11025 standard; Protein; 393 AA.  
XX  
AC AAV11025;  
XX  
DT 08-JUN-1999 (first entry)  
XX  
DE H. pylori ORF 02ge41622\_14875000\_c2\_65 outer membrane protein.  
XX  
KW Vaccine; probe; diagnostic; ORF; cell envelope protein;  
KW secreted protein; cytoplasmic protein; cellular protein.  
XX  
OS Helicobacter pylori.  
XX  
PN WO9824475-A1.  
XX  
PD 11-JUN-1998.  
XX  
PF 05-DEC-1997; 97WO-US22104.  
XX  
PR 14-JUL-1997; 97US-0891928.  
PR 05-DEC-1996; 96US-0759625.  
PR 25-MAR-1997; 97US-0823745.  
XX  
PA (ASTR ) ASTRA AB.  
XX  
PI Alm RA, Castriotta LM, Dolg PC, Kabok Z, Smith D;

DR WPI; 1998-133051/29.  
 DR N-PSDB; AAX30554.  
 XX  
 PT New isolated *Helicobacter pylori* nucleic acids - used to develop  
 products for the diagnosis, prevention and treatment of infection by  
 PT *H. pylori* and other *Helicobacter* species  
 XX  
 PS Claims 37, 41; Page 187-188; 339pp; English.  
 XX  
 CC Recombinant or substantially pure preparations of *H. pylori* polypeptides  
 CC are disclosed, together with the nucleic acids encoding them. In all,  
 CC 97 ORFs are shown. The proteins are variously cell envelope proteins,  
 CC cytoplasmic proteins, secreted proteins or other cellular proteins.  
 CC Vaccines containing the nucleic acids or proteins are claimed, as are  
 CC probes containing at least 8 nucleotides from the nucleic acid  
 CC sequences. The vaccines are useful for treating or reducing the risk of  
 CC -*H. pylori* infections, and the probes can be used diagnostically for  
 CC detecting the presence of *Helicobacter* in a sample. The products are  
 CC also of use in screening for compounds having the ability to interfere  
 CC with the *H. pylori* life cycle or to inhibit *H. pylori* infection.  
 CC  
 SQ Sequence 393 AA;  
 XX  
 Query Match 88.9%; Score 32; DB 19; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+02; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0;  
 QY 2 DMSYL 6  
 |||||  
 Db 284 DMSYL 288  
 XX  
 RESULT 13  
 AAU76667  
 ID AAU76667 standard; Protein: 393 AA.  
 XX  
 AC AAU76667;  
 XX  
 DT 21-MAY-2002 (first entry)  
 XX  
 DE *Helicobacter pylori* LPS biosynthesis enzyme HP1031 from strain J99.  
 XX  
 KM LPS; lipopolysaccharide; biosynthesis enzyme; HP1031, strain J99;  
 KM antibiotic; vaccine; human self epitope.  
 XX  
 OS *Helicobacter pylori*.  
 OS  
 PN WO200207763-A2.  
 XX  
 PD 31-JAN-2002.  
 XX  
 PF 12-JUL-2001; 2001WO-IB01536.  
 XX  
 PR 12-JUL-2000; 2000GB-0017149.  
 XX  
 PA (CHIR-) CHIRON SPA.  
 PI Del Giudice G, Rappuoli R;  
 XX  
 DR WPI; 2002-217026/27.  
 XX  
 PT Novel *Helicobacter pylori* useful for prophylaxis and treatment of  
 PT *Helicobacter pylori* infection, comprises mutation that prevents  
 PT synthesis of auto-reactive lipopolysaccharide -  
 XX  
 PS Disclosure; Fig 1; 23pp; English.  
 XX  
 CC The present invention relates to a new *Helicobacter pylori* bacterium  
 CC having a mutation that affects lipopolysaccharide (LPS) biosynthesis,  
 CC where either LPS is not expressed or LPS which is expressed does not  
 CC induce antibodies which cross-react with human self epitopes. The  
 CC invention is useful for treating or preventing, and in the manufacture  
 CC of a vaccine for treatment or prophylaxis of *Helicobacter pylori*

CC infection. The vaccine does not induce antibodies which cross-react  
 CC with human self epitopes. The present amino acid sequence represents  
 CC the *Helicobacter pylori* LPS biosynthesis enzyme HP1031 that was  
 CC isolated from strain J99 and was used in the methods of the invention.  
 XX  
 SQ Sequence 393 AA;  
 XX  
 Query Match 88.9%; Score 32; DB 23; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+02; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0;  
 QY 2 DMSYL 6  
 |||||  
 Db 284 DMSYL 288  
 XX  
 RESULT 14  
 AAG82777  
 ID AAG82777 standard; Protein: 455 AA.  
 XX  
 AC AAG82777;  
 XX  
 DT 03-SEP-2001 (first entry)  
 XX  
 DE S. epidermidis open reading frame protein sequence SEQ ID NO:2648.  
 XX  
 KW *Staphylococcus epidermidis* SRI strain; infection; diagnosis;  
 KW vaccination; endocarditis.  
 XX  
 OS *Staphylococcus epidermidis*.  
 XX  
 PN WO200134809-A2.  
 XX  
 PD 17-MAY-2001.  
 XX  
 PF 09-NOV-2000; 2000WO-US30782.  
 XX  
 PR 09-NOV-1999; 99US-0164258.  
 XX  
 PA (GLAXO) GLAXO GROUP LTD.  
 XX  
 PI Kimerly WJ;  
 XX  
 DR WPI; 2001-316495/33.  
 XX  
 DR N-PSDB; AAX53627.  
 XX  
 PT Nucleic acids encoding polypeptides from *Staphylococcus epidermidis*,  
 PT useful for vaccinating against infections, e.g. endocarditis -  
 XX  
 PS Claim 18; Page 694-695; 2188pp; English.  
 XX  
 CC AAH53304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
 CC (II), given in AAG81454 to AAG83120, from *Staphylococcus epidermidis*.  
 CC (I) and (II) can have antibacterial activity and therefore can be used  
 CC in vaccination. The nucleic acids (I) may be used to produce the  
 CC S. epidermidis polypeptides (II) via the production of vectors  
 CC containing them which are used to produce host cells which express the  
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
 CC used to vaccinate subjects and to raise antibodies against the bacteria.  
 CC The polypeptides may also be used to assay for other inhibitors of their  
 CC activity and therefore identify compounds that may be used for the  
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to  
 CC AAH55090 represent specifically claimed S. epidermidis genomic DNA  
 CC polynucleotide sequences from the present invention. AAH55091 to  
 CC AAH55098 represent oligonucleotide sequences and primers which are used  
 CC in the exemplification of the present invention.  
 CC N.B. The present invention specifically claims all the polynucleotide  
 CC sequences given in the sequence listing of the present specification,  
 CC however the sequence listing only goes up to SEQ ID NO:4454 so even  
 CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,  
 CC no sequences are present for SEQ ID NO:4455 to 4464.  
 XX  
 SQ Sequence 455 AA;

Query Match 88.9%; Score 32; DB 22; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSY 5  
 |||||  
 DB 152 LDMSY 156

## RESULT 15

ABP39455  
 ID ABP39455 standard; Protein; 462 AA.

XX AC ABP39455;

XX DT 24-JUL-2002 (first entry)

XX DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4300.

XX KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;

XX KM antibacterial; gene therapy.

XX OS Staphylococcus epidermidis.

XX PN US6380370-B1.

XX PD 30-APR-2002.

XX PF 13-AUG-1998; 98US-0134001.

XX PR 14-AUG-1997; 97US-055779P.

XX PR 08-NOV-1997; 97US-064964P.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PI Doucette-Stamm LA, Bush D;

XX DR WPI; 2002-381255/41.

XX DR N-PSDB; ABN92000.

XX PT Novel isolated nucleic acid encoding a Staphylococcus epidermidis  
 XX PR polypeptide, useful for diagnosing and treating bacterial infections -

XX PS Disclosure; SEQ ID 4300; 267bp; English.

XX CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading  
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences  
 CC given in ABP35124 to ABP37960. The S. epidermidis sequences have  
 CC antibacterial activity and can be used in gene therapy. The sequences  
 CC can also be used in the diagnosis and treatment of bacterial infections,  
 CC particularly S. epidermidis infections. The sequences can be used to  
 CC screen for compounds able to interfere with the S. epidermidis life  
 CC cycle or inhibit S. epidermidis infection.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from the  
 CC USPTO web site.

XX SQ Sequence 462 AA;

Query Match 88.9%; Score 32; DB 22; Length 462;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSY 5  
 |||||  
 DB 159 LDMSY 163

Search completed: February 18, 2004, 14:26:25  
 Job time : 22.7763 secs

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OM proteain - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds  
(without alignments)  
89.145 Million cell updates/sec

Title: US-09-643-260-14

Perfect score: 35  
Sequence: 1 LDMSFL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_ricent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	136	P72919	P72919 synechocyst
2	35	100.0	362	044634	044634 caenorhabdi
3	35	100.0	573	08YXB1	08YXB1 anabaena sp
4	35	100.0	2621	09JLM23	09JLM23 arabidopsis
5	35	100.0	2658	09SGR4	09SGR4 arabidopsis
6	33	94.3	208	08E014	08E014 streptococc
7	33	94.3	216	08B659	08B659 streptococc
8	33	94.3	556	08DC15	08DC15 vibrio vuln
9	33	94.3	608	09YXS9	09YXS9 drosophila
10	33	94.3	732	061565	061565 crassostrea
11	33	94.3	962	09SVS7	09SVS7 arabidopsis
12	33	91.4	176	044486	044486 caenorhabdi
13	32	91.4	203	098GA7	098GA7 rhizobium 1
14	32	91.4	203	08UDW9	08UDW9 agrobacteri
15	32	91.4	284	086850	086850 streptomyce
16	32	91.4	284	09RKS7	09RKS7 streptomyce

17	32	91.4	339	09CE52	09CE52 lactococcus
18	32	91.4	377	09Z4X8	09Z4X8 streptomyce
19	32	91.4	556	055814	055814 synechocyst
20	32	91.4	744	08N261	08N261 homo sapien
21	32	91.4	870	048N639	048N639 homo sapien
22	32	91.4	927	092882	092882 listeria in
23	32	91.4	927	08Y482	08Y482 listeria in
24	32	91.4	939	08Y0R3	08Y0R3 anabaena sp
25	32	91.4	1466	042930	042930 schizosacch
26	31	88.6	124	09D247	09D247 mus musculu
27	31	88.6	131	09Q0P1	09Q0P1 tomato leaf
28	31	88.6	134	08QXY7	08QXY7 tomato leaf
29	31	88.6	134	088558	088558 tomato leaf
30	31	88.6	134	08Q110	08Q110 tobacco cur
31	31	88.6	134	056991	056991 papaya leaf
32	31	88.6	134	072708	072708 cotton leaf
33	31	88.6	134	091MP1	091MP1 pepper leaf
34	31	88.6	134	099DR2	099DR2 chili leaf
35	31	88.6	134	08V019	08V019 cotton leaf
36	31	88.6	134	099319	099319 tomato leaf
37	31	88.6	134	098742	098742 tomato leaf
38	31	88.6	134	08J216	08J216 tomato leaf
39	31	88.6	134	08J110	08J110 cotton leaf
40	31	88.6	134	072711	072711 cotton leaf
41	31	88.6	134	091BQ2	091BQ2 ageratum ye
42	31	88.6	134	08V012	08V012 hollyhock l
43	31	88.6	134	091GX4	091GX4 tobacco gem
44	31	88.6	134	091N49	091N49 cotton leaf
45	31	88.6	134	09QDE5	09QDE5 tomato leaf

#### ALIGNMENTS

RESULT 1  
ID P72919 PRELIMINARY: PRT: 136 AA.  
AC P72919:  
DT 01-FEB-1997 (TRENBLrel. 02, Created)  
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)  
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)  
DE Hypothetical protein slr1082.  
GN slr1082.  
OS Synechocystis sp. (strain PCC 6803).  
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
OK NCBI\_taxid=1148;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97061201; PubMed=8905231;  
RA Kaneko T., Sato S., Kozami H., Tanaka A., Asanizu E., Nakamura Y.,  
RA Miyajima N., Hirosewa M., Sugita M., Sasaoka S., Kimura T.,  
RA Hosouchi T., Matsuno A., Muraki A., Nakasaki N., Nario K., Okumura S.,  
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M.,  
RA Tabata S.,  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the  
RT entire genome and assignment of potential protein-coding regions."  
RL DNA Res. 3:109-136 (1996).  
DR EMBL; D90901; BAA16936.1;  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 136 AA; 15774 MW; E80414D06029605E CRC64;

Query Match 100.0%; Score 35; DB 16; Length 136;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
Db 42 LDMSFL 47

RESULT 2  
044634

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ID 044634 PRELIMINARY; PRT; 362 AA.
AC 044634;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical 42.3 kDa protein.
GN P16B4.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RL investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Davidson S., Wohlmann P., Bauer C., O'Neal D.;
RT "The sequence of C. elegans cosmid P16B4.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF039048; AAB94233.1; -.
DR WormPep; P16B4.2; CE17012.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
KM Hypothetical protein.
SQ SEQUENCE 362 AA; 4225 MW; 33D99BF0FD14006 CRC64;

Query Match 100.0%; Score 35; DB 5; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
DB 26 LDMSFL 31

RESULT 3
08YXB1 PRELIMINARY; PRT; 573 AA.
ID 08YXB1;
AC 08YXB1;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Sulfate permease family protein.
GN ALI1304.
OS Arabidopsis sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxId=103690;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21595285; PubMed=11759840;
RA Kaneo T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriyuchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RL cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213 (2001).
DR EMBL; AF003585; BAB73261.1; -.
DR InterPro; IPR002645; STAS.
DR InterPro; IPR001902; Sulph_transpt.

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DR Pfam; PF01740; STAS; 1.
DR Pfam; PF00916; Sulfate_transp; 1.
DR PROSITE; PS0801; STAS; 1.
KM Complete proteome.
SQ SEQUENCE 573 AA; 60239 MW; F2D1C2P6A8B36CC CRC64;

Query Match 100.0%; Score 35; DB 16; Length 573;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
DB 357 LDMSFL 362

RESULT 4
09LMZ3 PRELIMINARY; PRT; 2621 AA.
ID 09LMZ3;
AC 09LMZ3;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE T6D22.24.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altafi H., Bel Q., Chin C., Chou J., Choi E., Corn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharly N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thavert A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Becker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC T6D22 from chromosome
RT 1.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Becker J.R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Becker J.R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bel B., Chin C., Chou J., Choi E.,
RA Corn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu S., Mukharly N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thavert A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Becker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC026875; AAF79832.1; -.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
SQ SEQUENCE 2621 AA; 297067 MW; B3534E176F237044 CRC64;

Query Match 100.0%; Score 35; DB 10; Length 2621;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
DB 2184 LDMSFL 2189

RESULT 5

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09SGE4  
ID 09SGE4 PRELIMINARY; PRT; 2658 AA.  
AC 09SGE4;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE T23G18.2.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC euroside II; Brassicales; Brassicaceae; Arabidopsie.  
NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,  
RA Kim C., Alcafi H., Bel O., Chin C., Chlou J., Choi E., Conn L.,  
RA Conway A., Gonzales A., Hansen N., Howling B., Koo T., Lam B., Lee J.,  
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukherjee N., Nguyen M.,  
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,  
RA Tortum M., Vayberg M., Yu G., Federpfeil N.A., Theologis A.,  
RA Ecker J.R.;  
RT "Genomic sequence for Arabidopsis thaliana BAC T23G18 from chromosome  
RT 1."  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC011438; AAP18257.1; -  
DR InterPro; IPR006153; Na\_H\_porter.  
DR Pfam; PF00999; Na\_H\_exchanger; 1.  
SQ SEQUENCE 2658 AA; 301830 MW; 77ECF9366784293F CRC64;  
Query Match 100.0%; Score 35; DB 10; Length 2658;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LDMSFL 6  
Db 2221 LDMSFL 2226  
RESULT 6  
Q8E014 PRELIMINARY; PRT; 208 AA.  
ID 08E014;  
AC 08E014;  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Riboflavin synthase, alpha subunit.  
GN RIBE OR SAG0747.  
OS Streptococcus agalactiae (serotype V).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
NCBI\_TaxID=216466;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=2603 V/R / Serotype V;  
RC MEDLINE=22222988; PubMed=12200547;  
RA Tettein H., Masjumi V., Cieslewicz M.J., Eisen J.A., Peterson S.,  
RA Wessels M.E., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,  
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,  
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,  
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,  
RA Carey H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,  
RA Iacobini E.T., Bretton C., Galli G., Mariani M., Vegni F., Malone D.,  
RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,  
RA Frazer C.M.;  
RT "Complete genome sequence and comparative genomic analysis of an  
RT emerging human pathogen, serotype V Streptococcus agalactiae.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).  
DR EMBL; AE014225; AAM99634.1; -  
DR TIGR; SAG0747; -  
KW Complete proteome.  
SQ SEQUENCE 208 AA; 22666 MW; 4C25AB59FC1BE601 CRC64;  
Query Match 94.3%; Score 33; DB 16; Length 208;

Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LDMSFL 6  
Db 198 MDMSFL 203  
RESULT 7  
Q8E659 PRELIMINARY; PRT; 216 AA.  
ID 08E659;  
AC 08E659;  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
GN GBS0768.  
OS Streptococcus agalactiae (serotype III).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
NCBI\_TaxID=216495;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NEM316 / Serotype III;  
RC MEDLINE=22242508; PubMed=12354221;  
RA Glaeser P., Rusniok C., Buchliesser C., Chevalier F., Frangeul L.,  
RA Msaek T., Zouine M., Couve E., Lalloui L., Poyart C., Trieu-Cuot P.,  
RA Kunat F.;  
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing  
RT invasive neonatal disease.";  
RL Mol. Microbiol. 45:1499-1513(2002).  
DR EMBL; AL766847; CAD46412.1; -  
DR Sagaliet; gbs0768; -  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 216 AA; 23587 MW; B55556D5F751CEBF CRC64;  
Query Match 94.3%; Score 33; DB 16; Length 216;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LDMSFL 6  
Db 206 MDMSFL 211  
RESULT 8  
Q8DC15 PRELIMINARY; PRT; 556 AA.  
ID 08DC15;  
AC 08DC15;  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Sulfate permease and.  
GN VVI1638.  
OS Vibrio vulnificus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrrio.  
NCBI\_TaxID=672;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CMCP6;  
RC Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,  
RA Choy H.E.;  
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";  
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE016802; AA010056.1; -  
KW Complete proteome.  
SQ SEQUENCE 556 AA; 59064 MW; 1EC2AC082F0602DA CRC64;  
Query Match 94.3%; Score 33; DB 16; Length 556;  
Best Local Similarity 83.3%; Pred. No. 4.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
 Db 356 LDMSFL 361

RESULT 9  
 QYX69 PRELIMINARY; PRT; 608 AA.

AC QYX69; (TEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)  
 DE CG9220 protein.  
 GN CG9220.  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NC NCBI\_TaxID=7227;  
 RX MEDLINE=2019606; PubMed=10731132;  
 RP STRAIN=Berkley;  
 RC STRAIN=Berkley;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutcliffe G.A., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers J.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,  
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,  
 RA Beeson K.Y., Berns P.V., Berman B.P., Bhandari D., Bolintsov S.,  
 RA Borkova D., Botchan M.R., Boutin J., Brokstein P., Brotlier P.,  
 RA Burlingame A., Buzam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo J., Delcher A., Deng Z., Dey A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W.,  
 RA Foster C., Gabrielian A.B., Gary N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Hariri N.L., Harvey D., Heilmann T.J., Hernandez J.R., Houck J.,  
 RA Hostin M., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kenton J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Labko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Paclet J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,  
 RA Shue B.C., Siden-Klamor I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spadling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Zheng H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
 RA Barton J., An H., Baldwin D., Barton J., Beeson K.Y., Buzam D.A.,  
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
 RA Ferreira S., Frise E., Galle R.F., Gary N.S., George R.A.,  
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howard L.J.,  
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
 RA Paclet J., Paragas V., Park S., Patel S., Pfeiffer B.,

RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RT "Sequencing of Drosophila melanogaster genome.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RA Mira S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.B., Smith C.D.,  
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.B.,  
 RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Seale S.M.J., Smith B., Shu S., Smucniak F., Whitfield B.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 RT "Annotation of Drosophila melanogaster genome.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RN SEQUENCE FROM N.A.  
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RN SEQUENCE FROM N.A.  
 RA FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF003499; AAF46479.2; --  
 DR FlyBase; FBgn0030662; CG9220.  
 SQ SEQUENCE 608 AA; 70423 MW; 9278ADDA4A3745CA CRC64;

Query Match 94.3%; Score 33; DB 5; Length 608;  
 Best Local Similarity 83.3%; Pred. No. 5; 1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
 Db 151 LDMSFL 156

RESULT 10  
 ID 061565 PRELIMINARY; PRT; 732 AA.

AC 061565;  
 DT 01-AUG-1998 (TEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TEMBLrel. 07, Last sequence update)  
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)  
 DE 1-keppa-B kinase.  
 GN 1-keppa-B kinase.  
 GN 1-keppa-B kinase.  
 OS Craspedostrea gigas (Pacific oyster).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;  
 OC Ostreoidae; Ostreidae; Craspedostrea.  
 NC NCBI\_TaxID=29159;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA MEDLINE=99332074; PubMed=10405163;  
 RA Bescoubas J.M., Briant L., Montagnani C., Hez S., Devaux C., Roch P.;  
 RT "Oyster Ixk-1-like protein shares structural and functional properties  
 with its mammalian homologues.";  
 RL FEBS Lett. 453:293-298(1999).  
 RT -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; AF051320; AAC05683.1; --  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_Thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PRODOM; PD000001; Prot\_kinase; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_SF; 1.  
 KW ATP-binding, kinase, Serine/threonine-protein kinase, Transferase.  
 SQ SEQUENCE 732 AA; 84215 MW; 871EB8D1CA3E33AF CRC64;

Query Match 94.3%; Score 33; DB 5; Length 732;  
 Best Local Similarity 83.3%; Pred. No. 6; 1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
:|||||  
Db 719 LDMSFL 724

## RESULT 11

Q9SVS7 PRELIMINARY; PRT; 962 AA.  
AC Q9SVS7  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical 108.9 kDa protein.  
GN F1722.160 OR AT4G21700.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC euroside II; Brassicales; Brassicaceae; Arabidopsi.  
OX NCBI\_TaxId=3702;

RP SEQUENCE FROM N.A.  
RA Bevan M., Van Der Schueren J., Chuang Y.-J., Voet M., Robben J.,  
RA Volckaert G., Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.;  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Van Der Schueren J., Vandebussche F., Chuang Y.J., Breken M.,  
RA Robben J., Volckaert G., Mewes H.W., Lemcke K., Mayer K.F.X.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL035527; CAB36814.1; -  
DR EMBL; AL161555; CAB81277.1; -  
DR InterPro; IPR000269; CUNH\_oxidase.  
DR PROSITE; PS01164; COPPER\_AMINE\_OXID\_1; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 962 AA; 108894 MW; 5F48A946474B8927 CRC64;

Query Match 94.3%; Score 33; DB 10; Length 962;  
Best Local Similarity 83.3%; Pred. No. 8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
:|||||  
Db 889 LDMSFL 894

## RESULT 12

O44486 PRELIMINARY; PRT; 176 AA.  
AC O44486  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical 20.6 kDa protein.  
GN F42A6.5

OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nemata; Chordata; Rhabdita; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxId=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Br15C01 N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RA None;  
RT "Genome sequence of the nematode C. elegans: a platform for

RT Investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018 (1998).

RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Br15C01 N2;  
RA Du Z., Scheet P., Andrews S.;  
RT "The sequence of C. elegans cosmid F42A6".  
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Br15C01 N2;  
RA Waterston R.;  
RT "Direct Submission".  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF038613; AAB92050.1; -  
DR WormPep; F42A6.5; CEI7057.  
DR InterPro; IPR001357; BRCT.  
DR Pfam; PF00533; BRCT; 1.  
DR SMART; SM00292; BRCT; 1.  
DR PROSITE; PS50172; BRCT; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 176 AA; 20612 MW; 1F8E5E23AF3E25BD CRC64;

Query Match 91.4%; Score 32; DB 5; Length 176;  
Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
:|||||  
Db 37 LDMSFL 42

## RESULT 13

Q98GA7 PRELIMINARY; PRT; 203 AA.  
AC Q98GA7  
DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Hypothetical protein m113416.  
GN M113416.  
OS Rhizobium loti (Mesorhizobium loti).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Phyllobacteriaceae; Mesorhizobium.  
OX NCBI\_TaxId=381;

RP SEQUENCE FROM N.A.  
RC STRAIN=MAFF303099;  
RX MEDLINE=21082930; PubMed=11214968;  
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A.,  
RA Mochizuki Y., Nakayama S., Nakazaki N., Shlimpo S., Sugimoto M.,  
RA Takeuchi C., Yamada M., Tabata S.;  
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
Mesorhizobium loti".  
RL DNA Res. 7:331-338 (2000).  
DR EMBL; AP003001; BAB50309.1; -  
DR InterPro; IPR000534; Semialdh.  
DR Pfam; PF01118; Semialdehyde dh.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 203 AA; 21716 MW; FC61A883F2E3EEF CRC64;

Query Match 91.4%; Score 32; DB 16; Length 203;  
Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
:|||||  
Db 140 LDMSFL 145

## RESULT 14

Q8UDW9- PRELIMINARY; PRT; 203 AA.  
 ID Q8UDW9  
 AC Q8UDW9;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Hypothetical protein AtU1999.  
 GN AtU1999 OR AGR\_C\_3633.  
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Rhizobium.  
 OX NCBI\_TaxID=176299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21608550; PubMed=11743193;  
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitzajima J.P.,  
 Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,  
 Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyce D. Sr.,  
 Chapman P., Clendinning J., Deatherage G., Gillet W., Grant C.,  
 Kutayavin T., Levy R., Li M.-J., McClelland E., Palmer A.,  
 Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,  
 Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
 Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
 Chunley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
 Neeter E.W.;  
 RA "The genome of the natural genetic engineer Agrobacterium tumefaciens  
 C58."  
 RT Science 294:2317-2323(2001).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21608551; PubMed=11743194;  
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
 Quirillo B., Goldman B.S., Cao Y., Askenazi M., Halling L.,  
 Houmel K., Gordon J., Vaubin M., Iartchouk O., Epp A., Liu F.,  
 William C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,  
 Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,  
 Cielo C., Slater S.;  
 RA "Genome sequence of the plant pathogen and biotechnology agent  
 Agrobacterium tumefaciens C58."  
 RT Science 294:2323-2328(2001).  
 RL EMBL/ AB009151; AAL42992.1; -;  
 DR EMBL/ AB008117; AAK87755.1; -;  
 KW Hypothetical protein, Complete proteome  
 SQ SEQUENCE 203 AA; 21846 MW; D5BF6AC9E3C6B7CB CRC64;  
 Query Match 91.4%; Score 32; DB 16; Length 203;  
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDWSFL 6  
 DB 140 LDWTFPL 145  
 RESULT 15  
 ID 086850 PRELIMINARY; PRT; 284 AA.  
 AC 086850;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Hypothetical 31.0 kDa protein.  
 GN ORPA.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycinae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=M145;  
 RA Takano E., Chakraborty R., Mihira T., Yamada Y., Bibb M.;  
 RT "Characterisation of acbR, and acbA genes involved in gamma-  
 butyrolactone binding and synthesis in Streptomyces coelicolor.";

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ007731; CA07626.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 284 AA; 30969 MW; 38DE00712A09BE7D CRC64;  
 Query Match 91.4%; Score 32; DB 2; Length 284;  
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDWSFL 6  
 DB 125 LDWTFPL 130

Search completed: February 18, 2004, 14:35:55  
 Job time: 18.3684 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds

(without alignments)  
87.531 Million cell updates/sec

Title: US-09-643-260-14

Sequence: 1 LDMSFL 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

PIR 76:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	136	S74785	hypothetical prote
2	35	100.0	362	T32669	hypothetical prote
3	35	100.0	573	AE1969	sulfate permease f
4	35	100.0	2658	A86216	protein T23G18.2 (
5	33	94.3	962	T05845	hypothetical prote
6	32	91.4	176	T32618	hypothetical prote
7	32	91.4	203	AB2822	conserved hypothet
8	32	91.4	203	B97600	hypothetical prote
9	32	91.4	339	C86874	ABC transporter pe
10	32	91.4	377	T36246	hypothetical glycolate
11	32	91.4	404	A64151	hypothetical prote
12	32	91.4	556	S76624	integral membrane
13	32	91.4	927	AG1739	transmembrane prot
14	32	91.4	927	AH1369	transmembrane prot
15	32	91.4	939	AE2275	hypothetical prote
16	32	91.4	1466	T39557	vacuolar protein s
17	31	88.6	21	A60420	lens intrininc mem
18	31	88.6	134	S59886	C2 protein - tomat
19	31	88.6	135	QCCY4	AL2 protein - tomat
20	31	88.6	135	S07593	hypothetical prote
21	31	88.6	204	AB0188	phosphoribosyl-ATP
22	31	88.6	225	T17795	hypothetical prote
23	31	88.6	242	B96571	hypothetical prote
24	31	88.6	264	S51829	alpha-amylase inti
25	31	88.6	264	B84848	hypothetical prote
26	31	88.6	350	AG2880	dibenzothioephene d
27	31	88.6	350	G98302	thermophilic deaul
28	31	88.6	355	A12867	endo-1,4-Delta-xyla
29	31	88.6	356	A42053	gap junction prote

30	31	88.6	357	2	A49024	connexin40 - dog
31	31	88.6	358	2	S23111	connexin 40 - mouse
32	31	88.6	358	2	I38429	connexin40 - human
33	31	88.6	365	2	E97644	endo-1,4-beta-xyla
34	31	88.6	369	2	B37819	connexin-42 - chic
35	31	88.6	383	2	T38772	protein phosphates
36	31	88.6	400	2	T11921	NADH2 dehydrogenas
37	31	88.6	400	2	I50219	connexin 45.6 - ch
38	31	88.6	402	2	I46053	connexin44 - bovin
39	31	88.6	416	2	S25764	connexin 46 - rat
40	31	88.6	432	2	I39176	intrinsic membrane
41	31	88.6	440	2	I49624	gap junction prote
42	31	88.6	510	2	A45338	connexin-56 - chic
43	31	88.6	569	2	T43531	probable potassium
44	31	88.6	570	2	H87368	copper-binding pro
45	31	88.6	575	2	D84668	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

S74785 hypothetical protein elr1082 - *Synechocystis* sp. (strain PCC 6803)

C.Species: *Synechocystis* sp.

A.Variety: PCC 6803

C.Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 21-Jul-2000

C.Accession: S74785

R.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.

O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yanada, M.; Yasu

DNA Res. 3, 109-136, 1996

A>Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

A.Reference number: S74322; MUID:97061201; PMID:8905231

A.Accession: S74785

A>Status: preliminary

A.Molecule type: DNA

A.Residues: 1-136 <KAN>

A.Cross-references: EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BA16936.1; PID:g16521

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C.Superfamily: *Synechocystis* hypothetical protein elr0489

Query Match Best Local Similarity 100.0%; Score 35; DB 2; Length 136;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
DB 42 LDMSFL 47

RESULT 2  
T32669 hypothetical protein F16B4.2 - *Caenorhabditis elegans*

C.Species: *Caenorhabditis elegans*

C.Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

R.Davidson, S.; Wohlmann, P.; Bauer, C.; O'Neal, D.

submitted to the EMBL Data Library, December 1997

A.Description: The sequence of C. elegans cosmid F16B4.

A.Reference number: Z31208

A.Accession: T32669

A>Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-362 <DAV>

A.Cross-references: EMBL:AF039048; PIDN:AA94233.1; GSPDB:GN00023; CESP:F16B4.2

A.Experimental source: strain Bristol N2; clone F16B4

C.Genetics:

A.Gene: CESP:F16B4.2

A.Map position: 5

A.Introns: 48/2; 112/2; 160/3; 255/3; 291/2; 333/3

Query Match 100.0%; Score 35; DB 2; Length 362;

Best Local Similarity 100.0%; Pred. No. 46;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
|||||  
Db 26 LDMSFL 31

RESULT 3  
AB1969  
sulfate permease family protein [imported] - Nostoc sp. (strain PCC 7120)

C/Species: Nostoc sp. PCC 7120

A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002

C/Accession: AB1969

R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Ref. 8, 205-213, 2001

A/Title: Complete genomic sequence of the filamentous Nitrogen-fixing Cyanobacterium Anabaena

A/Reference number: AB1907; MUID:21595285; PMID:11759840

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-573 <XLR>

A/Cross-references: GB:BA000019; PIDN:BA073261.1; PID:q17130651; GSPDB:GN00179

A/Experimental source: strain PCC 7120

C/Genetics:

A/Gene: all1304

C/Superfamily: integral membrane protein HP0228

Query Match Best Local Similarity 100.0%; Score 35; DB 2; Length 573;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
|||||  
Db 357 LDMSFL 362

RESULT 4

AB6216  
protein T23G18.2 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C/Accession: AB6216

R/Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.P.; Hughes, B.; Hutzar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: AB6141; MUID:21016719; PMID:11130712

A/Accession: AB6216

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-2658 <STO>

A/Cross-references: GB:AE005172; NID:96579214; PIDN:AA018257.1; GSPDB:GN00141

C/Genetics:

A/Gene: T23G18.2

A/Map position: 1

Query Match Best Local Similarity 100.0%; Score 35; DB 2; Length 2658;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
|||||  
Db 2221 LDMSFL 2226

RESULT 5  
T05845  
hypothetical protein F17L22.160 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 09-Apr-1999 #sequence\_revision 09-Apr-1999 #text\_change 24-Nov-1999

C/Accession: T05845

R/Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; I

submitted to the Protein Sequence Database, February 1999

A/Reference number: Z15454

A/Accession: T05845

A/Molecule type: DNA

A/Residues: 1-962 <BEV>

A/Cross-references: EMBL:AL035527

A/Experimental source: cultivar Columbia; BAC clone F17L22

C/Genetics:

A/Map position: 4

A/Note: F17L22.160

C/Superfamily: Arabidopsis thaliana hypothetical protein F17L22.160

Query Match Best Local Similarity 94.3%; Score 33; DB 2; Length 962;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
|||||  
Db 889 LDMSFL 894

RESULT 6

T32618  
hypothetical protein F42A6.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

C/Accession: T32618

R/Du, Z.; Scheet, P.; Andrews, S.

submitted to the EMBL Data Library, December 1997

A/Description: The sequence of C. elegans cosmid F42A6.

A/Reference number: Z21201

A/Accession: T32618

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-176 <DUZ>

A/Cross-references: EMBL:AF038613; PIDN:AB92050.1; GSPDB:GN00022; CESP:F42A6.5

A/Experimental source: strain Bristol N2; Clone F42A6

C/Genetics:

A/Gene: CESP:F42A6.5

A/Map position: 4

A/Introns: 51/3; 109/3

Query Match Best Local Similarity 91.4%; Score 32; DB 2; Length 176;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
|||||  
Db 37 LDMSFL 42

RESULT 7

AB2822  
conserved hypothetical protein Atu1999 [imported] - Agrobacterium tumefaciens (strain C)

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002

C/Accession: AB2822

R/Wood, D.W.; Sebubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavln, T.; Levy, R.; Li, M.; McCle;

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, B.W.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AB2822  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-203 <KUR>  
 A:Cross-references: GB:AE008688; PIDN:AA14292.1; PID:g17740453; GSPDB:GN00186  
 C:Genetics:  
 A:Gene: Atul999  
 A:Map position: circular chromosome  
 Query Match 91.4%; Score 32; DB 2; Length 203;  
 Best Local Similarity 83.3%; Pred. No. 89;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSFL 6  
 DB 140 LDMTFL 145  
 RESULT 8  
 B97600  
 hypothetical protein AGR\_C\_3633 [imported] - Agrobacterium tumefaciens (strain C58, Cere  
 C:Species: Agrobacterium tumefaciens  
 C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002  
 C:Accession: B97600  
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
 A.; Liu, F.; Wollem, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;  
 Science 294, 2323-2328, 2001  
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
 A:Reference number: A97359; MUID:21608551; PMID:11743194  
 A:Accession: B97600  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-203 <KUR>  
 A:Cross-references: GB:AE007669; PIDN:AAK8755.1; PID:g15157123; GSPDB:GN00169  
 C:Genetics:  
 A:Gene: AGR\_C\_3633  
 A:Map position: circular chromosome  
 Query Match 91.4%; Score 32; DB 2; Length 203;  
 Best Local Similarity 83.3%; Pred. No. 89;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSFL 6  
 DB 140 LDMTFL 145  
 RESULT 9  
 C86874  
 ABC transporter permease protein ecab [imported] - Lactococcus lactis subsp. lactis (str  
 C:Species: Lactococcus lactis subsp. lactis  
 C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
 C:Accession: C86874  
 R:Boletorin, A.; Winkler, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrli  
 Genome Res. 11, 731-753, 2001  
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s  
 A:Reference number: AB6625; MUID:21235186; PMID:11337471  
 A:Accession: C86874  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-339 <STO>  
 A:Cross-references: GB:AE005176; PID:g12725040; PIDN:AAK06093.1; GSPDB:GN00146  
 A:Experimental source: strain IL1403  
 C:Genetics:  
 A:Gene: ecab  
 Query Match 91.4%; Score 32; DB 2; Length 339;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSFL 6  
 DB 140 LDMTFL 145

DB 158 LDMAFL 163  
 RESULT 10  
 T36246  
 probable glycolate oxidase - Streptomyces coelicolor  
 C:Species: Streptomyces coelicolor  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 28-Jul-2000  
 C:Accession: T36246  
 R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.  
 submitted to the EMBL Data Library, March 1999  
 A:Reference number: Z21602  
 A:Accession: T36246  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-377 <SAU>  
 A:Cross-references: EMBL:AL035640; PIDN:CA838520.1; GSPDB:GN00070; SCODEB:SCE63.05  
 A:Experimental source: strain A3(2)  
 C:Genetics:  
 A:Gene: SCODEB:SCE63.05  
 A:Superfamily: (S)-2-hydroxy-acid oxidase/ (S)-2-hydroxy-acid oxidase homology  
 P:2-296/Domain: (S)-2-hydroxy-acid oxidase homology <2HY>  
 Query Match 91.4%; Score 32; DB 2; Length 377;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSFL 6  
 DB 207 LDMSFL 212  
 RESULT 11  
 A64151  
 hypothetical protein HI0396 - Haemophilus influenzae (strain Rd KW20)  
 C:Species: Haemophilus influenzae  
 C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 08-Oct-1999  
 C:Accession: A64151  
 R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage,  
 J.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,  
 D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.  
 Science 269, 496-512, 1995  
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
 A:Reference number: A64000; MUID:95350630; PMID:7542800  
 A:Accession: A64151  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-404 <TTGR>  
 A:Cross-references: GB:U52723; GB:L42023; MID:g1573363; PIDN:AAK22055.1; PID:g1573367;  
 A>Note: best homolog was a hypothetical protein from Escherichia coli  
 Query Match 91.4%; Score 32; DB 2; Length 404;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSFL 6  
 DB 366 LDMAFL 371  
 RESULT 12  
 S76624  
 integral membrane protein HP0228 homolog 2 - Synecocystis sp. (strain PCC 6803)  
 N:Alternate names: low affinity sulfate transporter; protein slr0096  
 C:Species: Synecocystis sp.  
 A:Variety: PCC 6803  
 C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
 C:Accession: S76624  
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, B.; Nakamura, Y.; Miyajima, N.  
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud  
 DNA Res. 3, 109-136, 1996  
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocyst

8.  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S76624  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-556 <KAN>  
A:Cross-references: EMBL:D64004; GB:AB001339; NID:g1001701; PIDN:BA10568.1; PID:g100173  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Superfamily: Integral membrane protein HP0228

Query Match 91.4%; Score 32; DB 2; Length 556;  
Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
DB 364 VDMWFL 369

## RESULT 13

AG1739  
transmembrane protein [imported] - *Listeria innocua* (strain C14p11262)  
C:Species: *Listeria innocua*  
C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AG1739  
R:Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entlian, K.D.; Feihl, H.; Science 294, 849-852, 2001  
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madeno, E.; Maltournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlant, A.; Title: Comparative genomics of *Listeria* species  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AG1739  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-927 <GLA>  
A:Cross-references: GB:AL592022; PIDN:CAC97687.1; PID:G16414982; GSPDB:GN00178  
A:Experimental source: strain C14p11262  
C:Genetics:  
A:Gene: 11n2460

Query Match 91.4%; Score 32; DB 2; Length 927;  
Best Local Similarity 83.3%; Pred. No. 4.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
DB 83 LDMSFL 88

## RESULT 14

AH1369  
transmembrane protein [imported] - *Listeria monocytogenes* (strain EGD-e)  
C:Species: *Listeria monocytogenes*  
C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AH1369  
R:Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entlian, K.D.; Feihl, H.; Science 294, 849-852, 2001  
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madeno, E.; Maltournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlant, A.; Title: Comparative genomics of *Listeria* species  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AH1369  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-927 <GLA>  
A:Cross-references: GB:NC\_003210; PIDN:CAD00438.1; PID:G16411848; GSPDB:GN00177  
C:Experimental source: strain EGD-e  
C:Genetics:  
Gene: 1m02360

Query Match 91.4%; Score 32; DB 2; Length 927;  
Best Local Similarity 83.3%; Pred. No. 4.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
DB 83 LDMSFL 88

## RESULT 15

AE2275  
hypothetical protein alr3756 [imported] - *Nostoc* sp. (strain PCC 7120)  
C:Species: *Nostoc* sp. PCC 7120  
A>Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C:Accession: AE2275  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001  
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *N*  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AE2275  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-939 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BA075455.1; PID:G17132890; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr3756

Query Match 91.4%; Score 32; DB 2; Length 939;  
Best Local Similarity 83.3%; Pred. No. 4.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
DB 648 LDMSFL 653

Search completed: February 18, 2004, 14:38:50  
Job time : 7.5921 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds

(Without alignments)  
41.814 Million cell updates/sec

Title: US-09-643-260-14

Perfect score: 35

Sequence: 1 LDMSPF 6

Scoring table: BLOSUM62

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter 45 summaries

Database :  
1: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1980.DAT:\*  
2: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1981.DAT:\*  
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7: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1986.DAT:\*  
8: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1987.DAT:\*  
9: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1988.DAT:\*  
10: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1989.DAT:\*  
11: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1990.DAT:\*  
12: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1991.DAT:\*  
13: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1992.DAT:\*  
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15: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1994.DAT:\*  
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19: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1998.DAT:\*  
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21: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA2000.DAT:\*  
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23: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA2002.DAT:\*  
24: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	23	ABB08736
2	35	100.0	6	23	AA48519
3	35	100.0	6	24	ABU08429
4	35	100.0	23	ABB77300	Human NEMO binding
5	33	94.3	59	22	AAU58740
6	33	94.3	208	23	ABP30274
7	33	94.3	216	23	ABP25952
8	33	94.3	788	22	ABB64315
9	32	91.4	6	23	ABB08737

10	32	91.4	6	23	AA48520	NBD mutant peptide
11	32	91.4	6	24	ABU08430	Human NEMO binding
12	32	91.4	37	21	AA659894	Arabidopsis thaliana
13	32	91.4	37	21	AA660632	Arabidopsis thaliana
14	32	91.4	56	22	ABB03835	Human musculoskeletal
15	32	91.4	56	24	ABU13129	Novel human musc
16	32	91.4	339	23	ABB55349	Lactococcus lactis
17	32	91.4	756	23	ABB77301	Human IKKbeta muta
18	32	91.4	927	23	ABB49720	Listeria monocytog
19	31	88.6	71	22	AAU63276	Propionibacterium
20	31	88.6	83	21	AAU00107	Human secreted pro
21	31	88.6	97	22	AAU55876	Propionibacterium
22	31	88.6	124	21	AA558122	Lung cancer associ
23	31	88.6	137	22	AA67051	Human dilydroxota
24	31	88.6	149	21	AA623584	Arabidopsis thaliana
25	31	88.6	150	21	AA635712	Citric AC3 protein
26	31	88.6	157	22	AA691029	C glutamylum prote
27	31	88.6	178	21	AA623583	Arabidopsis thaliana
28	31	88.6	234	21	AA648093	Arabidopsis thaliana
29	31	88.6	234	21	AA648116	Arabidopsis thaliana
30	31	88.6	242	23	ABB91342	Herbicideally activ
31	31	88.6	259	21	AA626244	Zea mays zmc2b me
32	31	88.6	264	21	AA616701	Bacteriophage Dp-1
33	31	88.6	266	21	AA611935	Arabidopsis thaliana
34	31	88.6	277	15	AA648747	G-protein coupled
35	31	88.6	277	17	AA602719	G-protein coupled
36	31	88.6	280	21	AA611934	Arabidopsis thaliana
37	31	88.6	315	21	AA649092	Arabidopsis thaliana
38	31	88.6	315	21	AA649115	Arabidopsis thaliana
39	31	88.6	317	22	AA669701	Arabidopsis thaliana
40	31	88.6	317	23	ABG56907	Human NOV protein
41	31	88.6	343	21	AA649114	Arabidopsis thaliana
42	31	88.6	358	23	AA623968	Connexin protein C
43	31	88.6	373	23	ABP65723	Blifidobacterium lo
44	31	88.6	382	17	AAW00496	Candida albicans s
45	31	88.6	417	19	AAW49009	Mouse alpha 3 con

#### ALIGNMENTS

RESULT 1	ABB08736	standard; peptide; 6 AA.
ID	ABB08736	standard; peptide; 6 AA.
AC	ABB08736	
XX		
DT	14-JUN-2002	(first entry)
DE	Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 14.	
XX		
XX	IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;	
KW	kinase activation; leukocyte; inflammation; B-selectin; osteoclast;	
KW	autoimmune disease; transplant rejection; osteoporosis; cancer;	
KW	Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;	
KW	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;	
KW	corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;	
KW	osteopathia; cystostatic; nootropic; neuroprotective; anti-HIV; human;	
KW	antiartherosclerotic; virucide; antiasthmatic; antiallergic;	
KW	dermatological; antibacterial; antiproliferative; antineoplastic;	
KW	antiarthritic; osteopathia; antitumor; mutant; mutcin.	
OS	Homo sapiens.	
OS	Synthetic.	
FT	Key	Location/Qualifiers
FT	Misc-difference 5	
FT		/note="Wildtype Trp substituted by Phe"
PN	WO200183547-A2.	
XX		
PD	08-NOV-2001.	
XX		

PF 02-MAY-2001; 2001WO-US40654.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S;  
 XX  
 DR WPI; 2002-179350/23.  
 XX  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorder, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 XX  
 XX Claim 23; Page 45; 82pp; English.  
 XX  
 CC The invention relates to modulating NF-kappaB (NF-KB) induction in a cell  
 CC comprising contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-KB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-KB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC polyarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polyarthritis, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections,  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
 CC binding domain of IKKbeta.  
 XX  
 SQ Sequence 6 AA;  
 QY  
 DB 1 LDMSFL 6  
 1 LDMSFL 6  
 Query Match 100.0%; Score 35; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 2  
 AAM48519  
 ID AAM48519 standard; Peptide; 6 AA.  
 XX  
 AC AAM48519;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE NBD mutant peptide SEQ ID NO 14.

XX  
 XX Antiinflammatory; antiaesthetic; cytostatic; antipsoriatic; neurotropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200183554-A2.  
 PN  
 XX  
 PD 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 PF  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECTS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Fandels MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Example 6; Page 48; 86pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC nootropic, immunosuppressive, dermatological, neuroprotective,  
 CC antioptic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 6 AA;  
 QY  
 DB 1 LDMSFL 6  
 1 LDMSFL 6  
 Query Match 100.0%; Score 35; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 3  
 ABU08429  
 ID ABU08429 standard; peptide; 6 AA.

XX AC ABU08429;  
 XX DT 12-JUN-2003 (first entry)  
 XX DE Human NEMO binding site (NBD) mutant peptide #12.  
 XX KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;  
 KW IKKbeta kinase-beta; IKKalpha kinase-alpha; IKKalpha; NF-kappaB;  
 KW nuclear factor-kappaB induction; inflammatory disorder;  
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;  
 KW atherosclerosis; viral infection; Ataxia telangiectasia;  
 KW transplacental detection; immunosuppressive; osteopathic;  
 KW cytosolic; notropic; neuroprotective; antiatherosclerotic; virucide;  
 KW vasotropic; antineumatic; antitartaric; mutant; mutein.  
 XX KW Homo sapiens.  
 OS Synthetic.  
 XX PN US2002156000-A1.  
 XX PD 24-OCT-2002.  
 XX PF 02-MAY-2001; 2001US-0847940.  
 XX PR 02-MAY-2000; 2000US-201261P.  
 XX PR 22-AUG-2000; 2000US-0643260.  
 XX PA (MAYM/) MAY M J.  
 XX PA (GHOS/) GHOSH S.  
 XX PI May MJ, Ghosh S;  
 XX DR WPI; 2003-209142/20.  
 XX PT Novel antiinflammatory peptide compounds comprising NEMO binding  
 PT domain, useful for modulating NF-kappaB induction in a cell and for  
 PT creating NF-kappaB-mediated inflammation disorders e.g., asthma,  
 PT psoriasis, vasculitis -  
 XX PS Claim 22; Page 17; 47pp; English.  
 XX CC The present invention relates to antiinflammatory compounds comprising  
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are  
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha  
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention  
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction  
 CC in a cell, where the compounds are capable of blocking the interaction  
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The  
 CC antiinflammatory compound further comprises at least one membrane  
 CC translocation domain. The compounds are useful for treating  
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia  
 CC telangiectasia, and for transplacental detection. The compounds of  
 CC the invention block NF-kappaB induction by IKK but do not inhibit  
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human  
 CC NBD mutant peptides.  
 XX SQ Sequence 6 AA;  
 SQ Query Match 100.0%; Score 35; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSFL 6  
 1 LDMSFL 6  
 Db 1 LDMSFL 6  
 RESULT 4  
 ABB77300 standard; protein; 756 AA.  
 ID ABB77300  
 XX

AC ABB77300;  
 XX DT 14-JUN-2002 (first entry)  
 XX DE Human IKKbeta mutant W741F.  
 XX KW IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;  
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;  
 KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;  
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;  
 KW osteopathic; cytosolic; notropic; neuroprotective; anti-HIV; human;  
 KW dermatological; antiviral; antiparasitic; antiallergic;  
 KW antitartaric; osteopathic; antitumor; mutant; mutein.  
 XX KW Homo sapiens.  
 OS Synthetic.  
 XX PN WO200183547-A2.  
 XX PD 08-NOV-2001.  
 XX PF 02-MAY-2001; 2001WO-US40654.  
 XX PR 02-MAY-2000; 2000US-201261P.  
 XX PR 22-AUG-2000; 2000US-0643260.  
 XX PA (UYVA ) UNIV YALE.  
 XX PI May MJ, Ghosh S;  
 XX DR WPI; 2002-179350/23.  
 XX PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 XX PS Example 11; Page -; 82pp; English.  
 XX CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprises contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of IkappaB. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,

CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplant and cancer therapy. Also for identifying  
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of an IKK $\beta$  gene  
 CC mutant, useful in examples of the invention.  
 CC Note: The present sequence is not given in the specification but is  
 CC derived from Genbank Accession No. 014920 (AB077294).  
 XX

SO Sequence 756 AA;

Query Match 100.0%; Score 35; DB 23; Length 756;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
 :|||||  
 Db 737 LDMSFL 742

RESULT 5  
 ID AAU58740 standard; Protein: 59 AA.  
 XX  
 AC AAU58740;  
 XX  
 DT 13-FEB-2002 (first entry)  
 XX  
 DE Propionibacterium acnes immunogenic protein #19636.  
 XX  
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
 KW dermatological; osteopetrotic; neuroprotectant.  
 XX  
 OS Propionibacterium acnes.  
 XX  
 PN WO200181581-A2.  
 XX  
 PD 01-NOV-2001.  
 XX  
 PF 20-APR-2001; 2001WO-US12865.  
 XX  
 PR 21-APR-2000; 2000US-199047P.  
 PR 02-JUN-2000; 2000US-208841P.  
 PR 07-JUL-2000; 2000US-216747P.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Skelky YAM, Persing DH, Mitcham JT, Wang SS, Bhatia A;  
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;  
 XX  
 DR WPI: 2001-616774/71.  
 DR N-PSDB: AAS59594.  
 XX  
 PT Propionibacterium acnes polypeptides and nucleic acids useful for  
 PT vaccinating against and diagnosing infections, especially useful for  
 PT treating acne vulgaris -  
 XX

Example 1, SEQ ID No 19935; 1069pp; English.

Sequences AAU93105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and endophthalmitis. nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The

CC polypeptides may be used as antigens in the production of antibodies  
 CC specific for P. acnes proteins. These antibodies can be used to  
 CC downregulate expression and activity of P. acnes polypeptides and  
 CC therefore treat P. acnes infections. The antibodies may also be used as  
 CC diagnostic agents for determining P. acnes presence, for example, by  
 CC enzyme linked immunosorbent assay (ELISA).  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX

SO Sequence 59 AA;

Query Match 94.3%; Score 33; DB 22; Length 59;  
 Best Local Similarity 83.3%; Pred. No. 61;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
 :|||||  
 Db 18 LDMSFL 23

RESULT 6  
 ID ABP30274 standard; Protein: 208 AA.  
 XX  
 AC ABP30274;  
 XX  
 DT 02-JUL-2002 (first entry)  
 XX  
 DE Streptococcus polypeptide SEQ ID NO 9724.  
 XX  
 KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
 XX  
 OS Streptococcus agalactiae.  
 XX  
 PN WO200234771-A2.  
 XX  
 PD 02-MAY-2002.  
 XX  
 PF 29-OCT-2001; 2001WO-GB04789.  
 XX  
 PR 27-OCT-2000; 2000GB-0026333.  
 PR 24-NOV-2000; 2000GB-0028727.  
 PR 07-MAR-2001; 2001GB-0005640.  
 XX  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 XX  
 PI Telford J, Maignan V, Margatit Ros YI, Grandi G, Fraser C;  
 PI Tettelin H;  
 XX  
 DR WPI: 2002-352536/38.  
 DR N-PSDB: ABN70905.  
 XX  
 PT New Streptococcus protein for the treatment or prevention of infection  
 PT or disease caused by Streptococcus bacteria, such as meningitis, and  
 PT for detecting a compound that binds to the protein -  
 XX

Claim 1, Page 4099; 4525pp; English.

The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus (GBS) (Streptococcus agalactiae) or group A streptococcus (GAS) (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (1), nucleic acids encoding (1), ABN6044-ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyogenes. Nucleic acids encoding (1) are used to detect Streptococcus in a biological sample. (1) is used to determine whether a compound binds to (1). A composition comprising (1) or a nucleic acid encoding (1), may be

CC used as a vaccine or diagnostic composition. The disease caused by  
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
 CC acid encoding (I) may be used to recombinantly produce (I) and may be  
 CC used in gene therapy. Antibodies to (I) are used for affinity  
 CC chromatography, immunoassays, and distinguishing/identifying  
 CC Streptococcus proteins.  
 XX  
 SQ Sequence 208 AA;  
 Query Match 94.3%; Score 33; DB 23; Length 208;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSFL 6  
 DB 198 MDMSFL 203  
 RESULT 7  
 ABB25952  
 ID ABB25952 standard; Protein; 216 AA.  
 XX  
 AC ABB25952;  
 XX  
 DT 02-JUL-2002 (first entry)  
 XX  
 DE Streptococcus polypeptide SEQ ID NO 1080.  
 XX  
 XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
 KM antiinflammatory; infection; vaccine; meningitis; gene therapy.  
 XX  
 OS Streptococcus agalactiae.  
 XX  
 WO200234771-A2.  
 XX  
 PN 02-MAY-2002.  
 XX  
 PF 29-OCT-2001; 2001WO-GB04789.  
 XX  
 XX 27-OCT-2000; 2000GB-0026333.  
 PR 24-NOV-2000; 2000GB-0028727.  
 PR 07-MAR-2001; 2001GB-0005640.  
 XX  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 XX  
 PI Telford J, Maignant V, Margart Ros YI, Grandi G, Fraser C;  
 PI Tettein H;  
 XX  
 DR WPI; 2002-352536/38.  
 DR N-PSDB; ABB6583.  
 XX  
 PT New Streptococcus protein for the treatment or prevention of infection  
 PT or disease caused by Streptococcus bacteria, such as meningitis, and  
 PT for detecting a compound that binds to the protein -  
 XX  
 PS Claim 1; Page 3263; 4525pp; English.  
 XX  
 CC The invention relates to a protein (ABB25413-ABB30895) from group B  
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
 CC the specification. The proteins have antibacterial and antiinflammatory  
 CC activity. (I), nucleic acid encoding (I), ABB6044-ABB71526 and  
 CC antibodies that bind (I) are used in the manufacture of medicaments for  
 CC the treatment or prevention of infection or disease caused by  
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
 CC biological sample. (I) is used to determine whether a compound binds to  
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
 CC used as a vaccine or diagnostic composition. The disease caused by  
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
 CC acid encoding (I) may be used to recombinantly produce (I) and may be

CC used in gene therapy. Antibodies to (I) are used for affinity  
 CC chromatography, immunoassays, and distinguishing/identifying  
 CC Streptococcus proteins.  
 XX  
 SQ Sequence 216 AA;  
 Query Match 94.3%; Score 33; DB 23; Length 216;  
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSFL 6  
 DB 206 MDMSFL 211  
 RESULT 8  
 ABB64315  
 ID ABB64315 standard; Protein; 788 AA.  
 XX  
 AC ABB64315;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 19737.  
 XX  
 XX Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 FN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PP 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers BW;  
 DR WPI; 2001-656860/75.  
 DR N-PSDB; ABL08418.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 XX Disclosure; SEQ ID NO 19737; 21pp + Sequence Listing; English.  
 XX  
 PS The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins  
 CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 788 AA;  
 Query Match 94.3%; Score 33; DB 22; Length 788;  
 Best Local Similarity 83.3%; Pred. No. 9.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSFL 6  
 DB 331 LDMSFL 336

RESULT 9  
 ABB08737  
 ID ABB08737 standard; peptide; 6 AA.  
 XX  
 AC ABB08737;  
 XX  
 DT 14-JUN-2002 (first entry)  
 XX  
 DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 15.  
 XX  
 KW IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
 KW kinase activation; leukocyte; inflammation; B-selectin; osteoclast;  
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;  
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;  
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 KW corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;  
 KW osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;  
 KW antiarteriosclerotic; virucide; antiasclerotic; anti-allergic;  
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;  
 KW antiarthritic; osteopathic; antitumor; mutant; mutagen.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT MISC-difference 5 /note= "Wildtype Trp substituted by Tyr"  
 FT  
 XX  
 PN W0200183547-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US40654.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S;  
 XX  
 DR WPI; 2002-179350/23.  
 XX  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 XX  
 PS Claim 23; Page 45; 82pp; English.  
 XX  
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprises contacting a cell with an anti-inflammatory compound  
 CC (ABB08737-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of IkbppaB. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and

CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
 CC binding domain of IKKbeta.  
 XX  
 SQ Sequence 6 AA;  
 XX  
 QY Query Match 91.4%; Score 32; DB 23; Length 6;  
 DB Best Local Similarity 83.3%; Pred No. 9.3e-05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSFL 6  
 DB 1 LDMSYL 6  
 XX  
 RESULT 10  
 AAM48520  
 ID AAM48520 standard; Peptide; 6 AA.  
 XX  
 AC AAM48520;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE NBD mutant peptide SEQ ID NO 15.  
 XX  
 KW Antiinflammatory; antiasclerotic; cytostatic; antipsoriatic; nootropic;  
 KW antineumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 OS  
 XX  
 PN W0200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Fandels MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Example 6; Page 48; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15

CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM8525-AAM4619). The antiinflammatory compounds have antiasthmatic,  
 CC cycostatic, antiproliferative, antirheumatic, antiallergic, osteoprotective,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC neurotropic, antithrombotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
 CC activation by blocking interaction of I-kappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of I-kappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.

CC  
 XX  
 SQ Sequence 6 AA;

Query Match 91.4%; Score 32; DB 23; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6  
 |||||  
 Db 1 LDMSYL 6

RESULT 11

ABU08430  
 ID ABU08430 standard; peptide; 6 AA.

XX AC ABU08430;

XX DT 12-UTN-2003 (first entry)

XX DE Human NEMO binding site (NBD) mutant peptide #13.

XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;  
 KW I-kappaB kinase-beta; I-kappaB kinase-alpha; IKKalpha; NF-kappaB;  
 KW nuclear factor-kappaB induction; inflammatory disorder;  
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;  
 KW atherosclerosis; viral infection; Ataxia telangiectasia;  
 KW transplantation detection; immunosuppressive; osteopathic;  
 KW cytoskeletal; neurotropic; neuroprotective; antithrombotic; virucide;  
 KW vasotropic; antirheumatic; antiallergic; mutant; mutein.

OS Homo sapiens.  
 OS Synthetic.

XX PN US2002156000-A1.

XX PD 24-OCT-2002.

XX PF 02-MAY-2001; 2001US-0847940.

XX PR 02-MAY-2000; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

XX PA (MATM/) MAY M J.

XX PA (GHOS/) GHOSH S.

XX PI May MJ, Ghosh S;

XX DR MPI: 2003-209142/20.

XX DR N-PSDB; ABX94271, ABX94272.

XX PT Novel antiinflammatory peptide compounds comprising NEMO binding  
 PT domain, useful for modulating NF-kappaB induction in a cell and for  
 PT creating NF-kappaB-mediated inflammation disorders e.g., asthma,

PT psoriasis, vasculitis -  
 XX  
 PS Claim 22; Page 17; 47pp; English.

CC The present invention relates to antiinflammatory compounds comprising  
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are  
 CC found on I-kappaB kinase-beta (IKKbeta) and I-kappaB kinase-alpha  
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention  
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction  
 CC in a cell, where the compounds are capable of blocking the interaction  
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The  
 CC antiinflammatory compound further comprises at least one membrane  
 CC translocation domain. The compounds are useful for treating  
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia  
 CC telangiectasia, and for transplantation detection. The compounds of  
 CC the invention block NF-kappaB induction by IKK but do not inhibit  
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human  
 CC NBD mutant peptides.

XX  
 XX SQ Sequence 6 AA;

Query Match 91.4%; Score 32; DB 24; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6  
 |||||  
 Db 1 LDMSYL 6

RESULT 12

AAG59894  
 ID AAG59894 standard; Protein; 37 AA.

XX AC AAG59894;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 77522.

XX Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

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XX PR 06-MAY-1999; 99US-0132486.





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PR 26-OCT-1999; 99US-0161360.  
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Query Match 91.4%; Score 32; DB 21; Length 37;  
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OY 1 LDMSPL 6  
DB 3 LDMAFL 8

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AC AAG60632;  
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XX  
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XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
XX Arabidopsis thaliana.  
XX  
XX EP1033405-A2.  
XX  
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XX  
XX 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-012180.  
PR 09-MAR-1999; 99US-0123548.  
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PR 24-JUN-1999; 99US-0140695.  
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Best Local Similarity 83.3%; Pred. No. 57;  
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Qy 1 LDMSFL 6  
Db 3 LDMAFL 8  
  
RESULT 14  
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ID ABR03835 standard; Protein; 56 AA.  
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AC ABR03835;  
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DT 08-JAN-2002 (first entry)  
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XX  
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;  
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
KW cariant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; human; secreted protein;  
KW musculoskeletal system.  
XX  
OS Homo sapiens.  
XX  
PN WO200155367-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01338.  
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 PR 01-DEC-2000; 2000US-0250160.  
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 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.

PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX WPI; 2001-451937/48.  
 DR N-PSDB; AAL35417.  
 XX  
 PT Isolated polypeptide for treating, preventing and/or prognosing  
 PT disorders related to the musculoskeletal system including  
 PT musculoskeletal cancers and also for testing and detection e.g.  
 PT diagnosis -  
 PT  
 PS Claim 11; SEQ ID NO 1782; 781bp + Sequence Listing; English.  
 XX  
 CC The invention relates to novel genes (AAL34669-AAL37666) and proteins  
 CC (ABR03087-ABR04109) associated with the musculoskeletal system useful  
 CC for preventing, treating or ameliorating medical conditions e.g. by  
 CC protein or gene therapy. The genes are isolated from a range of human  
 CC tissues disclosed in the specification. The nucleic acids, proteins,  
 CC antibodies and (ant)agonists are useful in the diagnosis, treatment  
 CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and  
 CC other cancers of the adrenal gland, bone, bone marrow, breast,  
 CC gastrointestinal tract, liver, lung, or urogenital; (b) immune  
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;  
 CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound  
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;  
 CC and (f) infectious diseases such as viral, bacterial, fungal and  
 CC parasitic infections.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
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SQ Sequence 56 AA;

Query Match 91.4%; Score 32; DB 22; Length 56;  
 Best Local Similarity 83.3%; Pred. No. 87;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSFL 6  
Db 27 LDMSFL 32

RESULT 15  
ABU13129 standard; Protein; 56 AA.

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AC ABU13129;  
XX 26-FEB-2003 (first entry)  
XX  
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XX  
XX Musculoskeletal system antigen; cancer; metastasis;  
XX re-vascularisation; thrombosis; arteriosclerosis; mineral content;  
XX cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;  
XX post-operative tissue repair; limb regeneration; neuronal growth;  
XX neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
XX AIDS-related complex; chondrocyte growth; bone regeneration;  
XX periodontal regeneration; tissue transport; bone graft; skin aging;  
XX keratinocyte growth; hair loss; melanocyte growth; cell proliferation;  
XX cell growth; organ transplant; cell differentiation; body height;  
XX weight; hair colour; eye colour; skin; percentage of adipose tissue;  
XX pigmentation; cosmetic surgery; metabolism; biorhythm; cardiac rhythm;  
XX depression; tendency for violence; pain; reproductive capability;  
XX hormone level; endocrine level; appetite; libido; memory; stress;  
XX storage capability; fat content; lipid content; protein content;  
XX carbohydrate content; vitamin content; cofactor content;  
XX nutritional component.  
XX  
XX Homo sapiens.  
XX OS  
XX US2002147140-A1.  
XX  
XX 10-OCT-2002.  
XX  
XX 17-JAN-2001; 2001US-0764877.  
XX  
XX 31-JAN-2000; 2000US-179065P.  
XX 04-FEB-2000; 2000US-180628P.  
XX 28-JUN-2000; 2000US-214886P.  
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XX 01-SEP-2000; 2000US-229345P.  
XX 05-SEP-2000; 2000US-229509P.  
XX 05-SEP-2000; 2000US-229511P.  
XX 08-SEP-2000; 2000US-231413P.  
XX 21-SEP-2000; 2000US-234223P.  
XX 21-SEP-2000; 2000US-234274P.  
XX 25-SEP-2000; 2000US-234977P.  
XX 27-SEP-2000; 2000US-235834P.  
XX 29-SEP-2000; 2000US-236327P.  
XX 29-SEP-2000; 2000US-236367P.

PR 29-SEP-2000; 2000US-236368P.  
PR 29-SEP-2000; 2000US-236369P.  
PR 29-SEP-2000; 2000US-236370P.  
PR 02-OCT-2000; 2000US-236802P.  
PR 02-OCT-2000; 2000US-237037P.  
PR 02-OCT-2000; 2000US-237038P.  
PR 02-OCT-2000; 2000US-237039P.  
PR 02-OCT-2000; 2000US-237040P.  
PR 13-OCT-2000; 2000US-239335P.  
PR 20-OCT-2000; 2000US-240960P.  
PR 20-OCT-2000; 2000US-241785P.  
PR 20-OCT-2000; 2000US-241809P.  
PR 01-NOV-2000; 2000US-244617P.  
PR 17-NOV-2000; 2000US-249299P.  
PR 08-DEC-2000; 2000US-251856P.  
PR 08-DEC-2000; 2000US-251868P.  
PR 08-DEC-2000; 2000US-251869P.

XX (ROSE/) ROSEN C A.  
XX (RUBEN/) RUBEN S M.  
XX (BARA/) BARASH S C.  
XX  
XX Rosen CA, Ruben SM, Barash SC;  
XX WPI; 2003-128199/12.  
XX N-PSDB; ABX58405.  
XX  
XX Isolated nucleic acid molecules encoding musculoskeletal system  
XX associated polypeptides, useful for detecting disorders, e.g. cancer -  
XX  
XX Claim 11; SEQ ID NO 1782; 321pp; English.

CC The invention describes an isolated nucleic acid molecule comprising a  
CC sequence encoding musculoskeletal system associated polypeptides useful  
CC for detecting disorders, e.g., cancer or cancer metastases, in animals  
CC or humans. The nucleic acid; stimulates re-vascularisation of ischemic  
CC tissues associated with conditions such as thrombosis, arteriosclerosis,  
CC and other cardiovascular conditions; treats wounds due to injuries,  
CC burns, post-operative tissue repair, and ulcers; stimulates angiogenesis  
CC and limb regeneration; stimulates neuronal growth; can treat and prevent  
CC neuronal damage occurring in certain disorders or neurodegenerative  
CC conditions, such as, Alzheimer's disease, Parkinson's disease, and  
CC AIDS-related complex; stimulates chondrocyte growth, thus they can be  
CC used to enhance bone and periodontal regeneration and aid in tissue  
CC transplants or bone grafts; prevents skin aging due to sunburn by  
CC stimulating keratinocyte growth; prevents hair loss, since FGF family  
CC members activate hair-forming cells and promotes melanocyte growth;  
CC stimulates growth and differentiation of hematopoietic cells and bone  
CC marrow cells when used in combination with other cytokines; maintains  
CC organs before transplantation or for supporting cell culture of primary  
CC tissues; induces tissue of mesodermal origin to differentiate in early  
CC embryos; increases or decreases the differentiation or proliferation of  
CC embryonic stem cells, besides, haematopoietic lineage; modulates  
CC mammalian characteristics, such as, body height, weight, hair colour, eye  
CC colour, skin, percentage of adipose tissue, pigmentation, size, and shape  
CC (e.g., cosmetic surgery); modulates mammalian metabolism; changes  
CC mammalian's mental state or physical state by influencing biorhythms,  
CC cardiac rhythms, depression, tendency for violence, tolerance for pain,  
CC reproductive capabilities, hormonal or endocrine levels, appetite,  
CC libido, memory, or stress; increases or decreases storage capabilities,  
CC fat content, lipid, protein, carbohydrate, vitamin, minerals, cofactors  
CC or other nutritional components. This is the amino acid sequence of a  
CC novel human musculoskeletal system antigen.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?DocID=20020147140.  
XX  
XX SQ Sequence 56 AA;

Query Match 91.4%; Score 32; DB 24; Length 56;  
Best Local Similarity 83.3%; Pred. No. 87;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	LDMSFL	6
Db	27	LDMSFL	32

Search completed: February 18, 2004, 14:26:25  
Job time : 23.7763 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds  
(without alignments)  
89.145 Million cell updates/sec

Title: US-09-643-260-13

Perfect score: 33

Sequence: 1 LDM5AL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: SPTRMBL.23.\*  
2: sp\_archaea.\*  
3: sp\_bacteria.\*  
4: sp\_fungi.\*  
5: sp\_human.\*  
6: sp\_invertebrate.\*  
7: sp\_mammal.\*  
8: sp\_mhc.\*  
9: sp\_organelle.\*  
10: sp\_phage.\*  
11: sp\_plant.\*  
12: sp\_rodent.\*  
13: sp\_virus.\*  
14: sp\_vertebrate.\*  
15: sp\_unclassified.\*  
16: sp\_virus.\*  
17: sp\_bacteriophage.\*  
18: sp\_bacteriophage.\*  
19: sp\_bacteriophage.\*  
20: sp\_bacteriophage.\*  
21: sp\_bacteriophage.\*  
22: sp\_bacteriophage.\*  
23: sp\_bacteriophage.\*  
24: sp\_bacteriophage.\*  
25: sp\_bacteriophage.\*  
26: sp\_bacteriophage.\*  
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30: sp\_bacteriophage.\*  
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34: sp\_bacteriophage.\*  
35: sp\_bacteriophage.\*  
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38: sp\_bacteriophage.\*  
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40: sp\_bacteriophage.\*  
41: sp\_bacteriophage.\*  
42: sp\_bacteriophage.\*  
43: sp\_bacteriophage.\*  
44: sp\_bacteriophage.\*  
45: sp\_bacteriophage.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	295	16	Q9RL11
2	31	93.9	192	16	Q9PCP5
3	31	93.9	266	2	Q9EUB5
4	31	93.9	345	5	Q9YXR2
5	31	93.9	399	5	Q9NE98
6	31	93.9	455	16	Q8PM34
7	31	93.9	652	5	Q9V553
8	31	93.9	666	2	Q8L311
9	31	93.9	1006	5	Q8SX14
10	31	93.9	1040	3	Q94147
11	31	93.9	1394	3	Q08409
12	31	93.9	2297	16	Q54155
13	31	93.9	10917	2	Q93NM6
14	31	93.9	90	2	Q50164
15	30	90.9	124	5	Q9VP65
16	30	90.9	124	5	Q9VP65

17	30	90.9	154	5	Q9NSH2	Q9NSH2 caenorhabd
18	30	90.9	163	17	Q9P6E2	Q9P6E2 halobacteri
19	30	90.9	208	16	Q9RY28	Q9RY28 deinococcus
20	30	90.9	231	2	Q9RHB7	Q9RHB7 bradyrhizob
21	30	90.9	256	11	Q9CUA9	Q9CUA9 mus musculu
22	30	90.9	256	11	Q9CXU7	Q9CXU7 mus musculu
23	30	90.9	280	16	Q97GH1	Q97GH1 clostridium
24	30	90.9	360	5	Q16933	Q16933 ancylostoma
25	30	90.9	365	16	Q9KL23	Q9KL23 vibrio chol
26	30	90.9	380	16	Q9KPM8	Q9KPM8 vibrio chol
27	30	90.9	384	16	Q8ZGR2	Q8ZGR2 yersinia pe
28	30	90.9	391	16	Q9BPD4	Q9BPD4 rhizobium l
29	30	90.9	401	16	Q916R0	Q916R0 pseudomonas
30	30	90.9	403	16	Q9L111	Q9L111 streptomyce
31	30	90.9	407	16	Q8DKX4	Q8DKX4 synchococc
32	30	90.9	442	5	Q19242	Q19242 caenorhabd
33	30	90.9	476	16	Q9PFA6	Q9PFA6 xylella fas
34	30	90.9	547	10	Q8LR21	Q8LR21 oryza sativ
35	30	90.9	547	11	Q8BXR2	Q8BXR2 mus musculu
36	30	90.9	564	11	Q9CTV2	Q9CTV2 mus musculu
37	30	90.9	572	12	Q9S1S8	Q9S1S8 streptomyce
38	30	90.9	574	12	Q8B400	Q8B400 porcine lym
39	30	90.9	578	12	Q8B417	Q8B417 porcine lym
40	30	90.9	578	12	Q8B3X0	Q8B3X0 porcine lym
41	30	90.9	580	12	Q8UYD0	Q8UYD0 porcine lym
42	30	90.9	600	4	Q9UF13	Q9UF13 homo sapien
43	30	90.9	638	16	Q9RXV9	Q9RXV9 deinococcus
44	30	90.9	660	2	Q8GR31	Q8GR31 streptomyce
45	30	90.9	1026	3	Q42948	Q42948 schizosacch

## ALIGNMENTS

RESULT 1  
Q9RL11 PRELIMINARY; PRT; 295 AA.  
ID Q9RL11  
AC Q9RL11  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein SC00307.  
GN SC00307 OR SC5G9.16.  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Streptomyces.  
OX NCBI\_Taxid=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Redenbach M., Kleier H.M., Denepate D., Eichner A., Cullum J.,  
RX Kinashi H., Hopwood D.A.;  
RT "A set of ordered cosmids and a detailed genetic and physical map for  
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
RL Mol. Microbiol. 21:77-96(1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2) / M145;  
RX MEDLINE=21996410; PubMed=12000953;  
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
Thompson N.R., James K.D., Harris D.B., Quail M.A., Kleier H.,  
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

No art

RA Cronin A., Frazer A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 RA Huang C.-H., Kleiser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabbinowitch E., Rajendram M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wierzok A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete Streptomyces  
 RT coelicolor A3(2).";  
 RL Nature 417:141-147(2002).  
 DR EMBL: AL939105; CAB55664.1; -  
 DR InterPro: IPR002086; Aldehyde\_dehydr.  
 DR InterPro: IPR001387; HTH\_3.  
 DR Pfam: PF01381; HTH\_3; 1.  
 DR SMART: SMO0530; HTH\_XRE; 1.  
 DR PROSITE: PS00687; ALDEHYDE\_DEHYDR\_GLU; 1.  
 KM Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 295 AA; 32188 MW; 91AF744D7736075 CRC64;

Query Match 100.0%; Score 33; DB 16; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSAL 6  
 Db 234 LDMSAL 239

## RESULT 2

Q9PCP5 PRELIMINARY; PRT; 192 AA.  
 AC Q9PCP5;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Tyrocyphos repressor binding protein.  
 GN Xp1733.  
 OS Xylella fastidiosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 OC Xanthomonadaceae; Xylella.  
 NCBI\_Taxid=2371;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=965C;  
 RX MEDLINE=20365717; PubMed=10910347;  
 RA Simpson A.J.G., Reinhard P.C., Arruda P., Abreu F.A., Acencio M.,  
 RA Alvares R., Alves L.M.C., Araya J.B., Baia G.S., Baptista C.S.,  
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Bionese M.R.S.,  
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carer H.,  
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,  
 RA Faciniani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,  
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,  
 RA Gartner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,  
 RA Ho P.L., Honneisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,  
 RA Klieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,  
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,  
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,  
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsumura A.Y.,  
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,  
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,  
 RA Nhami A.J., Nobrega F.G., Nunes L.R., Oliveira M.A.,  
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,  
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A.Jr., Pesquero J.B.,  
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,  
 RA de Rosa V.B., Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,  
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A.Jr.,  
 RA da Silva J.F., Silvestri M.L.Z., Siqueira M.J., de Souza A.A.,  
 RA de Souza A.P., Terenzi W.F., Truffi D., Tsai S.M., Tsunako M.H.,  
 RA Valada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,  
 RA Zago M.A., Zatz M., Meidanis J., Secubal J.C.;  
 RT "The genome sequence of the plant pathogen Xylella fastidiosa";  
 RL Nature 406:151-159(2000).  
 DR EMBL: AB003996; AAP84542.1; -

DR InterPro: IPR001226; Flavodoxin.  
 DR Pfam: PF00258; Flavodoxin; 1.  
 DR PROSITE: PS00201; FLAVODOXIN; 1.  
 KM Complete proteome.  
 SQ SEQUENCE 192 AA; 20309 MW; 38474F2CAC40A7D4 CRC64;

Query Match 93.9%; Score 31; DB 16; Length 192;  
 Best Local Similarity 83.3%; Pred. No. 3.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSAL 6  
 Db 43 LDMSAL 48

## RESULT 3

Q9EUB5 PRELIMINARY; PRT; 266 AA.  
 AC Q9EUB5;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Hypothetical 29.4 kDa protein.  
 GN ORF55.  
 OS Corynebacterium equi (Rhodococcus equi).  
 OG Plasmid PREAT701 (p33701), and Plasmid virulence.  
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;  
 OC Corynebacteriaceae; Nocardia; Rhodococcus.  
 NCBI\_Taxid=43767;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC33701, and 103; PLASMID=PREAT701 (p33701), and virulence;  
 RX Takai S., Sekizaki T., Kakuda T., Nakamura M., Suzuki K., Ogino N.,  
 RL Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.  
 GN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC33701, and 103; PLASMID=PREAT701 (p33701), and virulence;  
 RX PubMed=11083803;  
 RA Takai S., Hines S.A., Sekizaki T., Nicholson V.M., Alberin D.A.,  
 RA Oseki M., Takamatsu D., Nakamura M., Suzuki K., Ogino N., Kakuda T.,  
 RA Dan H., Prescott J.F.;  
 RT "DNA sequence and comparison of virulence plasmids from Rhodococcus  
 RT equi ATCC 33701 and 103.";  
 RL Infect. Immun. 68:6840-6847(2000).  
 DR EMBL: AP001204; BAB16664.1; -  
 DR EMBL: AP016907; AAG21758.1; -  
 KM Hypothetical protein; Plasmid.  
 SQ SEQUENCE 266 AA; 29450 MW; 26B9B0B9717FF8B6 CRC64;

Query Match 93.9%; Score 31; DB 2; Length 266;  
 Best Local Similarity 83.3%; Pred. No. 4.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSAL 6  
 Db 30 LDMSAL 35

## RESULT 4

Q9YXR2 PRELIMINARY; PRT; 345 AA.  
 AC Q9YXR2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE CG8191 protein (RE17655p).  
 GN CG8191.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachytera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_Taxid=7227;  
 RX [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zheng Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Chame M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,  
 RA Butris K.C., Busen D.A., Butler H., Cadieu L.B., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davernport L.B., Davies P.,  
 RA de Pablos B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 RA Foster C., Gabriellian A.B., Garg N.S., Gelbart W.M., Glaeser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
 RA Jalali M., Katush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laevo F., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murthy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,  
 RA Relarte K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Klamas I., Simpson M., Skupski M.P., Smith T.,  
 RA Spletter E., Spiraling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tecor C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*."; Science 287:2185-2195 (2000).  
 RL  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Chame M., Chavez C., Dorsett V., Drensek D., Farfan D., Fries B.,  
 RA Harris R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Munguel C.J., Nunco J., Pacleb J., Pargass V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celinker S.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003500; AAF48496.1; -;  
 DR EMBL; AY071134; AAL48756.1; -;  
 DR Playbase; Fggn0030675; CG8191.  
 SQ SEQUENCE 345 AA; 39831 MW; 0613409F8F007B9C CRC64;

Query Match 93.9%; Score 31; DB 5; Length 345;  
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LDMSAL 6  
 Db 136 LDMSAL 141

RESULT 5  
 Q9NE98 PRELIMINARY; PRT; 399 AA.  
 AC Q9NE98;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE Hypothetical 43.5 kDa protein.

GN L4803.06.  
 OS Leishmania major.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 OX NCBI\_TaxID=5664;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Friedlin;  
 RA Maury D., Furnelle B., Goffeau A., Ivens A.C., Quail M.,  
 RA Rajandream M.A., Barrell B.G.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Friedlin;  
 RX MEDLINE=98146435; PubMed=9477341;  
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,  
 RA Smith D.F.;  
 RT "A physical map of the *Leishmania major* Friedlin genome."; Genome Res. 8:135-145(1998).  
 RL EMBL; AL161416; CAB77684.1; -;  
 DR KW Hypothetical protein.  
 SQ SEQUENCE 399 AA; 43458 MW; BB86021C2BB3E18 CRC64;

Query Match 93.9%; Score 31; DB 5; Length 399;  
 Best Local Similarity 83.3%; Pred. No. 6.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LDMSAL 6  
 Db 388 LDMSAL 393

RESULT 6  
 Q8PM34 PRELIMINARY; PRT; 455 AA.  
 AC Q8PM34;  
 DT 01-OCT-2002 (TREMblrel. 22, Created)  
 DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Xanthomine 3-monoxygenase.  
 GN XAC1600.  
 OS Xanthomonas axonopodis (pv. citri).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 OC Xanthomonadaceae; Xanthomonas.  
 OX NCBI\_TaxID=92829;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=306 / ATCC 13902 / XV 101;  
 RX MEDLINE=22022145; PubMed=12024217;  
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furian L.R.,  
 RA Queiroz R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,  
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,  
 RA Camarotte G., Cammaran F., Cardoso J., Chambergo F., Clapina L.P.,  
 RA Ciccarelli R.M.B., Coutinho L.L., Curcio-Santos J.R., El-Dorri H.,  
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,  
 RA Formiglieri E.F., Franco M.C., Greggio C.C., Gruber A.,  
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,  
 RA Lacerda E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,  
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,  
 RA Spindola L.A.F., Takita M.A., Tamara R.B., Teixeira E.C., Tezza R.I.D.,  
 RA Trindade dos Santos M., Truffi D., Teal S.M., White F.F.,  
 RA Setubal J.C., Kitajima J.P.;  
 RT "Comparison of the genomes of two *Xanthomonas* pathogens with differing host specificities"; Nature 417:459-463(2002).  
 RL EMBL; AE011792; AAM36468.1; -;  
 DR InterPro; IPR000733; Flav\_monoxygenase.  
 DR InterPro; IPR003042; Rng\_mnoxygenase.  
 DR Pfam; PF01360; Monoxygenase; 1.  
 DR PRINTS; PR00420; RINGMONOXGNASE.  
 KW Monoxygenase; Complete proteome.  
 SQ SEQUENCE 455 AA; 50857 MW; DAD9F44B9761A618 CRC64;



Query Match 93.9%; Score 31; DB 16; Length 455;  
 Best Local Similarity 83.3%; Pred. No. 7.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSAL 6  
 Db 435 LDMSAL 440

## RESULT 7

Q9V553 PRELIMINARY; PRT; 652 AA.  
 AC Q9V553;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE CG8027 protein.  
 GN CG8027.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NC NCB1\_Taxid=7227;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RC STRAIN=BERKELEY;  
 RP SEQUENCE FROM N.A.

RA Adams M.D., Cealiner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Suton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,  
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abriil J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bertan B.P., Bhandari D., Bolshakov S.,  
 RA Borova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahike C., Dayenport L.B., Davies P.,  
 RA de Pabloe B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasseer K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,  
 RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mactel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Mostreli A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reene M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Ventler E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang X., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Ventler J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AF003834; AAF58967.1; -  
 DR FLYBase; FBgn0033392; CG8027.  
 DR InterPro; IPR000800; Notch.  
 DR Pfam; PF00066; notch; 1.  
 SO SEQUENCE 652 AA; 75752 MW; 2728764810039458 CRC64;

Query Match 93.9%; Score 31; DB 5; Length 652;

Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSAL 6  
 Db 447 LDMSAL 452

## RESULT 8

Q8L311 PRELIMINARY; PRT; 666 AA.  
 AC Q8L311;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Cytochrome b subunit B.  
 GN CYOB.  
 OS Vitreoscilla sp. (strain C1).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Nisseriales;  
 OC Neisseriaceae; Vitreoscilla.  
 NC NCB1\_Taxid=96942;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=C1;  
 RA Webster D.A., Hwang K.-W., Kim S.-K., Kim K.-J., Chung Y.-T.,  
 RA Stark B.C.;  
 RT "Sequence and characterization of the cytochrome b operon of  
 RT Vitreoscilla.";  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.  
 DR EMBL; AF439739; AAM20915.1; -  
 DR InterPro; IPR000883; COX1.  
 DR PRINTS; PR01165; CYCOXIDASE1.  
 DR PROSITE; PS00077; COX1. 1.  
 KW Copper; Electron transport; Heme; Oxidoreductase; Respiratory chain;  
 KW Transmembrane; Transport.  
 SQ SEQUENCE 666 AA; 74470 MW; B5F3EAB67282E7C CRC64;

Query Match 93.9%; Score 31; DB 2; Length 666;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSAL 6  
 Db 5 LDMSAL 10

## RESULT 9

Q8SX14 PRELIMINARY; PRT; 666 AA.  
 AC Q8SX14;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE RE350339.  
 GN CG8027.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NC NCB1\_Taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Dreanek D., Farfan D., Fries E.,  
 RA George R., Gonzalez W., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nuno J., Pacleb J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Cealiner S.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY089618; AAL90356.1; -

```

DR  P1yBase: F6gn003392; CCG8027.
DR  InterPro: IPR000800; Notch.
DR  Pfam: PF00066; notch.1.
SQ  SEQUENCE 666 AA; 77745 MW; F6FDB6D1C39248 CRC64;

Query Match
Best Local Similarity 93.9%; Score 31; DB 5; Length 666;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 LDMSAL 6
Db  461 LDMSAM 466

RESULT 10
ID  Q07324 PRELIMINARY; PRT; 1006 AA.
AC  Q07324;
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-NOV-1996 (TrEMBLrel. 23, Last annotation update)
DE  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  ATP dependent permease (Yeast homolog).
OS  Saccharomyces cerevisiae (Baker's yeast).
OC  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC  Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
CX  NCBI_TaxID=4932;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=FY1679;
RA  De haan M.;
RL  Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=FY1679;
RX  MEDLINE=94019318; PubMed=8413243;
RA  Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G.,
RA  Sherman F.;
RT  "CYC2 encodes a factor involved in mitochondrial import of yeast
RT  cytochrome c.";
RL  Mol. Cell. Biol. 13:6442-6451(1993).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=FY1679;
RX  MEDLINE=94169519; PubMed=7764548;
RA  Lee Y.S., Shintzu J., Yoda K., Yamasaki M.;
RT  "Molecular cloning of a gene, DHS1, which complements a drug-
RT  hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
RL  Biotech. Biochem. 58:391-395(1994).
DR  EMBL; X87331; CAA60760.1; -.
DR  InterPro: IPR003593; AAA_ATPase.
DR  InterPro: IPR003439; ABC_transporter.
DR  InterPro: IPR001202; WW_Reps_WWP.
DR  Pfam; PF00005; ABC_tran.1.
DR  ProDom; PD000006; ABC_transporter; 1.
DR  SMART; SM00382; AAA; 1.
DR  PROSITE; PS01159; WW_DOMAIN_1; 1.
KM  ATP-binding.
SQ  SEQUENCE 1006 AA; 113961 MW; 0EA9409A1AD1CA7F CRC64;

Query Match
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 LDMSAL 6
Db  629 LDMSAL 634

RESULT 11
ID  Q94147 PRELIMINARY; PRT; 1040 AA.
AC  Q94147;
DT  01-MAY-1999 (TrEMBLrel. 10, Created)

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DT  01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  ORF YOR011W (fragment).
OS  Saccharomyces cerevisiae (Baker's yeast).
OC  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC  Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
CX  NCBI_TaxID=4932;
RN  [1]
RP  SEQUENCE OF 1-488 FROM N.A.
RA  Petersson B., Sterky F., Uhlen M.;
RL  Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RA  De haan M., Grivell L.A., Maarse A.C.;
RL  Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN  [3]
RP  SEQUENCE FROM N.A.
RC  Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR  EMBL; Z74920; CAA99202.1; -.
DR  InterPro: IPR003593; AAA_ATPase.
DR  InterPro: IPR003439; ABC_transporter.
DR  InterPro: IPR001202; WW_Reps_WWP.
DR  Pfam; PF00005; ABC_tran.1.
DR  ProDom; PD000006; ABC_transporter; 1.
DR  SMART; SM00382; AAA; 1.
DR  PROSITE; PS01159; WW_DOMAIN_1; 1.
KM  ATP-binding.
FT  NON TER
SQ  SEQUENCE 1040 AA; 117840 MW; B32B0F1D33906B5C CRC64;

Query Match
Best Local Similarity 93.9%; Score 31; DB 3; Length 1040;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 LDMSAL 6
Db  663 LDMSAL 668

RESULT 12
ID  Q08409 PRELIMINARY; PRT; 1394 AA.
AC  Q08409;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Chromosome XV reading frame ORF YOR011W.
GN  AUS1 OR YOR011W.
OS  Saccharomyces cerevisiae (Baker's yeast).
OC  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC  Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
CX  NCBI_TaxID=4932;
RN  [1]
RP  SEQUENCE OF 1-842 FROM N.A.
RA  Petersson B., Sterky F., Uhlen M.;
RL  Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  SEQUENCE OF 355-1394 FROM N.A.
RA  De haan M., Grivell L.A., Maarse A.C.;
RL  Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN  [3]
RP  SEQUENCE FROM N.A.
RC  Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR  EMBL; Z74919; CAA99199.1; -.
DR  SGD; S000537; AUS1.
DR  InterPro: IPR003593; AAA_ATPase.
DR  InterPro: IPR003439; ABC_transporter.
DR  InterPro: IPR001202; WW_Reps_WWP.
DR  Pfam; PF00005; ABC_tran.2.
DR  ProDom; PD000006; ABC_transporter; 2.
DR  SMART; SM00382; AAA; 1.

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DR PROSITE; PS00211; ABC\_TRANSPORTER; 1.  
 DR PROSITE; PS01159; MW\_DOMAIN\_1; 1.  
 DR ATP-binding.  
 SQ SEQUENCE 1394 AA; 157749 MW; 357A35A0FCFC93B CRC64;

Query Match 93.9%; Score 31; DB 3; Length 1394;  
 Best Local Similarity 83.3%; Pred. No. 2.4e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
 :|||||  
 Db 1017 IDMSAL 1022

RESULT 13  
 ID 054155 PRELIMINARY; PRT; 2297 AA.  
 AC 054155;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Polyketide synthase.  
 GN SC05692 OR SC37.12.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Oliver K., Harris D.,  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Parkhill J., Barrell B.G., Rajandream M.A.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA MEDLINE=97000351; PubMed=8843436;  
 RX MEDLINE=21996410; PubMed=12000953;  
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Klee H.,  
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornby T., Howarth S.,  
 RA Huang C.H., Klee H., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabbittowitch E., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wieroszek A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete Streptomyces  
 coelicolor A3(2)."  
 RL Nature 417:141-147(2002).  
 DR EMBL; AL339125; CAA16183.1; -.  
 DR HSSP; P25715; IMLA.  
 DR InterPro; IPR001227; Ac transferase.  
 DR InterPro; IPR003408; Ala synthase.  
 DR InterPro; IPR004839; aminotransf.2.  
 DR InterPro; IPR000873; AMP-bind.  
 DR InterPro; IPR000794; ketoacyl-synt.  
 DR InterPro; IPR001917; Nitransf.2.  
 DR InterPro; IPR006163; Pp bind.  
 DR Pfam; PF00698; Acyl transf. 1.  
 DR Pfam; PF02490; Ala\_synthase; 1.

DR Pfam; PF00155; aminotran\_1.2; 1.  
 DR Pfam; PF00501; AMP-binding; 1.  
 DR Pfam; PF00109; ketoacyl-synt; 1.  
 DR Pfam; PF02801; ketoacyl-synt C; 1.  
 DR Pfam; PF00550; pp-binding; 1.  
 DR PROSITE; PS00599; AA\_TRANSPER\_CLASS\_2; 1.  
 DR PROSITE; PS00751; ACI\_DOMAIN; 2.  
 DR PROSITE; PS00606; B\_KETOACYL\_SYNTHASE; 1.  
 DR Phosphopantetheine; Transferase; Complete proteome.  
 SQ SEQUENCE 2297 AA; 241989 MW; C67B5846153EB46 CRC64;

Query Match 93.9%; Score 31; DB 16; Length 2297;  
 Best Local Similarity 83.3%; Pred. No. 4e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
 :|||||  
 Db 1641 IDMSAL 1646

RESULT 14  
 ID 093NW6 PRELIMINARY; PRT; 10917 AA.  
 AC 093NW6;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE AmpHC.  
 GN AMPHC.  
 OS Streptomyces nodosus.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.  
 OX NCBI\_TaxID=40318;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Caffrey P., Lynch S.V., Flood E.M., Finnan S.M., O'Leary M.;  
 RT "The amphoterin biosynthetic gene cluster from Streptomyces  
 nodosus."  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- COFACTOR: ZINC (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE  
 FAMILY  
 CC  
 DR EMBL; AF357202; AAK7514.1; -.  
 DR InterPro; IPR001227; Ac transferase.  
 DR InterPro; IPR002328; Adh\_zinc.  
 DR InterPro; IPR002085; Adh\_zn\_family.  
 DR InterPro; IPR004410; FADd.  
 DR InterPro; IPR000794; ketoacyl-synt.  
 DR InterPro; IPR006162; Ppantne\_attach.  
 DR InterPro; IPR006163; Pp\_bind.  
 DR Pfam; PF00698; Acyl\_transf. 6.  
 DR Pfam; PF00107; ketoacyl-synt; 1.  
 DR Pfam; PF00109; ketoacyl-synt; 6.  
 DR Pfam; PF02801; ketoacyl-synt C; 6.  
 DR Pfam; PF00550; pp-binding; 6.  
 DR TIGRPFAM; TIGR00128; FADd; 6.  
 DR PROSITE; PS00751; ACI\_DOMAIN; 6.  
 DR PROSITE; PS00059; ADH\_ZINC; 1.  
 DR PROSITE; PS00606; B\_KETOACYL\_SYNTHASE; 6.  
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 5.  
 DR Metal-binding; Oxidoreductase; Phosphopantetheine; Transferase; Zinc.  
 SQ SEQUENCE 10917 AA; 1132905 MW; 15AC5956B5810A1 CRC64;

Query Match 93.9%; Score 31; DB 2; Length 10917;  
 Best Local Similarity 83.3%; Pred. No. 1.9e+04;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
 :|||||  
 Db 8165 IDMSAL 8170

RESULT 15

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OS0164
ID OS0164 PRELIMINARY; PRT; 90 AA.
AC OS0164;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TRENBLrel. 01, Last annotation update)
DE U2968.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Robison K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U15187; AAA63116.1; -.
SQ SEQUENCE 90 AA; 9642 MW; F0187130F41A846 CRC64;

Query Match          90.9%; Score 30; DB 2; Length 90;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWSAL 6
   ||||:
Db 65 LDWSAV 70

```

Search completed: February 18, 2004, 14:35:54  
 Job time : 19.3684 secs

GenCore version 5.1.6  
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OM protease - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds  
(without alignments)  
79.423 Million cell updates/sec

Title: US-09-643-260-13

Perfect score: 33

Sequence: 1 LDMSAL 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	330	YD31_ARCFU	O28938 archaeoglob
2	31	93.9	226	CXB2_SHEEP	P46691 ovls arles
3	31	93.9	333	Y237_SYNY3	O55480 synochocyt
4	31	93.9	666	COL4_BRAJA	P98057 bradyrhizob
5	31	93.9	984	PKL2_HUMAN	Q16513 homo sapien
6	30	90.9	208	TRPF_DEIRA	Q9128 delnococcus
7	30	90.9	261	YFUR_BACSU	O34669 bacillus su
8	30	90.9	377	Y4WD_RHISN	P55682 rhizobium s
9	30	90.9	516	PROD_HUMAN	O43272 homo sapien
10	29	87.9	223	SAMP_HUMAN	P02743 homo sapien
11	29	87.9	224	SAMP_PIG	O19663 sus scrofa
12	29	87.9	234	SAMP_MESAU	P07629 mesocricetu
13	29	87.9	286	CXAE_RAT	P28233 rattus norv
14	29	87.9	286	SGBU_ECOLI	P37679 escherichia
15	29	87.9	296	CYCG_RHOSH	O53143 rhodospirillum rubrum
16	29	87.9	313	Y763_TREPA	O83744 treponema p
17	29	87.9	378	CXAI_XENLA	P16663 xenopus lae
18	29	87.9	380	CXAI_BRARA	O57474 brachydanio
19	29	87.9	381	CXAI_CHICK	P14554 gallus galli
20	29	87.9	381	CXAI_HUMAN	P17302 homo sapien
21	29	87.9	381	CXAI_MOUSE	P23242 mus musculu
22	29	87.9	381	CXAI_RAT	P08050 rattus norv
23	29	87.9	382	CXAI_BOVIN	P18246 bos taurus
24	29	87.9	394	PGK_BACST	P18912 bacillus st
25	29	87.9	446	SHR_BOMMO	Q17239 bombyx mori
26	29	87.9	451	GUH_PSRPU	P42206 pseudomonas
27	29	87.9	455	UHPT_CHLPN	O92798 chlamydia p
28	29	87.9	456	UHPT_CHLMU	O92798 chlamydia p
29	29	87.9	456	UHPT_CHLTR	O84548 chlamydia m
30	29	87.9	482	TRPE_SPIAU	P21690 spirochaeta
31	29	87.9	517	LADI_HUMAN	O00515 homo sapien
32	29	87.9	518	LADI_MOUSE	P57016 mus musculu
33	29	87.9	548	NOL0_BRAJA	Q45269 bradyrhizob

34	29	87.9	600	1	GLMS_HALNI	O9ht00 h glucosami
35	29	87.9	630	1	GLMS_SYNY3	P72720 s glucosami
36	29	87.9	644	1	VP4_BTV11	P33428 bluetongue
37	29	87.9	644	1	VP4_BTV13	P33429 bluetongue
38	29	87.9	644	1	VP4_BTV2A	P33427 bluetongue
39	29	87.9	654	1	VP4_BTV10	P07132 bluetongue
40	29	87.9	754	1	RIR1_BP74	P32282 bacteriophag
41	29	87.9	842	1	PKL2_RAT	O08874 rattus norv
42	29	87.9	926	1	MAY3_SCHCO	P37934 schizophyll
43	29	87.9	941	1	GCSP_MYCTU	O50601 mycobacteri
44	29	87.9	946	1	PKL1_RAT	O63433 rattus norv
45	29	87.9	958	1	YA7B_SCHRO	O09764 schizosacch

## ALIGNMENTS

RESULT 1  
ID YD31\_ARCFU STANDARD; PRT; 330 AA.  
AC O28938;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypothetical protein AF1331.  
GN AF1331.  
OS Archaeoglobus fulgidus.  
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;  
OC Archaeoglobaceae; Archaeoglobus.  
OX NCBI\_TaxId=2234;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
RX MEDLINE=98049343; PubMed=9389475;  
RA Kleink H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
RA Richardson D.L., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
RA Fleischmann R.D., Ketchum K.A., Smith T.A., Venter J.C.,  
RA Kirschner E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,  
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,  
RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,  
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
RA Venter J.C.;  
RT "The complete genome sequence of the hyperthermophilic, sulphate-  
reducing archaeon Archaeoglobus fulgidus.";  
RL Nature 390:364-370 (1997).  
CC -----  
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CC -----  
CC EMBL, AB01012; AAB89926.1; -  
CC DR PIR, B69416; B69416.  
CC TIGR, AF1331, -  
CC DR TIGR, AF1331, -  
CC KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 330 AA; 38741 MW; 1B32F8BF59C7621 CRC64;  
Query Match 100.0%; Score 33; DB 1; Length 330;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
LDMSAL 6  
177 LDMSAL 182  
RESULT 2

CX82\_SHEEP STANDARD; PRT; 226 AA.  
 ID\_CX82\_SHEEP  
 AC P46651;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Gap junction beta-2 protein (Connexin 26) (Cx26).  
 GN Cx26  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OC NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cornea;  
 RA Dong Y., Green C., Donaldson P.J., Kistler J.;  
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: One gap junction consists of a cluster of closely packed  
 CC pairs of transmembrane channels, the connexons, through which  
 CC materials of low mw diffuse from one cell to a neighboring cell.  
 CC -1- SUBUNIT: A connexon is composed of a hexamer of connexins.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. BETA-TYPE (GROUP 1)  
 CC SUBFAMILY.  
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 CC  
 CC EMBL; U17592; AAA67446.1; -;  
 CC InterPro; IPR000500; Connexin.  
 CC Pfam; PF00029; connexin; 1.  
 CC DR PRINTS; PR00206; CONNEXIN.  
 CC SMART; SM00037; CNX; 1.  
 CC DR PROSITE; PS00407; CONNEXINS\_1; 1.  
 CC DR PROSITE; PS00408; CONNEXINS\_2; 1.  
 CC KW Gap junction; Transmembrane.  
 CC FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 21 40 POTENTIAL.  
 CC FT DOMAIN 41 75 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 76 98 POTENTIAL.  
 CC FT DOMAIN 99 131 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 132 154 POTENTIAL.  
 CC FT DOMAIN 155 192 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 193 215 POTENTIAL.  
 CC FT DOMAIN 216 226 CYTOPLASMIC (POTENTIAL).  
 CC SQ SEQUENCE 226 AA; 26215 MW; DCE2F0C1B4FCEFD CRC64;  
 Query Match 93.9%; Score 31; DB 1; Length 226;  
 Best Local Similarity 83.3%; Pred. No. 61;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LDMSAL 6  
 Db 1 MDMSAL 6  
 RESULT 3  
 YZ37\_SYNV3 STANDARD; PRT; 333 AA.  
 AC Q55480;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical sugar kinase slr0537.  
 GN slr0537.  
 OS Synechocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.

OX NCBI\_TaxID=1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=96127529; PubMed=8590279;  
 RA Kaneko T., Tanaka A., Sato S., Kocant H., Sazuka T., Miyajima N.,  
 RA Sugita M., Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb  
 RT region from map positions 64% to 92% of the genome.";  
 RL DNA Res. 2:153-166(1995).  
 CC -1- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.  
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 CC  
 CC EMBL; D64006; BAA10827.1; -;  
 CC FIR; S75980; S75980.  
 CC HSP; G9TW2; 1DG.  
 CC DR InterPro; IPR002173; PFKB.  
 CC DR InterPro; IPR002139; Ribokinase.  
 CC DR Pfam; PF00294; PFKB; 1.  
 CC DR PRINTS; PR00990; RIBOKINASE.  
 CC DR PROSITE; PS00583; PFKB\_KINASES\_1; FALSE NEG.  
 CC DR PROSITE; PS00584; PFKB\_KINASES\_2; 1.  
 CC KW Hypothetical protein; Transferrase; Kinase; Complete proteome.  
 CC SQ SEQUENCE 333 AA; 35184 MW; CBCE13D0FEE90D CRC64;  
 Query Match 93.9%; Score 31; DB 1; Length 333;  
 Best Local Similarity 83.3%; Pred. No. 89;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LDMSAL 6  
 Db 146 MDMSAL 151  
 RESULT 4  
 CO14\_BRAJA STANDARD; PRT; 666 AA.  
 ID\_CO14\_BRAJA  
 AC P98057;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Probable cytochrome c oxidase polypeptide I (EC 1.9.3.1) (Fourth  
 DE terminal oxidase).  
 GN blr2715  
 OS Bradyrhizobium japonicum.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae; Bradyrhizobium.  
 OC NCBI\_TaxID=375;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=94259305; PubMed=8200541;  
 RA Surpin M.A., Moshiri F., Murphy A.M., Maier R.J.;  
 RT "Genetic evidence for a fourth terminal oxidase in Bradyrhizobium  
 RT japonicum.";  
 RL Gene 143:73-77(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USDA 110;  
 RX MEDLINE=22484998; PubMed=12597275;  
 RA Kaneko T., Nakamura Y., Sato S., Minamisaawa K., Uchiyama T.,  
 RA Sasano S., Watanabe A., Idegawa K., Iritsugu M., Kawashima K.,  
 RA Kohara M., Matsumoto M., Shimpo S., Teurroka H., Wada T., Yamada M.,  
 RA "Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
 RT Bradyrhizobium japonicum USDA110.";  
 RL DNA Res. 9:189-197(2002).

```

CC -1- CATALYTIC ACTIVITY: 4 ferricytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- PATHWAY: Respiratory chain; terminal step.
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
CC -----
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CC -----
DR EMBL; L25841; AAA26210.1; -.
DR EMBL; AF005944; BAC47980.1; -.
DR HSSP; P18401; 1FT.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PR01165; CYCOXIDASE1.
DR PROSITE; PS00077; COX1; 1.
KW Oxidoreductase; Heme; Copper; Transmembrane; Respiratory chain;
KW Complete proteome.
FT METAL 105 105
FT FT METAL 283 283
FT FT METAL 287 287
FT FT METAL 332 332
FT FT METAL 333 333
FT FT METAL 418 418
FT FT METAL 420 420
FT FT METAL 420 420
FT FT CROSSLINK 283 287
FT FT CONFLICT 204 204
SQ SEQUENCE 666 AA; 74469 MW; F04F4870CD039861 CRC64;

Query Match 93.9%; Score 31; DB 1; Length 666;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
Db 5 LDMSAL 10

RESULT 5
PKL2 HUMAN STANDARD; PRT; 984 AA.
AC 016513; O9H1W4;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C-like 2 (EC 2.7.1.-) (Protein-kinase C-related kinase
DE 2).
GN PRKCL2 OR PRK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95080426; PubMed=7986719;
RA Palmer R.H., Ridden J., Parker P.J.;
RT "Identification of multiple, novel, protein kinase C-related gene
RT products.";
RL FEBS Lett. 356:5-8(1994).
RP [2]
RP SEQUENCE FROM N.A.
RX TISSUE=B-cell;
RX MEDLINE=95154310; PubMed=7851406;
RA Palmer R.H., Ridden J., Parker P.J.;
RT "Cloning and expression patterns of two members of a novel protein-
RT kinase-C-related kinase family.";
```

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RL Eur. J. Biochem. 227:344-351(1995).
RN [3]
RP SEQUENCE OF 17-984 FROM N.A.
RA Brown A.;
RL Submitted (OCT-2000) to the EMBL/Genbank/DDJ databases.
CC -1- FUNCTION: EXHIBITS A PREFERENCE FOR HIGHLY BASIC PROTEIN
CC SUBSTRATES (BY SIMILARITY).
CC -1- ENZYME REGULATION: ACTIVATED BY LIPIDS, PARTICULARLY CARDIOLIPIN
CC AND TO A LESSER EXTENT BY OTHER ACIDIC PHOSPHOLIPIDS AND
CC UNSATURATED FATTY ACIDS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- PTM: AUTOPHOSPHORYLATED.
CC -1- PTM: ACTIVATED BY LIMITED PROTEOLYSIS WITH TRYPSIN (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC -----
DR EMBL; U33052; AAC50208.1; -.
DR EMBL; S75548; AAB33346.1; -.
DR EMBL; AL136381; CAC17575.1; -.
DR PIR; S67527; S67527.
DR HSSP; O63450; 1A06.
DR Genew; HGNC:9406; PRKCL2.
DR MIM; 602549; -.
DR GO; GO:000468; P:protein amino acid phosphorylation; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR000008; C2.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR000861; REM_repeat.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF02185; HRI; 3.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00074; HRI; 3.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; ATP-binding; Serine/threonine-protein kinase;
KW Phosphorylation.
FT DOMAIN 657 916
FT NP BIND 663 671
FT BINDING 666 686
FT ACT_SITE 782 782
FT CONFLICT 207 207
SQ SEQUENCE 984 AA; 112034 MW; 687EC417A0F51CID CRC64;

Query Match 93.9%; Score 31; DB 1; Length 984;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
Db 919 LDMSAL 924

RESULT 6
TRPF DEIRA
ID TRPF DEIRA STANDARD; PRT; 208 AA.
AC O9RYZ8;
DT 15-SEP-2003 (Rel. 42, Created)
```

DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE N-(5'-phosphoribosyl)anthranilate isomerase (EC 5.3.1.24) (PRAI).  
 GN TRPF OR DR0123.  
 OS Deinococcus radiodurans.  
 OC Bacteriæ; Deinococcus-Thermus; Deinococci; Deinococcales;  
 OC Deinococcaceæ; Deinococcus.  
 NC NCBI\_TaxID=1299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RI / ATCC 13939 / DSM 20539 / NCIB 9279;  
 RX MEDLINE=20036896; PubMed=10567266;  
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
 Dodson R.J., Helt D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,  
 Klotzel K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
 Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,  
 Makarewicz K.S., Aravind L., Minton K.W., Fleischmann R.D.,  
 Ratzburg K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,  
 Fraser C.M.;  
 RA "Genome sequence of the radioreistant bacterium Deinococcus  
 RT radiodurans R1.";  
 RL Science 286:1571-1577(1999).  
 CC -1- CATALYTIC ACTIVITY: N-(5'-phospho-beta-D-riboseyl)-anthranilate = 1-  
 CC (2-carboxyphenylamino)-1-deoxy-D-ribose 5-phosphate.  
 CC -1- PATHWAY: Tryptophan biosynthesis; third step.  
 CC -1- SIMILARITY: BELONGS TO THE TRPF FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AEO01875; AAF09715.1; -;  
 DR PIR; D75556; D75556.  
 DR HSP; Q56320; IDL3.  
 DR TIGR; DR0123; -;  
 DR HAMAP; MF\_00135; -1.  
 DR InterPro; IPR001240; PRAI.  
 DR Pfam; PF00697; PRAI.1.  
 KM Isomerase: Tryptophan biosynthesis; Complete proteome.  
 SQ SEQUENCE 208 AA; 21156 MW; CF98D22E23AC2833 CRC64;  
 Query Match 90.9%; Score 30; DB 1; Length 208;  
 Best Local Similarity 83.3%; Pred. No. 85;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSAL 6  
 Db 144 LDMSAL 149  
 RESULT 7  
 YFJR\_BACSU STANDARD; PRT; 261 AA.  
 ID YFJR\_BACSU  
 AC O34969;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical oxidoreductase yfjr (EC 1.1.-.-).  
 GN YFJR.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 NC NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AC227;  
 RX MEDLINE=97124190; PubMed=8696503;  
 RA Yamamoto H., Uchiyama S., Sekiguchi J.,  
 RT "Cloning and sequencing of a 40.6 kb segment in the 73 degrees-76  
 degrees region of the Bacillus subtilis chromosome containing genes

RT for trehalose metabolism and acetoin utilization.";  
 RL Microbiology 142:3057-3065(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=98044033; PubMed=9384377;  
 RA Kunet F., Ogasawara N., Moszer I., Albertini A.M., Allont G.,  
 Azevedo V., Bartero M.G., Bessieres P., Bolotin A., Borchert S.,  
 Borriess R., Bourlier L., Brans A., Braun M., Briganti S.C., Bron S.,  
 Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,  
 Choi S.K., Codani J.J., Conerton I.F., Cumming N.J., Daniel R.A.,  
 Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
 Entian K.D., Errington J., Fabre C., Ferrari E., Fougere D.,  
 Frit C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
 Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grand G.,  
 Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,  
 Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 Joris B., Karamata D., Kasahara Y., Kjaer-Blanchard M., Klein C.,  
 Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
 Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,  
 Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
 Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,  
 Paro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
 Presecan E., Puig C., Purnelle B., Rapoport G., Ray M., Reynolds S.,  
 Rieger M., Rivolta E., Rochna E., Roche R., Rose M., Sadale Y.,  
 Sato T., Scanlan B., Schleich S., Schroeder R., Scifone F.,  
 Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S., Soldo B.,  
 Sorokin A., Taccoti B., Takegi T., Takahashi H., Takemura K.,  
 Takeuchi M., Tamakoshi A., Tanaka T., Tempstra P., Tognoni A.,  
 Toker V., Uchiyama S., Vandenbol M., Vannier F., Vassarelli A.,  
 Viari A., Wandt R., Wedler E., Wedler H., Weizenegger T.,  
 Winters P., Wipat A., Yamamoto H., Yamane K., Yasuno K., Yata K.,  
 Yoshida K., Yoshikawa H.F., Zumbstein B., Yoshikawa H., Darchin A.,  
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus  
 RT subtilis.";  
 RL Nature 390:249-256(1997).  
 CC -1- SIMILARITY: BELONGS TO THE 3-HYDROXYISOBUTYRATE DEHYDROGENASE  
 CC FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; D83967; BAA23388.1; -;  
 DR EMBL; D78509; BAA24303.1; -;  
 DR EMBL; Z59108; CAB12628.1; -;  
 DR PIR; A69807; A69807.  
 DR Subtillet; BG12914; YfJR.  
 DR InterPro; IPR002204; 3-hydroxyisobut DH.  
 DR PROSITE; PS00895; 3-HYDROXYISOBUT DH; FALSE NEG.  
 KM Hypothetical protein: Oxidoreductase; NAD: Complete proteome.  
 FT ACT\_SITE 146 146  
 SQ SEQUENCE 261 AA; 27866 MW; 6C9A8CAC8C71CA66 CRC64;  
 Query Match 90.9%; Score 30; DB 1; Length 261;  
 Best Local Similarity 83.3%; Pred. No. 11e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSAL 6  
 Db 251 LDMSAL 256  
 RESULT 8  
 Y4WD\_RHSN STANDARD; PRT; 377 AA.  
 ID Y4WD\_RHSN  
 AC P55682;  
 DT 01-NOV-1997 (Rel. 35, Created)



DT 01-NOV-1997 (Rel. 35, last sequence update)  
 DT 01-NOV-1997 (Rel. 35, last annotation update)  
 DE Hypothetical transport protein Y4WD.  
 GN Y4WD.  
 OS Rhizobium sp. (strain NGR234).  
 OC Plasmid sym pNGR234.  
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 CC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.  
 OK NCBI\_TaxID=394;  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97305956; PubMed=9163424;  
 RA Feilberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,  
 RA Perret X.;  
 RT "Molecular basis of symbiosis between Rhizobium and legumes";  
 RL Nature 387:394-401(1997).  
 CC -1- FUNCTION: COULD BE INVOLVED IN A TRANSPORT SYSTEM.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -1- SIMILARITY: TO R.MBLIOTI M08C.  
 CC  
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 CC -----  
 CC EMBL; AB000103; AAB91911.1; -  
 CC InterPro; IPR007114; MFS.  
 DR Hypothetical protein; Transmembrane; Transport; Plasmid.  
 KM  
 FT TRANSMEM 4 24 POTENTIAL.  
 FT TRANSMEM 41 61 POTENTIAL.  
 FT TRANSMEM 85 105 POTENTIAL.  
 FT TRANSMEM 134 154 POTENTIAL.  
 FT TRANSMEM 159 179 POTENTIAL.  
 FT TRANSMEM 192 212 POTENTIAL.  
 FT TRANSMEM 278 298 POTENTIAL.  
 FT TRANSMEM 301 321 POTENTIAL.  
 FT TRANSMEM 327 347 POTENTIAL.  
 FT TRANSMEM 356 376 POTENTIAL.  
 SQ SEQUENCE 377 AA; 39051 MW; 49CFEB4A4AD74BD CRC64;  
 SQ

Query Match 90.9%; Score 30; DB 1; Length 377;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
 Db 221 LDMSAV 226

RESULT 9  
 PROD HUMAN  
 ID PROD HUMAN STANDARD; PRT; 516 AA.  
 AC 043272;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, last sequence update)  
 DT 15-SEP-2003 (Rel. 42, last annotation update)  
 DE Proline oxidase, mitochondrial precursor (EC 1.5.3.-) (Proline  
 DE dehydrogenase).  
 GN PRODH.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OK NCBI\_TaxID=9606;  
 [1]  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98046348; PubMed=9385373;  
 RA Campbell H.D., Webb G.C., Young I.G.;  
 RT "A human homologue of the Drosophila melanogaster elugfish-A (proline  
 RT oxidase) gene maps to 22q11.2, and is a candidate gene for type-I

RT hyperprolinaemia.";  
 RL Hum. Genet. 101:69-74(1997).  
 RN  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cerebellum, and Kidney;  
 RX MEDLINE=99206616; PubMed=10192398;  
 RA Gogoe J.A., Sartha M., Takacs Z., Beck K.D., Luine V., Lucas L.R.,  
 RA Nadler J.V., Karayorgou M.;  
 RT "The gene encoding proline dehydrogenase modulates sensorimotor gating  
 RT in mice.";  
 RL Nat. Genet. 21:434-439(1999).  
 CC -1- FUNCTION: CONVERTS PROLINE TO DELTA-1-PYRROLINE-5-CARBOXYLATE.  
 CC -1- PATHWAY: Conversion from proline to glutamate, first step.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SKELETAL MUSCLE AND BRAIN,  
 CC TO A LESSER EXTENT IN HEART AND KIDNEY, AND WEAKLY IN LIVER,  
 CC PLACENTA AND PANCREAS.  
 CC -1- DISEASE: Defects in PRODH are the cause of type I hyperprolinaemia  
 CC [MIM:239500], a disorder characterized by elevated serum proline  
 CC levels. May be involved in the psychiatric and behavioral  
 CC phenotypes associated in the 22q11 velocardiofacial syndrome.  
 CC -1- SIMILARITY: BELONGS TO THE PROLINE OXIDASE FAMILY.  
 CC  
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 CC -----  
 CC EMBL; U82381; AAB88789.1; -  
 CC EMBL; AF120278; AAD24775.1; -  
 CC Genew; HGNC:9453; PRODH.  
 DR GK; 043272; -  
 DR MIM; 606810; -  
 DR MIM; 239500; -  
 DR GO; GO:0004657; P:proline dehydrogenase activity; TNS.  
 DR InterPro; IPR002872; Pro\_dh.  
 DR Pfam; PF01619; Pro\_dh; 1.  
 KM Oxidoreductase; Proline metabolism; Mitochondrion; Transic peptide.  
 FT TRANSIT 1 7 POTENTIAL.  
 FT CHAIN 1 7 MITOCHONDRION (POTENTIAL).  
 FT CONFLICT 80 80 S -> T (IN REF. 2).  
 SQ SEQUENCE 516 AA; 59216 MW; 2FA5B1E4461C450A CRC64;  
 SQ

Query Match 90.9%; Score 30; DB 1; Length 516;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
 Db 231 LDMSL 236

RESULT 10  
 SAMP HUMAN  
 ID SAMP HUMAN STANDARD; PRT; 223 AA.  
 AC P02743;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1995 (Rel. 31, last sequence update)  
 DT 15-SEP-2003 (Rel. 42, last annotation update)  
 DE Serum amyloid P-component precursor (SAP) (9.5S alpha-1-glycoprotein).  
 GN APCS OR PTX2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OK NCBI\_TaxID=9606;  
 [1]  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85207628; PubMed=2987268;  
 RA Mantzouras E.C., Dowton S.B., Whitehead A.S., Edge M.D.,  
 RA Bruns G.A.P., Colten H.R.;

RT "Human serum amyloid P component. cDNA isolation, complete sequence  
 RT of pre-serum amyloid P component, and localization of the gene to  
 RT Chromosome 1.";  
 RL J. Biol. Chem. 260:7752-7756(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8713751; PubMed=3029048;  
 RA Ohnishi S., Maeda S., Shimada K., Arai T.;  
 RT "Isolation and characterization of the complete complementary and  
 RT genomic DNA sequences of human serum amyloid P component.";  
 RL J. Biochem. 100:849-858(1986).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Skeletal muscle;  
 RX MEDLINE=22386257; PubMed=12477932;  
 RA Strauberg R.L., Feinberg E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datsenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carinici P., Prange C.,  
 RA Rana S.S., Loguigliano N.A., Peters G.J., Adamson R.D., Mullaly S.J.,  
 RA Bork S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Small D.B.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP SEQUENCE OF 20-223.  
 RX MEDLINE=86033713; PubMed=4055725;  
 RA Prell P., Fras M., Frangione B.;  
 RT "The primary structure of human tissue amyloid P component from a  
 RT patient with primary idiopathic amyloidosis.";  
 RL J. Biol. Chem. 260:12895-12898(1985).  
 RN [5]  
 RP SEQUENCE OF 20-49.  
 RX MEDLINE=79042150; PubMed=81686;  
 RA Thompson A.R., Enfield D.L.;  
 RT "Human plasma P component: isolation and characterization.";  
 RL Biochemistry 17:4304-4311(1978).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=94159098; PubMed=8114934;  
 RA Emley J., White H.E., O'Hara B., Oliva G., Srinivasan N.,  
 RA Tickle I.J., Blundell T.L., Pepys M.B., Wood S.P.;  
 RT "Structure of pentameric human serum amyloid P component.";  
 RL Nature 367:338-345(1994).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
 RX MEDLINE=97360233; PubMed=9217261;  
 RA Hohenester E., Hutchinson W.L., Pepys M.B., Wood S.P.;  
 RT "Crystal structure of a decameric complex of human serum amyloid P  
 RT component with bound dAMP.";  
 RL J. Mol. Biol. 269:570-578(1997).  
 CC -1- FUNCTION: CAN INTERACT WITH DNA AND HISTONES AND MAY SCAVENGE  
 CC NUCLEAR MATERIAL RELEASED FROM DAMAGED CIRCULATING CELLS. MAY ALSO  
 CC FUNCTION AS A CALCIUM-DEPENDENT LECTIN.  
 CC -1- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISC  
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND  
 CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.  
 CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.  
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 CC -----  
 DR EMBL; D00097; BA00060.1; -;  
 DR EMBL; M10944; AAA60302.1; -;  
 DR EMBL; X04608; CAA28275.1; -;  
 DR EMBL; BC007039; AAH07039.1; -;  
 DR EMBL; BC007058; AAH07058.1; -;  
 DR PIR; A25503; YLHUP.  
 DR PDB; 1SAC; 31-JUL-94.  
 DR PDB; 1LGN; 24-DEC-97.  
 DR GLYCOSULEDB; P02743; -;  
 DR SWISS-2DPAGE; P02743; HUMAN.  
 DR Genew; HGNC:584; APCs.  
 DR MIM; 104770; -;  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0003794; F:acute-phase response protein activity; TAS.  
 DR GO; GO:0005208; F:amyloid protein; TAS.  
 DR GO; GO:0003754; F:chaperone activity; TAS.  
 DR GO; GO:0005211; F:plasma glycoprotein; TAS.  
 DR GO; GO:0005209; F:plasma protein; TAS.  
 DR GO; GO:0006462; F:protein complex assembly, multichaperone pa. . .; TAS.  
 DR InterPro; IPR001759; Pentaxin.  
 DR Pfam; PF00354; Pentaxin; 1.  
 DR PRINTS; PR00895; PENTAXIN.  
 DR Prodom; PD002153; Pentaxin; 1.  
 DR SMART; SM00159; PTX; 1.  
 DR PROSITE; PS00289; PENTAXIN; 1.  
 DR Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin; Signal; Polymorphism;  
 KW 3D-structure.  
 FT SIGNAL 1 19  
 FT CHAIN 20 223  
 FT DOMAIN 20 223  
 FT DISULFID 55 114  
 FT CARBOHYD 51 51  
 FT  
 FT VARIANT 152 152  
 FT  
 FT VARIANT 155 155  
 FT  
 FT VARIANT 158 158  
 FT  
 FT CONFLICT 101 101  
 FT STRAND 21 21  
 FT TURN 24 25  
 FT STRAND 26 30  
 FT STRAND 38 42  
 FT STRAND 49 49  
 FT STRAND 51 59  
 FT STRAND 66 73  
 FT TURN 74 75  
 FT STRAND 76 86  
 FT TURN 87 88  
 FT STRAND 89 94  
 FT TURN 95 96  
 FT STRAND 97 102  
 FT STRAND 111 118  
 FT TURN 119 121  
 FT STRAND 123 128  
 FT TURN 129 130  
 FT STRAND 131 132  
 FT STRAND 136 137  
 FT TURN 140 141  
 FT STRAND 144 144  
 FT STRAND 149 152  
 FT HELIX 165 167  
 FT STRAND 171 179  
 FT HELIX 185 193

FT TURN 194 194  
 FT STRAND 202 203  
 FT TURN 204 205  
 FT STRAND 207 212  
 FT STRAND 216 219  
 SQ SEQUENCE 223 AA; 25387 MW; 6C8BA515F8E8B93 CRC64;  
 Query Match 87.9%; Score 29; DB 1; Length 223;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMOAL 6  
 Db 202 LDMOAL 207

RESULT 11  
 SAMP\_PIG STANDARD; PRT; 224 AA.  
 AC 019063;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Serum amyloid P-component precursor (SAP).  
 GN APCS.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 NC NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Landrace; TISSUE=Liver;  
 RA Ozawa A., Matsumoto M., Kajikawa M., Hanazono M., Yasue H.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1 SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID  
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.  
 CC -1 SUBCELLULAR LOCATION: Secreted.  
 CC -1 DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND  
 CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.  
 CC -1 SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.  
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 CC -----  
 CC EMBL: AB005546; BAA21474.1; -  
 CC HSPF: P02743; ISAC.  
 DR InterPro: IPR001759; Pentaxin.  
 DR Pfam: PF000354; Pentaxin; 1.  
 DR PRINTS: PR00895; PENTAXIN.  
 DR ProDom: PD002153; Pentaxin; 1.  
 DR SMART: SM00159; PTX; 1.  
 DR PROSITE: PS00289; PENTAXIN; 1.  
 KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin; signal.  
 FT SIGNAL 19  
 FT CHAIN 1 224 SERUM AMYLOID P-COMPONENT.  
 FT DOMAIN 20 224 PENTAXIN.  
 FT DISULFID 55 114 BY SIMILARITY.  
 FT CARBOHYD 51 51 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 224 AA; 25641 MW; 9D18676918BEDC66 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 224;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMOAL 6  
 Db 203 LDMOAL 208

RESULT 12  
 SAMP\_MESAU STANDARD; PRT; 234 AA.  
 AC P07629;  
 DT 01-APR-1998 (Rel. 07, Created)  
 DT 01-FEB-1998 (Rel. 31, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Serum amyloid P-component precursor (Female protein) (FP) (SAP(FP)).  
 GN PTX2 OR SAP.  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 NC NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94012761; PubMed=7691816;  
 RA Rudnick C.M., Dowton S.B.;  
 RT "Serum amyloid P (female protein) of the Syrian hamster. Gene  
 RT structure and expression."  
 RL J. Biol. Chem. 268:21760-21769 (1993).  
 RN [2]  
 RP SEQUENCE OF 24-234 FROM N.A.  
 RX MEDLINE=85218787; PubMed=2408337;  
 RA Dowton S.B., Woods D.E., Mantzouranis E.C., Colten H.R.;  
 RT "Syrian hamster female protein: analysis of female protein primary  
 RT structure and gene expression."  
 RL Science 228:1206-1208 (1985).  
 RN [3]  
 RP SEQUENCE OF 25-48.  
 RX MEDLINE=81241327; PubMed=6166709;  
 RA Coe J.E., Margosian S.S., Slayter H.S., Sogn J.A.;  
 RT "Hamster female protein. A new Pentraxin structurally and  
 RT functionally similar to C-reactive protein and amyloid P component."  
 RL J. Exp. Med. 153:977-991 (1981).  
 RN [4]  
 RP 3D-STRUCTURE MODELING.  
 RX MEDLINE=95187705; PubMed=7881902;  
 RA Srinivasan N., White H.E., Emaley J., Wood S.P., Peyys M.B.,  
 RA Blundell T.L.;  
 RT "Comparative analyses of pentraxins: implications for proteome  
 RT assembly and ligand binding."  
 RL Structure 2:1017-1027 (1994).  
 CC -1 SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID  
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.  
 CC -1 SUBCELLULAR LOCATION: Secreted.  
 CC -1 MISCELLANEOUS: PLASMA CONCENTRATION OF PP ARE ALTERED BY SEX  
 CC STEROIDS AND BY STIMULI THAT ELICIT AN ACUTE PHASE RESPONSE.  
 CC -1 SIMILARITY: BELONGS TO THE PENTAXIN FAMILY. ORTHOLOG OF HUMAN SAP.  
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 CC -----  
 CC EMBL: L22024; AAA03577.1; -  
 CC PIR: M11342; AAA36980.1; -  
 DR PIR: A44177; A44177.  
 DR PIR: A48593; A48593.  
 DR PDB: 1HAS; 15-OCT-95.  
 DR InterPro: IPR001759; Pentaxin.  
 DR Pfam: PF000354; Pentaxin; 1.  
 DR PRINTS: PR00895; PENTAXIN.  
 DR ProDom: PD002153; Pentaxin; 1.  
 DR SMART: SM00159; PTX; 1.  
 DR PROSITE: PS00289; PENTAXIN; 1.  
 KW Lectin; Pentaxin; Plasma; Acute phase; signal; Amyloid; Glycoprotein;  
 KW 3D-structure.  
 FT SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 234 SERUM AMYLOID P-COMPONENT.  
 FT DOMAIN 23 234 PENTAXIN.  
 FT DISULFID 58 117 BY SIMILARITY.  
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CONFLICT 27 27 T -> S (IN REF. 3).  
 FT CONFLICT 43 43 K -> N (IN REF. 3).  
 FT CONFLICT 76 76 A -> T (IN REF. 2).  
 FT STRAND 24 24  
 FT TURN 27 28  
 FT STRAND 29 33  
 FT STRAND 41 44  
 FT STRAND 52 52  
 FT STRAND 54 62  
 FT STRAND 69 76  
 FT TURN 77 78  
 FT STRAND 79 89  
 FT TURN 90 91  
 FT STRAND 92 97  
 FT TURN 98 99  
 FT STRAND 100 105  
 FT STRAND 113 121  
 FT TURN 122 125  
 FT STRAND 126 131  
 FT TURN 132 133  
 FT STRAND 134 135  
 FT STRAND 139 140  
 FT TURN 143 144  
 FT STRAND 147 147  
 FT STRAND 152 155  
 FT HELIX 168 170  
 FT STRAND 174 182  
 FT HELIX 188 196  
 FT TURN 197 197  
 FT STRAND 205 205  
 FT TURN 207 208  
 FT STRAND 210 210  
 FT STRAND 212 215  
 FT STRAND 219 222  
 FT HELIX 226 234  
 SQ SEQUENCE 234 AA; 26463 MW; 6161F0383062D2DB CRC64;

Query Match 87.9%; Score 29; DB 1; Length 234;  
 Best Local Similarity 83.3%; Pred. NO. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DMSAL 6  
 Db 205 LDWQAL 210

RESULT 13  
 CXAG RAT STANDARD; PRT; 286 AA.  
 ID CXAG RAT  
 AC P2823;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Gap junction alpha-6 protein (Connexin 33) (Cx33).  
 GN GJA6 OR CXN-33.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92112940; PubMed=1370487;  
 RA Hefflinger J.-A., Bruzzone R., Jenkins N.A., Gilbert D.J.,  
 RA Copeland N.G., Paul D.L.;  
 RT "Four novel members of the connexin family of gap junction proteins.  
 RT Molecular cloning, expression, and chromosome mapping."  
 RT J. Biol. Chem. 267:2057-2064(1992).  
 CC -1- FUNCTION: One gap junction consists of a cluster of closely packed  
 CC pairs of transmembrane channels, the connexons, through which

CC materials of low mw diffuse from one cell to a neighboring cell.  
 CC -1- SUBUNIT: A connexon is composed of a hexamer of connexins.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Expressed in testis.  
 CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)  
 CC SUBFAMILY.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC DR EMBL, M76534; AAA0998.1; -.  
 CC DR PIR, C42053; C42053.  
 CC DR InterPro, IPR000500; Connexin.  
 CC DR Pfam, PF00029; connexin.1.  
 CC DR PRINTS, PR00206; CONNEXIN.  
 CC DR SMART, SM00037; CNX, 1.  
 CC DR PROSITE, PS00407; CONNEXINS\_1; 1.  
 CC DR PROSITE, PS00408; CONNEXINS\_2; 1.  
 CC KW Gap junction; Transmembrane.  
 CC FT DOMAIN 1 23  
 CC FT TRANSMEM 24 41 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 42 76 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 77 99 POTENTIAL.  
 CC FT DOMAIN 100 151 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 152 174 POTENTIAL.  
 CC FT DOMAIN 175 209 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 210 232 POTENTIAL.  
 CC FT DOMAIN 233 286 CYTOPLASMIC (POTENTIAL).  
 CC SQ SEQUENCE 286 AA; 32860 MW; A585266ACA2ACCF2 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 286;  
 Best Local Similarity 100.0%; Pred. NO. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSAL 6  
 Db 3 DMSAL 7

RESULT 14  
 SGBU ECOLI STANDARD; PRT; 286 AA.  
 ID SGBU ECOLI  
 AC P37679;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Putative hexulose-6-phosphate isomerase (EC 5.-.-.-) (HUMPI).  
 GN SGBU OR B3582.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=KL2 / MG1655;  
 RX MEDLINE=9416500; PubMed=8041620;  
 RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;  
 RA "Analysis of the Escherichia coli genome. V. DNA sequence of the  
 RT region from 76.0 to 81.5 minutes."  
 RT Nucleic Acids Res. 22:2576-2586(1994).  
 RN [2]  
 RP DISCUSSION OF SEQUENCE.  
 RA Reizer U., Charbit A., Reizer A., Sela M.H. Jr.;  
 RT "Novel phosphotransferases system genes revealed by bacterial genome  
 RT analysis: operons encoding homologues of sugar-specific permease  
 RT domains of the phosphotransferase system and pentose catabolic  
 RT enzymes."  
 RL Genome Sci. Technol. 1:53-75(1996).

```

CC -1- FUNCTION: ISOMERIZATION OF D-ARABINO-6-HEXULOSE 3-PHOSPHATE TO
CC D-FRUCTOSE 6-PHOSPHATE.
CC -1- PATHWAY: PROBABLY PART OF A SUGAR METABOLIC PATHWAY ALONG WITH
CC SGBH.
CC -1- SIMILARITY: BELONGS TO THE HUMPI FAMILY.
CC -----
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CC -----
DR EMBL; U00039; AAB18559.1; ALT INIT.
DR EMBL; AE000435; AAC76606.1; ALT_INIT.
DR Ecogene; EG12286; ggbu
DR InterPro; IPR004560; Hx16Piso_put.
DR Pfam; PF03809; Hx16Piso_put; 1.
DR TIGRfam; TIGR00542; Hx16Piso_put; 1.
DR Isomerase; Complete proteome.
SQ SEQUENCE 286 AA; 32455 MW; 4C849F575E937BF9 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSA 5
Db 48 LDMSA 52

RESULT 15
CYCG_RHOSH STANDARD; PRT; 296 AA.
AC Q53143;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Diheme cytochrome C-type.
GN CYCG.
OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP SEQUENCE FROM N.A..
RC STRAIN:ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX MEDLINE=95362655; PubMed=7543472;
RA Flory J.E., Donohue T.J.;
RT "Organization and expression of the Rhodobacter sphaeroides cycFG
RT operon.";
RL J. Bacteriol. 177:4311-4320 (1995).
CC -1- FUNCTION: DIHEME C-TYPE CYTOCHROME, THAT IS PARTICULARLY EXPRESSED
CC WHEN CELLS GENERATE ENERGY VIA AEROBIC RESPIRATION.
CC -1- SUBCELLULAR LOCATION: Membrane-bound.
CC -1- PTM: BINDS TWO HEME GROUPS PER MOLECULE (POTENTIAL).
CC -1- SIMILARITY: TO ACETOBACTER ALCOHOL DEHYDROGENASE CYTOCHROME C
CC SUBUNIT.
CC -----
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CC -----
DR EMBL; L36880; AAD09146.1; -
DR InterPro; IPR003088; CyC_C1.
DR InterPro; IPR003219; CyC adh.
DR InterPro; IPR000345; CyC_heme_bind.
DR Pfam; PF00034; Cytochrome_c; 1.

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DR ProDom; PD011584; CyC adh; 1.
DR PROSITE; PS00190; CYTOCHROME C; 2.
DR Electron transport; Heme; Membrane.
FT BINDING 52 52 HEME 1 (COVALENT) (BY SIMILARITY).
FT BINDING 55 55 HEME 1 (COVALENT) (BY SIMILARITY).
FT METAL 56 56 IRON (HEM 1 AXIAL LIGAND)
FT BINDING 202 202 HEME 2 (COVALENT) (BY SIMILARITY).
FT BINDING 205 205 HEME 2 (COVALENT) (BY SIMILARITY).
FT METAL 206 206 IRON (HEM 2 AXIAL LIGAND)
FT (BY SIMILARITY).
SQ SEQUENCE 296 AA; 31727 MW; 4C4A9D8F695B5BFD CRC64;

Query Match 87.9%; Score 29; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSA 5
Db 241 LDMSA 245

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Search completed: February 18, 2004, 14:28:11  
 Job time : 4.55263 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds  
(without alignments)  
87.531 Million cell updates/sec

Title: US-09-643-260-13

Perfect score: 33

Sequence: 1 LDMSAL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	330	2	B69416
2	31	93.9	192	2	P82645
3	31	93.9	333	2	S75980
4	31	93.9	984	2	S67527
5	31	93.9	1394	2	S66876
6	31	93.9	2297	2	T34918
7	30	90.9	163	2	D84320
8	30	90.9	208	2	D75556
9	30	90.9	261	2	A69807
10	30	90.9	280	2	D97195
11	30	90.9	365	2	P82398
12	30	90.9	380	2	D83048
13	30	90.9	384	2	AC0149
14	30	90.9	401	2	D83618
15	30	90.9	442	2	T20638
16	30	90.9	476	2	E82758
17	30	90.9	572	2	T37128
18	30	90.9	638	2	F75547
19	30	90.9	1026	2	T39612
20	30	90.9	1293	2	T30871
21	30	90.9	1471	2	F86218
22	30	90.9	1616	2	T00713
23	29	87.9	32	2	A24047
24	29	87.9	94	2	S77047
25	29	87.9	119	2	S74925
26	29	87.9	119	2	S75488
27	29	87.9	119	2	S74836
28	29	87.9	119	2	S75590
29	29	87.9	150	2	A83754

30	29	87.9	171	2	S75475	transposase glr152
31	29	87.9	177	2	A62498	hypothetical prote
32	29	87.9	211	2	A44177	female protein - g
33	29	87.9	214	2	G63488	probable permease
34	29	87.9	215	2	H82830	conserved hypothet
35	29	87.9	223	1	YLHUP	serum amyloid P-co
36	29	87.9	232	2	P82729	conserved hypothet
37	29	87.9	234	2	A48593	serum amyloid P-co
38	29	87.9	242	2	G87696	hypothetical prote
39	29	87.9	279	2	F70612	hypothetical prote
40	29	87.9	282	2	S76906	transposase glr023
41	29	87.9	282	2	S76382	transposase glr035
42	29	87.9	282	2	S76312	transposase glr135
43	29	87.9	282	2	S77237	transposase glr135
44	29	87.9	282	2	S75484	transposase glr135
45	29	87.9	286	1	C42053	gap junction prote

#### ALIGNMENTS

##### RESULT 1

B69416  
hypothetical protein AF1331 - Archaeoglobus fulgidus  
C:Species: Archaeoglobus fulgidus  
C:Date: 05-Dec-1997 #sequence\_reviseion 05-Dec-1997 #text\_change 22-Oct-1999  
C:Accession: B69416  
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A:Authors: Usterback, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kalne, B.P.; Sykes, S.; Smith, H.O.; Woese, C.R.; Venter, J.C.  
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae  
A:Reference number: A69250; PMID:98049343; PMID:9389475  
A:Accession: B69416  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-330 <KLE>  
A:Cross-references: GB:AE001012; GB:AE000782; NID:G2689335; PIDN:AAB89926.1; PID:G26492

Query Match 100.0%; Score 33; DB 2; Length 330;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LDMSAL 6  
Db 177 LDMSAL 182

##### RESULT 2

P82645  
tryptophan repressor binding protein XF1733 [imported] - Xylella fastidiosa (strain 9a;  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_reviseion 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: P82645  
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequ  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; PMID:20365717; PMID:10910347  
A>Note: for a complete list of authors see reference number A59328 below  
A:Accession: P82645  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-192 <SIM>  
A:Cross-references: GB:AE003996; GB:AE003849; NID:G9106790; PIDN:AAF94542.1; GSPDB:GNOC  
A:Experimental source: GB:AE003996  
R:Stimpson, A.J.G.; Reinach, F.C.; Arruda, A.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Brites, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrero, D.M.; Carrer, A.; Neto, E.; Docena, C.; El-Dorri, H.; Facinanca, A.P.; Ferreira, A.J.S.  
Submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frich J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.  
 A.; Nethers, Martins, E.M.F.; Matsushima, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
 Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawaak  
 A.; Authores, da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira  
 M.; Tanhako, M.H.; Vailhada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
 A.; Reference number: A59328  
 A;Contents: annotation  
 C;Genetics:  
 A;Gene: XP1733

Query Match 93.9%; Score 31; DB 2; Length 192;  
 Best Local Similarity 83.3%; Pred. No. 93;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
 :|||||  
 Db 43 MDMSAL 48

RESULT 3  
 S75980  
 hypothetical protein slr0537 - *Synechocystis* sp. (strain PCC 6803)

C;Species: *Synechocystis* sp.  
 A;Variety: PCC 6803  
 C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000

C;Accession: S75980  
 R;Kaneho, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
 DNA Res. 3: 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*  
 sp.  
 A;Reference number: S74322; MUID:97061201; PMID:8905231  
 A;Accession: S75980  
 A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA  
 A;Residues: 1333 <KAN>

A;Cross-references: EMBL:DD4006; GB:AB001339; NID:g1001291; PIDN:BA10827.1; PID:g100134  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Superfamily: probable ribokinase

Query Match 93.9%; Score 31; DB 2; Length 333;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
 :|||||  
 Db 146 MDMSAL 151

RESULT 4  
 S67527  
 protein kinase (EC 2.7.1.-) PRK2 - human

C;Species: *Homo sapiens* (man)  
 C;Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 21-Jul-2000

C;Accession: S67527; I67464  
 R;Palmer, R.H.; Ridden, J.; Parker, P.J.

Eur. J. Biochem. 227: 344-351, 1995

A;Title: Cloning and expression patterns of two members of a novel protein-kinase-C-rela  
 A;Reference number: I53327; MUID:95154310; PMID:7851406

A;Accession: S67527  
 A;Molecule type: mRNA

A;Residues: 1-984 <PML>  
 A;Cross-references: EMBL:S75548; NID:g914099; PIDN:AB33346.1; PID:g914100

A;Experimental source: fetal brain  
 A;Accession: I67464

A;Status: preliminary; translated from GB/EMBL/DBD  
 A;Molecule type: mRNA

A;Residues: 1-984 <RKS>  
 A;Cross-references: GB:S75548; NID:g914099; PIDN:AB33346.1; PID:g914100  
 C;Keywords: ATP; unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog  
 C;Keywords: ATP; unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog  
 F:655-916/Domain: protein kinase homology <KIN>

F:663-671/Region: protein kinase ATP-binding motif  
 F:686/Active site: Lys #status predicted

Query Match 93.9%; Score 31; DB 2; Length 984;  
 Best Local Similarity 83.3%; Pred. No. 5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
 :|||||  
 Db 919 IDMSAL 924

RESULT 5  
 S66876  
 ATP-dependent transport protein homolog YOR011w - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: ATP-dependent permease homolog; protein O2601; protein UNA841  
 C;Species: *Saccharomyces cerevisiae*

C;Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 19-Apr-2002

C;Accession: S66876; S66877; S54617; S61995; S72144  
 R;Peterson, B.; Sterky, F.; Uhlen, M.

submitted to the Protein Sequence Database, July 1996  
 A;Reference number: S66882

A;Accession: S66876  
 A;Molecule type: DNA

A;Residues: 1-841 <PBT>  
 A;Cross-references: EMBL:S74919; MIPS:YOR011w

A;Experimental source: strain S288C  
 R;de Haan, M.; Grivell, L.A.; Maarse, A.C.  
 submitted to the Protein Sequence Database, July 1996

A;Reference number: S66877  
 A;Accession: S66877

A;Molecule type: DNA  
 A;Residues: 355-1394 <DEM>

A;Cross-references: EMBL:S74919; MIPS:YOR011w  
 A;Experimental source: strain S288C

R;de Haan, M.; Maarse, A.C.; Grivell, L.A.  
 submitted to the EMBL Data Library, May 1995

A;Reference number: S54617  
 A;Accession: S54617

A;Molecule type: DNA  
 A;Residues: 355-1394 <DEM>

A;Cross-references: EMBL:X87331  
 R;Sterky, F.; Uhlen, M.

submitted to the EMBL Data Library, December 1995  
 A;Reference number: S61995

A;Accession: S61995  
 A;Molecule type: DNA

A;Residues: 389-841 <STB>  
 A;Cross-references: EMBL:U43491; NID:g1150992; PIDN:AA49491.1; PID:g1151007

R;Sterky, F.; Holmberg, A.; Pettersson, B.; Uhlen, M.  
 Yeast 12: 1091-1095, 1996

A;Title: The sequence of a 30 kb fragment on the left arm of chromosome XV from *Saccha*  
 A;Reference number: S72130; MUID:97051599; PMID:8896276

A;Accession: S72144  
 A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA  
 A;Residues: 389-841 <STB>

A;Cross-references: EMBL:U43491; NID:g1150992; PIDN:AA49491.1; PID:g1151007  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995

C;Genetics:  
 A;Gene: SGD:YUS1

A;Cross-references: SGD:S0005537  
 A;Map position: 15R  
 A;Note: YOR011w

C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology  
 C;Keywords: ATP; nucleotide binding; P-loop; transmembrane protein  
 F:49-249/Domain: ATP-binding cassette homology <ABC1>

F:391-407/Domain: transmembrane #status predicted <TM1>  
 F:421-437/Domain: transmembrane #status predicted <TM2>  
 F:476-492/Domain: transmembrane #status predicted <TM3>  
 F:501-517/Domain: transmembrane #status predicted <TM4>  
 F:527-543/Domain: transmembrane #status predicted <TM5>  
 F:640-656/Domain: transmembrane #status predicted <TM6>

F/766-954/Domain: ATP-binding cassette homology <ABC2>  
 F/762-789/Region: nucleotide-binding motif A (p-loop)  
 F/1107-1123/Domain: transmembrane #status predicted <TM7>  
 F/1166-1182/Domain: transmembrane #status predicted <TM8>  
 F/1226-1242/Domain: transmembrane #status predicted <TM9>

Query Match 93.9%; Score 31; DB 2; Length 1394;  
 Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
 DB 1017 LDMSAL 1022

RESULT 6  
 T34918  
 polyketide synthase - Streptomyces coelicolor

C/Species: Streptomyces coelicolor  
 C/Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 17-Nov-2000  
 C/Accession: T34918  
 R/Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, January 1998  
 A/Reference number: Z21558  
 A/Accession: T34918

A/status: preliminary; translated from GB/EMBL/DBD8  
 A/molecule type: DNA  
 A/residues: 1-2297 <OLI>  
 A/cross-references: EMBL:AL021409; PIDN:CAA16183.1; GSPDB:GNO00070; SCODEB:SC3F7.12  
 A/experimental source: strain A3(2)  
 C/genetics:

A/gene: SCODEB:SC3F7.12  
 C/superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology; acetate-CoA ligase  
 C/keywords: carrier protein  
 F/80-583/Domain: acetate-CoA ligase homology <ACL>  
 F/701-771/Domain: acyl carrier protein homology <ACP>  
 F/818-1205/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>  
 F/1315-1600/Domain: [acyl-carrier-protein] 5-malonyltransferase homology <AMT>

Query Match 93.9%; Score 31; DB 2; Length 2297;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
 DB 1641 LDMSAL 1646

RESULT 7  
 DB4320  
 hypothetical protein Vng1679h (imported) - Halobacterium sp. NRC-1  
 C/Species: Halobacterium sp. NRC-1  
 C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
 C/Accession: DB4320  
 R/Ng, W.V.; Kennedy, S.P.; Mahatras, G.G.; Bergiste, B.; Pan, M.; Shukla, H.D.; Laaky, S.  
 ; Leitauer, B.; Keller, K.; Cruz, R.; Danon, M.C.; Hough, D.W.; Maddocks, D.G.; Jablo  
 pong, K.H.; Alam, M.; Prellae, T.  
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A/authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
 A/title: Genome sequence of Halobacterium species NRC-1.  
 A/reference number: A84160; MID:20504483; PMID:11016550  
 A/Accession: DB4320

A/status: preliminary  
 A/molecule type: DNA  
 A/residues: 1-163 <STO>  
 A/cross-references: GB:AE004437; NID:G10581148; PIDN:AA31928.1; GSPDB:GNO0138  
 C/genetics:  
 A/gene: VNG1679H

Query Match 90.9%; Score 30; DB 2; Length 163;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
 DB 142 LDMSAL 147

RESULT 8  
 D75556  
 phosphoribosylanthranilate isomerase - Deinococcus radiodurans (strain R1)

C/Species: Deinococcus radiodurans  
 C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000  
 C/Accession: D75556  
 R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.  
 ; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S  
 .; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 Science 286, 1571-1577, 1999

A/title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
 A/reference number: A75250; MID:20036896; PMID:10567266

A/Accession: D75556  
 A/status: preliminary  
 A/molecule type: DNA  
 A/residues: 1-208 <WHI>  
 A/cross-references: GB:AE001875; GB:AE000513; NID:G6457790; PIDN:ANF09715.1; PID:G6457  
 A/experimental source: strain R1  
 C/genetics:

A/gene: DR0123  
 A/map position: 1  
 C/superfamily: phosphoribosylanthranilate isomerase; trpF homology

Query Match 90.9%; Score 30; DB 2; Length 208;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
 DB 144 LDMSAL 149

RESULT 9  
 A69807  
 3-hydroxyisobutyrate dehydrogenase homolog yfjR - Bacillus subtilis

C/Species: Bacillus subtilis  
 C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 18-Aug-2000  
 C/Accession: A69807  
 R/Kunst, F.; Ogatawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bert  
 C.; Bron, S.; Brouillet, S.; Bruscia, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; C  
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.  
 Nature 390, 249-256, 1997

A/authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall  
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.  
 Koester, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
 A/authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maguda, S.; Maue  
 Y, M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porterei  
 Rieger, M.; Rivolta, C.; Rooha, B.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon  
 A/authors: Schlach, S.; Schoeler, R.; Scofield, F.; Sekiguchi, J.; Sekowska, A.; Ser  
 akuchi, M.; Tanakoshi, A.; Tanaka, T.; Teppera, P.; Tognoni, A.; Tosato, V.; Uchiyam  
 A.; Whitters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida  
 A/authors: Yoshikawa, H.F.; Zumelelin, E.; Yoshikawa, H.; Danchin, A.

A/title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
 A/reference number: A69580; MID:98044033; PMID:9384377

A/Accession: A69807  
 A/status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/molecule type: DNA  
 A/residues: 1-261 <KUN>  
 A/cross-references: GB:Z99108; GB:AL009126; NID:G2631055; PIDN:CAB12628.1; PID:G263112  
 A/experimental source: strain 168  
 C/genetics:

A/gene: yfjR  
 C/superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase 1  
 F/2-240/Domain: 3-hydroxyisobutyrate dehydrogenase homology #status atypical <HIB>

Query Match 90.9%; Score 30; DB 2; Length 261;  
 Best Local Similarity 83.3%; Pred. No. 2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



Qy 1 LDMSAL 6  
|||:  
Db 251 LDMSAL 256

## RESULT 10

D97195  
Probable xylanase/chitin deacetylase [imported] - Clostridium acetobutylicum  
C/Species: Clostridium acetobutylicum  
C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
C/Accession: D97195  
R/Noiling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld  
A/Reference number: A96900; MUID:21359325; PMID:21359325  
A/Accession: D97195  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-280 <KUR>  
A/Cross-references: GB:AE001437; PIDN:AAK80351.1; PID:G15025409; GSPDB:GN00168  
C/Experimental source: Clostridium acetobutylicum ATCC824  
C/Genetic8:  
A/Gene: CAC2396

Query Match 90.9%; Score 30; DB 2; Length 280;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSAL 6  
|||:  
Db 212 LDMSAL 217

## RESULT 11

F82398  
Transcription regulator Arac/Xy1S family VCA0926 [imported] - Vibrio cholerae (strain NI  
C/Species: Vibrio cholerae  
C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C/Accession: F82398  
R/Heldberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gajim, M.L.; Dodson, R.J.;  
chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Baes, S.; Qin, H.; Dragol, I.; Sellers, F.  
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A/Reference number: A82035; MUID:20406833; PMID:10952301  
A/Accession: F82398  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-365 <HEI>  
A/Cross-references: GB:AE004420; GB:AE003853; NID:G9656361; PIDN:AAF96823.1; GSPDB:GN001  
A/Experimental source: serogroup O1, strain N16961, biotype El Tor  
C/Genetic8:  
A/Gene: VCA0926  
A/Map position: 2

Query Match 90.9%; Score 30; DB 2; Length 365;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSAL 6  
|||:  
Db 70 VDMASL 75

## RESULT 12

D82088  
Chromate resistance protein-related protein VC2339 [imported] - Vibrio cholerae (strain  
C/Species: Vibrio cholerae  
C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C/Accession: D82088  
R/Heldberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gajim, M.L.; Dodson, R.J.;

chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Baes, S.; Qin, H.; Dragol, I.; Sellers,  
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A/Reference number: A82035; MUID:20406833; PMID:10952301  
A/Accession: D82088  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-380 <HEI>  
A/Cross-references: GB:AE004304; GB:AE003852; NID:G9656905; PIDN:AAF95482.1; GSPDB:GNO  
A/Experimental source: serogroup O1, strain N16961, biotype El Tor  
C/Genetic8:  
A/Gene: VC2339  
A/Map position: 1  
C/Superfamily: chromate resistance protein A

Query Match 90.9%; Score 30; DB 2; Length 380;  
Best Local Similarity 83.3%; Pred. No. 2.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSAL 6  
|||:  
Db 344 LDMSAL 349

## RESULT 13

AG0149  
Probable membrane protein YPO1221 [imported] - Yersinia pestis (strain CO92)  
C/Species: Yersinia pestis  
C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C/Accession: AG0149  
R/Parhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.;  
demo-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.  
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett  
Nature 413, 523-527, 2001  
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A/Reference number: AB0001; MUID:21470413; PMID:11586360  
A/Accession: AG0149  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-384 <KUR>  
A/Cross-references: GB:AL590842; PIDN:CMC90058.1; PID:G15979278; GSPDB:GN00175  
C/Genetic8:  
A/Gene: YPO1221

Query Match 90.9%; Score 30; DB 2; Length 384;  
Best Local Similarity 83.3%; Pred. No. 2.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSAL 6  
|||:  
Db 228 LDMSAL 233

## RESULT 14

D83618  
beta-ketoadipyl CoA thiolase Pcaf PA0228 [imported] - Pseudomonas aeruginosa (strain P.  
C/Species: Pseudomonas aeruginosa  
C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C/Accession: D83618  
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mitsuuchi, S.D.; Warrenner, P.; Hickey, M.J.;  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Li  
Loay, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat.  
A/Reference number: A82950; MUID:20437337; PMID:10984043  
A/Accession: D83618  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-401 <STO>  
A/Cross-references: GB:AE004460; GB:AE004091; NID:G9946055; PIDN:AA03617.1; GSPDB:GNO  
A/Experimental source: strain PA01  
C/Genetic8:

A:Gene: pcaf; PA0228  
C:Superfamily: acetyl-CoA acetyltransferase

Query Match 90.9%; Score 30; DB 2; Length 401;  
Best Local Similarity 83.3%; Pred. No. 3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6  
:|||||  
Db 45 VDWSAL 50

## RESULT 15

T20638

hypothetical protein T06H11.4 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000

C/Accession: T20638; T24630

R/Kershaw, J.

submitted to the EMBL Data Library, June 1995

A/Reference number: Z19303

A/Accession: T20638

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-442 &lt;NT&gt;

A/Cross-references: EMBL:Z49887; PIDN:CAA90060.1; GSPDB:GN00028; CESP:T06H11.4

A/Experimental source: clone F0989

R/Kershaw, J.

submitted to the EMBL Data Library, June 1995

A/Reference number: Z19914

A/Accession: T24630

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-442 &lt;NT&gt;

A/Cross-references: EMBL:Z49889; PIDN:CAA90069.1; GSPDB:GN00028; CESP:T06H11.4

A/Experimental source: clone T06H11

C/Genetics:

A:Gene: CESP:T06H11.4

A/Map position: X

A/Intons: 45/1; 95/3; 150/2; 208/3; 250/2; 292/3

C:Superfamily: molybdenum cofactor biosynthesis protein moea-2

Query Match 90.9%; Score 30; DB 2; Length 442;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSAL 6  
:|||||  
Db 39 VDWSAL 44

Search completed: February 18, 2004, 14:38:49  
Job time : 7.5921 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 (without alignments)  
75.239 Million cell updates/sec

Title: US-09-643-260-13

Perfect score: 33

Sequence: 1 LDMSAL 6

Scoring table: BIOSIM62

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

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2: /cgn2_6/prodata/1/pubppa/US06_PUB_PUB.pep:*
3: /cgn2_6/prodata/1/pubppa/US06_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubppa/US07_PUB.pep:*
5: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubppa/US08_PUB.pep:*
7: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pep:*
8: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
9: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
11: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
12: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	6	10	US-09-847-940B-13
2	33	100.0	6	11	US-09-847-940B-13
3	31	93.9	53	12	US-10-148-786A-25
4	31	93.9	77	12	US-10-148-786A-8
5	31	93.9	333	12	US-10-369-493-2852
6	31	93.9	334	12	US-10-217-574-18
7	31	93.9	334	12	US-10-217-574-18
8	31	93.9	334	12	US-10-217-574-18
9	31	93.9	502	10	US-09-895-072-13
10	31	93.9	502	10	US-09-895-072-13
11	31	93.9	502	12	US-10-023-894-16
12	31	93.9	502	12	US-10-024-197-16
13	31	93.9	502	12	US-10-306-686-13
14	31	93.9	502	15	US-10-023-888-16
15	31	93.9	502	15	US-10-023-889-16
16	31	93.9	502	15	US-10-023-890-16

16	31	93.9	552	12	US-10-120-801-91	Sequence 91, Appl
17	31	93.9	984	12	US-10-354-358-106	Sequence 106, Appl
18	31	93.9	984	14	US-10-029-905-10	Sequence 10, Appl
19	31	93.9	1394	12	US-10-369-493-22253	Sequence 22353, A
20	30	90.9	138	12	US-10-029-386-34138	Sequence 34138, A
21	30	90.9	208	12	US-10-369-493-23401	Sequence 23401, A
22	30	90.9	403	15	US-10-156-761-14428	Sequence 14428, A
23	30	90.9	466	12	US-10-310-154-397	Sequence 397, Appl
24	30	90.9	516	14	US-10-119-635-2	Sequence 2, Appl
25	30	90.9	1293	12	US-10-084-846A-50	Sequence 50, Appl
26	30	90.9	2747	12	US-10-402-842-2	Sequence 2, Appl
27	30	90.9	19725	12	US-10-084-846A-4	Sequence 4, Appl
28	29	87.9	175	12	US-10-320-797-3024	Sequence 3024, Appl
29	29	87.9	203	12	US-10-262-473-4	Sequence 4, Appl
30	29	87.9	223	12	US-10-262-473-2	Sequence 2, Appl
31	29	87.9	228	12	US-10-084-846A-16	Sequence 16, Appl
32	29	87.9	267	15	US-10-156-761-14290	Sequence 14290, A
33	29	87.9	292	12	US-10-238-075-301	Sequence 301, Appl
34	29	87.9	297	11	US-09-557-796-30	Sequence 30, Appl
35	29	87.9	300	12	US-10-314-657-11	Sequence 11, Appl
36	29	87.9	344	15	US-10-156-761-7691	Sequence 7691, Appl
37	29	87.9	345	11	US-09-735-056-34	Sequence 34, Appl
38	29	87.9	352	12	US-10-289-762-702	Sequence 702, Appl
39	29	87.9	382	12	US-10-024-298A-113	Sequence 113, Appl
40	29	87.9	382	12	US-10-024-298A-115	Sequence 115, Appl
41	29	87.9	382	12	US-10-042-211A-113	Sequence 113, Appl
42	29	87.9	382	12	US-10-042-211A-115	Sequence 115, Appl
43	29	87.9	382	12	US-10-438-537-6	Sequence 6, Appl
44	29	87.9	382	12	US-10-372-683-28	Sequence 28, Appl
45	29	87.9	426	12	US-10-369-493-3236	Sequence 3236, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-847-940B-13
Sequence 13, Application US/09847940B
Patent No. US2002015600A1
GENERAL INFORMATION:
APPLICANT: May, Michael J.
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PRI-117P
CURRENT APPLICATION NUMBER: US/09/847,940B
PRIOR FILING DATE: 2001-05-02
PRIORITY APPLICATION NUMBER: 09/643,260
PRIORITY FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
US-09-847-940B-13
```

Query Match 100.0%; Score 33; DB 10; Length 6;  
Best local Similarity 100.0%; Pred. No. 7+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
Db 1 LDMSAL 6

RESULT 2  
US-09-847-946A-13  
Sequence 13, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J

```

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathy
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NBD peptide
US-09-847-946A-13

Query Match          100.0%; Score 33; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDWSAL 6
       :|||||
Db      1 LDWSAL 6

RESULT 3
US-10-148-786A-25
; Sequence 25, Application US/10148786A
; Publication No. US20030143656A1
; GENERAL INFORMATION:
; APPLICANT: Aleassi, Dario
; APPLICANT: Biondi, Riccardo
; TITLE OF INVENTION: Protein Kinase Regulation
; FILE REFERENCE: 002.00210
; CURRENT APPLICATION NUMBER: US/10/148,786A
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Polypeptide
US-10-148-786A-25

Query Match          93.9%; Score 31; DB 12; Length 53;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDWSAL 6
       :|||||
Db      12 IDWSAL 17

RESULT 4
US-10-148-786A-8
; Sequence 8, Application US/10148786A
; Publication No. US20030143656A1
; GENERAL INFORMATION:
; APPLICANT: Aleassi, Dario
; APPLICANT: Biondi, Riccardo
; TITLE OF INVENTION: Protein Kinase Regulation
; FILE REFERENCE: 002.00210
; CURRENT APPLICATION NUMBER: US/10/148,786A
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 68
```

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Polypeptide
US-10-148-786A-8

Query Match          93.9%; Score 31; DB 12; Length 77;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDWSAL 6
       :|||||
Db      12 IDWSAL 17

RESULT 5
US-10-369-493-2852
; Sequence 2852, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2852
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Synechocystis sp.
US-10-369-493-2852

Query Match          93.9%; Score 31; DB 12; Length 333;
Best Local Similarity 83.3%; Pred. No. 8.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDWSAL 6
       :|||||
Db      146 MDWSAL 151

RESULT 6
US-10-217-574-18
; Sequence 18, Application US/10217574
; Publication No. US20040005687A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemminger, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures
; FILE REFERENCE: 44237
; CURRENT APPLICATION NUMBER: US/10/217,574
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: GB 0216215.4
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
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```

; LENGTH: 334
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Sequence source
; OTHER INFORMATION: uncertain
; US-10-217-574-18

Query Match      93.9%; Score 31; DB 12; Length 334;
Best Local Similarity 83.3%; Pred. No. 8.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
DB      269 LDMSAL 274

RESULT 7
US-10-217-555-18
; Sequence 18, Application US/10217555
; Publication No. US2004009569A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemminge, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for
; FILE REFERENCE: 44236
; CURRENT APPLICATION NUMBER: US/10/217,555
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Sequence source
; OTHER INFORMATION: uncertain
; US-10-217-555-18

Query Match      93.9%; Score 31; DB 12; Length 334;
Best Local Similarity 83.3%; Pred. No. 8.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
DB      269 LDMSAL 274

RESULT 8
US-09-895-072-13
; Sequence 13, Application US/09895072
; Patent No. US2002002550A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM M
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
; FILE REFERENCE: 210119US00NT
; CURRENT APPLICATION NUMBER: US/09/895,072
; CURRENT FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; PRIOR APPLICATION NUMBER: US 09/635,872
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 502
```

```

; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-895-072-13

Query Match      93.9%; Score 31; DB 9; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
DB      372 LDMSAM 377

RESULT 9
US-09-986-552-13
; Sequence 13, Application US/09986552
; Patent No. US20020150981A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASE:
; FILE REFERENCE: 215089US77DIV
; CURRENT APPLICATION NUMBER: US/09/986,552
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 09/635,872
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-986-552-13

Query Match      93.9%; Score 31; DB 10; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
DB      372 LDMSAM 377

RESULT 10
US-10-023-894-16
; Sequence 16, Application US/10023894
; Publication No. US2003014369A1
; GENERAL INFORMATION:
; APPLICANT: KORNFIELD, Stuart
; APPLICANT: KORNFIELD, William
; TITLE OF INVENTION: EXPRESSION OF LYSOSOMAL HYDROLASE IN CELLS EXPRESSING PRO-N-
; FILE REFERENCE: 217139US77
; CURRENT APPLICATION NUMBER: US/10/023,894
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-10-023-894-16

Query Match      93.9%; Score 31; DB 12; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
DB      372 LDMSAM 377
```

```
RESULT 11
US-10-024-197-16
; Sequence 16, Application US/10024197
; Publication No. US2003013924A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, William
; TITLE OF INVENTION: HIGHLY PHOSPHORYLATED ACID BETA-GLUCOSEREBROSIDASE AND METHODS C
; TITLE OF INVENTION: TREATING GAUCHER'S DISEASE
; FILE REFERENCE: 209794US0
; CURRENT APPLICATION NUMBER: US/10/024,197
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-024-197-16

Query Match          93.9%; Score 31; DB 12; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
        |||||:
Db      372 LDMSAM 377

RESULT 12
US-10-306-686-13
; Sequence 13, Application US/10306686
; Publication No. US20030148460A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: PHOSPHODIESTER ALPHA-GLUCANASE OF THE LYSOSOMAL TARGETING PATHWAY
; FILE REFERENCE: 230397US77D1V
; CURRENT APPLICATION NUMBER: US/10/306,686
; CURRENT FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: 09/636,596
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-08-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-306-686-13

Query Match          93.9%; Score 31; DB 12; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
        |||||:
Db      372 LDMSAM 377

RESULT 13
US-10-023-888-16
; Sequence 16, Application US/10023888
; Publication No. US20030119086A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, William
; TITLE OF INVENTION: SOLUBLE GLCNAC PHOSPHOTRANSFERASE
; FILE REFERENCE: 203515US77
; CURRENT APPLICATION NUMBER: US/10/023,888
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 502
```

```
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-023-888-16

Query Match          93.9%; Score 31; DB 15; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
        |||||:
Db      372 LDMSAM 377

RESULT 14
US-10-023-889-16
; Sequence 16, Application US/10023889
; Publication No. US20030124652A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, William
; TITLE OF INVENTION: METHODS OF PRODUCING HIGH MANNOSE GLYCOPROTEINS IN COMPLEX CARB
; FILE REFERENCE: 203512US77
; CURRENT APPLICATION NUMBER: US/10/023,889
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-023-889-16

Query Match          93.9%; Score 31; DB 15; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
        |||||:
Db      372 LDMSAM 377

RESULT 15
US-10-023-890-16
; Sequence 16, Application US/10023890
; Publication No. US20030124653A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, William
; TITLE OF INVENTION: METHOD OF PRODUCING GLYCOPROTEINS HAVING REDUCED COMPLEX CARBOH
; FILE REFERENCE: 203510US77
; CURRENT APPLICATION NUMBER: US/10/023,890
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-023-890-16

Query Match          93.9%; Score 31; DB 15; Length 502;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDMSAL 6
        |||||:
Db      372 LDMSAM 377

Search completed: February 18, 2004, 15:41:59
Job time : 16.7529 secs
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PF	02-MAY-2001; 2001WO-US40654.
PR	02-MAY-2000; 2000US-201261P.
ER	22-AUG-2000; 2000US-064326O.
PA	(UYVA ) UNIV YALE.
XX	
P1	May MJ, Ghosh S;
XX	
DR	WPI; 2002-179350/23.
XX	
PS	Claim 23; Page 45; 82pp; English.
XX	
CC	The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC	comprises contacting a cell with an anti-inflammatory compound
CC	(ABB08725-ABB08742) comprising at least one NEMO binding domain
CC	(ABB77113). The compound has acts through selective inhibition of NEMO
CC	cyclo-oxygenase-mediated NF-kB activation by blocking the interaction of NEMO
CC	with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC	interaction results in inhibition of IKKbeta kinase activation and
CC	subsequent decreased phosphorylation of IkkappaB. The compound may also
CC	act (directly or indirectly) by blocking the recruitment of leukocytes
CC	into sites of acute and chronic inflammation, by down-regulating the
CC	expression of E-selectin on leukocytes or by blocking osteoclast
CC	differentiation. The compound is useful in treating NF-kB mediated
CC	conditions, where the condition is an inflammatory disorder, an
CC	autoimmune disease, transplant rejection, osteoporosis, cancer,
CC	Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC	telangiectasia. The inflammatory disorder is asthma, allergies,
CC	urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
CC	rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
CC	bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC	burns/diseases. The inflammatory disorder may also be dermatitis, eczema,
CC	psoriasis, osteoarthritis, psoriatic arthritis, lupus and
CC	spondyloarthritis. Also for Crohn's disease, ulcerative colitis,
CC	polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC	cryoglobulinemia or multiple sclerosis. For chronic viral infections
CC	caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
CC	diseases include HIV and influenza. The compound may also be useful for
CC	treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC	sunburn or aging. The compound may be used to replace corticosteroids in
CC	any application in which corticosteroids are used, including
CC	immunosuppression in transplants and cancer therapy. Also for identifying
CC	anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
CC	The compound may be administered alone or in combination with other known
CC	anti-inflammatory agents. The present sequence is that of a mutated NEMO
CC	binding domain of IKKbeta.
SQ	
XX	Sequence 6 AA;
DB	
OY	1 LDMSAL 6 
ID	Best Local Similarity 100.0%; Score 33; DB 23; Length 6; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0
RESULT 2	
AAM48518	
ID	AAM48518 standard; Peptide; 6 AA.
AC	
XX	AAM48518;
DT	
XX	20-MAR-2002 (first entry)
NBD	mutant peptide SEQ ID NO 13.

XX	Antiinflammatory; antiaesthetic; cyrostatic; antipsoriatic; nootropic;
KW	antirheumatic; antiarthritic; osteopathic; antibacterial; vitruclide;
KW	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW	antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW	cytokine; NKkappa; Ikappa kinase beta; IKKbeta; cancer; psoriasis;
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW	autoimmune disorder; multiple sclerosis; transplant rejection;
KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS	Synthetic.
PN	WO200183554-A2.
PN	
PD	08-NOV-2001.
PF	02-MAY-2001; 2001WO-US14346.
XX	
PR	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-0643260.
XX	
PA	(PRAE-) PRAECIS PHARM INC.
PA	(TYTA ) UNIT YALE.
PI	May MJ, Ghosh S, Findeis MA, Phillips K;
XX	
DR	WPI; 2002-121889/16.
XX	
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
XX	psoriasis -
PS	
XX	Example 6; Page 48; 88pp; English.
CC	The invention relates to an antiinflammatory compound (especially
CC	AMM48628-AMM48651), comprising a membrane translocation domain
CC	(AMM48620-AMM48627 or AMM48646-AMM48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AMM48525-AMM48619). The antiinflammatory compounds have antiaesthetic,
CC	cyrostatic, antipsoriatic, antineumatic, antiarthritic, osteopathic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	nootropic, antiatherosclerotic, vitruclide and antiallergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NKkappaB
CC	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of IkappaB. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
XX	
SQ	Sequence 6 AA;
QY	Query Match 100.0%; Score 33; DB 23; Length 6;
Db	Best Local Similarity 100.0%; Pred. No. 9.3e+05;
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	1 LDMSAL 6
	1 LDMSAL 6
RESULT 3	
ABU08428	
ID	ABU08428 standard; peptide; 6 AA.



XX AC ABU08428;  
 XX DT 12-JUN-2003 (first entry)  
 XX DE Human NEMO binding site (NBD) mutant peptide #11.  
 XX KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;  
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;  
 KW nuclear factor-kappaB induction; inflammatory disorder;  
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;  
 KW atherosclerosis; viral infection; Ataxia telangiectasia;  
 KW transplantation detection; immunosuppressive; osteopathic;  
 KW cytostatic; neutrotropic; neuroprotective; antitumorogenic; vincristine;  
 KW vasotropic; antineumatic; antitartaric; mutant; mutin.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN US2002156000-A1.  
 XX PD 24-OCT-2002.  
 XX PF 02-MAY-2001; 2001US-0847940.  
 XX PR 02-MAY-2000; 2000US-201261P.  
 XX PR 22-AUG-2000; 2000US-0643260.  
 XX PA (MAYM/) MAY M J.  
 XX PA (GHOS/) GHOSH S.  
 XX PI May MJ, Ghosh S;  
 XX DR WPI; 2003-209142/20.  
 XX PT Novel antiinflammatory peptide compounds comprising NEMO binding  
 PT domain, useful for mediating NF-kappaB induction in a cell and for  
 PT creating NF-kappaB-mediated inflammation disorders e.g., asthma,  
 PT psoriasis, vasculitis -  
 XX PS Claim 22; Page 17; 47pp; English.  
 XX CC The present invention relates to antiinflammatory compounds comprising  
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are  
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha  
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention  
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction  
 CC in a cell, where the compounds are capable of blocking the interaction  
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The  
 CC antiinflammatory compound further comprises at least one membrane  
 CC translocation domain. The compounds are useful for treating  
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia  
 CC telangiectasia, and for transplantation detection. The compounds of  
 CC the invention block NF-kappaB induction by IKK but do not inhibit  
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human  
 CC NBD mutant peptides.  
 XX SQ Sequence 6 AA;  
 XX

Query Match 100.0%; Score 33; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMASL 6  
 |||||  
 Db 1 LDMASL 6

RESULT 4  
 ABB77299 standard; protein; 756 AA.  
 XX

AC ABB77299;  
 XX DT 14-JUN-2002 (first entry)  
 XX DE Human IKKbeta mutant W741A.  
 XX KW IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;  
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;  
 KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;  
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;  
 KW osteopathic; cytostatic; neutrotropic; neuroprotective; anti-HIV; human;  
 KW dermatological; antiviral; antitumorogenic; antiallergic;  
 KW antitartaric; osteopathic; antitumor; mutant; mutin.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN WO200103547-A2.  
 XX PD 08-NOV-2001.  
 XX PF 02-MAY-2001; 2001WO-US40654.  
 XX PR 02-MAY-2000; 2000US-201261P.  
 XX PR 22-AUG-2000; 2000US-0643260.  
 XX PA (UYVA ) UNIV YALE.  
 XX PI May MJ, Ghosh S;  
 XX DR WPI; 2002-179350/23.  
 XX PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 XX PS Example 11; Page -; 82pp; English.  
 XX CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprises contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77213). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of IkappaB. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC burstitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polyomyelitis, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,

CC burnburn or aging. The compound may be used to replace corticosteroids in  
CC any application in which corticosteroids are used, including  
CC immunosuppression in transplants and cancer therapy. Also for identifying  
CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.  
CC The compound may be administered alone or in combination with other known  
CC anti-inflammatory agents. The present sequence is that of an IKK $\beta$  gene  
CC mutant, useful in examples of the invention.  
CC Note: The present sequence is not given in the specification but is  
CC derived from GenBank Accession No. 014920 (AB077294).  
XX  
SQ Sequence 756 AA;  
Query Match 100.0%; Score 33; DB 23; Length 756;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 737 LDMSAL 742  
QY 1 LDMSAL 6  
ID AAY94732 standard; peptide; 53 AA.  
XX AAY94732;  
XX  
DT 29-JAN-2001 (first entry)  
XX  
DE Region A of protein kinase C related protein kinase 2.  
XX  
KM Substrate specificity; phosphoinositide-dependent protein kinase 1;  
KM PDK1; protein kinase C related protein kinase 2; PKX2; cancer; apoptosis;  
KM mechanical tissue damage; ischemic disease; stroke;  
KM myocardial infarction; antigenic peptide.  
XX  
OS Unidentified.  
XX  
PN WO200056864-A2.  
XX  
PD 26-SEP-2000.  
XX  
PF 17-MAR-2000; 2000WO-GB01004.  
XX  
PR 19-MAR-1999; 99GB-0006245.  
XX  
PA (UYDU-) UNIV DUNDEE.  
XX  
PI Aleesi D, Balendran A, Deak M, Currie R, Downes P, Casamayor A;  
XX WPI; 2000-647155/62.  
XX  
PT Altering substrate specificity of phosphoinositide-dependent protein  
XX kinase 1 to phosphorylate Ser473 in addition to Thr308 by exposing to  
XX interacting polypeptide -  
XX  
PS Disclosure; Page 12; 103pp; English.  
XX  
CC This invention relates to a method for altering the substrate  
CC specificity of phosphoinositide-dependent protein kinase 1 (PDK1) by  
CC exposing it to an interacting polypeptide. Included in the invention are  
CC a preparation comprising PDK1 and an interacting polypeptide, PDK1 with  
CC altered specificity is useful for phosphorylating a residue corresponding  
CC to the Ser/Thr residue of a substrate with the following peptide  
CC Phe/Tyr-Xaa-Xaa-Phe/Tyr-Ser/Thr-Phe/Tyr. Altered PDK1 is also used for  
CC phosphorylating protein kinase C related protein kinase 2 (PKX2). The  
CC compound identified by methods of the invention that are capable of  
CC altering the substrate specificity of PDK1 are useful for manufacturing a  
CC medicament for treating a patient who is in need of modulation of the  
CC insulin signalling pathway and/or PDK1, PKX2 or PKX2 signalling. A  
CC compound that is capable of reducing the activity (i.e. the PDK1 and/or  
CC the PKX2 activity) of PDK1 may be useful in treating cancer. PDK1,  
CC e.g. via protein kinase B and/or SGK, may be capable of providing a

CC survival signal that protects cells from apoptosis induced in a variety  
CC of ways. Reduction of the activity of PDK1 may promote apoptosis and may  
CC be useful in treating cancer. Conditions in which aiding apoptosis may be  
CC of benefit may also include resolution of inflammation. A compound  
CC capable of increasing the activity of PDK1 may be useful in treating  
CC diabetes or obesity, or may be useful in inhibiting apoptosis. Increased  
CC activity of PDK1 may lead to increased levels of leptin, which may lead  
CC to weight loss. The compounds may suppress apoptosis, which may aid cell  
CC survival during or following cell damaging processes and in treating  
CC disease in which apoptosis is involved. Examples of the diseases include,  
CC mechanical (including heart) tissue injury or ischemic disease, for  
CC example stroke and myocardial infarction, or neural injury. The present  
CC sequence represents a region of protein kinase C related protein kinase  
CC 2 (PKX2) which interacts with PDK1.  
XX  
SQ Sequence 53 AA;  
Query Match 93.9%; Score 31; DB 21; Length 53;  
Best Local Similarity 83.3%; Pred. No. 91;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
DB 12 IDMSAL 17  
QY 1 LDMSAL 6  
ID AAB99802 standard; peptide; 53 AA.  
XX AAB99802;  
XX  
DT 20-SEP-2001 (first entry)  
XX  
DE Protein kinase derived interacting peptide #4.  
XX  
KM Protein kinase; identification; hydrophobic pocket; interacting;  
KM cancer; diabetes; inhibition; apoptosis; tissue injury;  
KM ischaemic injury; stroke.  
XX  
OS Homo sapiens.  
XX  
PN WO200144497-A2.  
XX  
PD 21-JUN-2001.  
XX  
PF 04-DEC-2000; 2000WO-GB04598.  
XX  
PR 02-DEC-1999; 99US-0168559.  
XX  
PA (UYDU-) UNIV DUNDEE.  
XX  
PI Aleesi D, Biondi R;  
XX WPI; 2001-390252/41.  
XX  
PT Identifying modulators of protein kinase (PK) activity, useful in  
XX developing drugs for treating cancer or diabetes, by measuring the  
XX ability of the compound to modulate or mimic the interaction of PK with  
XX interacting polypeptides -  
XX  
PS Disclosure; Page 25; 180pp; English.  
XX  
CC The present invention describes a method for identifying a compound that  
CC modulates protein kinase activity. The method comprises measuring the  
CC ability of the compound to inhibit, promote or mimic the interaction of  
CC a hydrophobic pocket-containing protein kinase with an interacting  
CC polypeptide. The interacting polypeptide interacts with the hydrophobic  
CC pocket of the protein kinase and/or comprises the amino acid sequence  
CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (I). The method is useful in screening assays  
CC for developing pharmaceutical compounds or drugs. Compounds, polypeptides  
CC or polynucleotides from the present invention are useful in medicine.

CC particularly in the manufacture of a medicament for treating a patient  
CC in need of modulation of signalling by a hydrophobic pocket-containing  
CC protein kinase. Specifically, the patient has cancer or diabetes or is  
CC in need of inhibition of apoptosis, e.g. a patient suffering from tissue  
CC injury or ischemic injury, including stroke. The compound or  
CC composition is also useful for inhibiting the degree or rate of  
CC phosphorylation by the protein kinase. The interacting polypeptide or  
CC compound is useful in methods of stabilising a hydrophobic pocket-  
CC containing protein kinase, where the protein kinase is exposed to the  
CC compound or polypeptide. AAB9786 to AAB9847 represent amino acid  
CC sequences, and AAH44210 and AAH44211 represent oligonucleotide sequences,  
CC used in the exemplification of the present invention.

XX  
SQ Sequence 53 AA;  
Query Match 93.9%; Score 31; DB 22; Length 53;  
Best Local Similarity 83.3%; Pred. No. 91;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
:|||||  
Db 12 IDMSAL 17

RESULT 7  
AAB9793 ID AAB9793 standard; Peptide; 77 AA.  
XX  
AC AAB9793;  
XX  
DT 20-SEP-2001 (first entry)  
XX  
DE 3-phosphoinositide-dependent protein kinase 1 binding peptide PIF.  
XX  
DE Protein kinase; identification; hydrophobic pocket; interacting;  
XX  
KW cancer; diabetes; inhibition; apoptosis; tissue injury;  
XX  
KW ischemic injury; stroke.  
XX  
OS Homo sapiens.  
XX  
OS Synthetic.  
XX  
PN WO20014497-A2.  
XX  
PD 21-JUN-2001.  
XX  
PF 04-DEC-2000; 2000WO-GB04598.  
XX  
PR 02-DEC-1999; 99US-0168559.  
XX  
PA (UYDU-) UNIV DUNDEE.  
XX  
PI Aleesi D, Blondi R;  
XX  
DR WPI; 2001-390252/41.  
XX  
PT Identifying modulators of protein kinase (PK) activity, useful in  
XX developing drugs for treating cancer or diabetes, by measuring the  
XX ability of the compound to modulate or mimic the interaction of PK with  
XX interacting polypeptides -  
XX  
PS Disclosure; Page 22; 180pp; English.

XX  
CC The present invention describes a method for identifying a compound that  
XX modulates protein kinase activity. The method comprises measuring the  
XX ability of the compound to inhibit, promote or mimic the interaction of  
XX a hydrophobic pocket-containing protein kinase with an interacting  
XX polypeptide. The interacting polypeptide interacts with the hydrophobic  
XX pocket of the protein kinase and/or comprises the amino acid sequence  
XX Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays  
XX for developing pharmaceutical compounds or drugs. Compounds, polypeptides  
XX or polynucleotides from the present invention are useful in medicine,  
XX particularly in the manufacture of a medicament for treating a patient  
XX in need of modulation of signalling by a hydrophobic pocket-containing

CC protein kinase. Specifically, the patient has cancer or diabetes or is  
CC in need of inhibition of apoptosis, e.g. a patient suffering from tissue  
CC injury or ischemic injury, including stroke. The compound or  
CC composition is also useful for inhibiting the degree or rate of  
CC phosphorylation by the protein kinase. The interacting polypeptide or  
CC compound is useful in methods of stabilising a hydrophobic pocket-  
CC containing protein kinase, where the protein kinase is exposed to the  
CC compound or polypeptide. AAB9786 to AAB9847 represent amino acid  
CC sequences, and AAH44210 and AAH44211 represent oligonucleotide sequences,  
XX used in the exemplification of the present invention.

XX  
SQ Sequence 77 AA;  
Query Match 93.9%; Score 31; DB 22; Length 77;  
Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
:|||||  
Db 12 IDMSAL 17

RESULT 8  
AAB9835 ID AAB9835 standard; Protein; 315 AA.  
XX  
AC AAB9835;  
XX  
DT 20-SEP-2001 (first entry)  
XX  
DE AGC protein kinase family member PRK2 protein sequence.  
XX  
DE Protein kinase; identification; hydrophobic pocket; interacting;  
XX  
KW cancer; diabetes; inhibition; apoptosis; tissue injury;  
XX  
KW ischemic injury; stroke.  
XX  
OS Homo sapiens.  
XX  
OS Synthetic.  
XX  
PN WO20014497-A2.  
XX  
PD 21-JUN-2001.  
XX  
PF 04-DEC-2000; 2000WO-GB04598.  
XX  
PR 02-DEC-1999; 99US-0168559.  
XX  
PA (UYDU-) UNIV DUNDEE.  
XX  
PI Aleesi D, Blondi R;  
XX  
DR WPI; 2001-390252/41.  
XX  
PT Identifying modulators of protein kinase (PK) activity, useful in  
XX developing drugs for treating cancer or diabetes, by measuring the  
XX ability of the compound to modulate or mimic the interaction of PK with  
XX interacting polypeptides -  
XX  
PS Disclosure; Fig 16; 180pp; English.

XX  
CC The present invention describes a method for identifying a compound that  
XX modulates protein kinase activity. The method comprises measuring the  
XX ability of the compound to inhibit, promote or mimic the interaction of  
XX a hydrophobic pocket-containing protein kinase with an interacting  
XX polypeptide. The interacting polypeptide interacts with the hydrophobic  
XX pocket of the protein kinase and/or comprises the amino acid sequence  
XX Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays  
XX for developing pharmaceutical compounds or drugs. Compounds, polypeptides  
XX or polynucleotides from the present invention are useful in medicine,  
XX particularly in the manufacture of a medicament for treating a patient  
XX in need of modulation of signalling by a hydrophobic pocket-containing  
XX protein kinase. Specifically, the patient has cancer or diabetes or is  
XX in need of inhibition of apoptosis, e.g. a patient suffering from tissue

CC Injury or ischemic injury, including stroke. The compound or  
CC composition is also useful for inhibiting the degree or rate of  
CC phosphorylation is also useful for inhibiting the degree or rate of  
CC compound is useful in methods of stabilizing a hydrophobic pocket-  
CC containing protein kinase, where the protein kinase is exposed to the  
CC compound or polypeptide. AAB99786 to AAB99847 represent amino acid  
CC sequences, and AAH44210 and AAH44211 represent oligonucleotide sequences,  
CC used in the exemplification of the present invention.

XX  
XX Sequence 315 AA;

Query Match 93.9%; Score 31; DB 22; Length 315;  
Best Local Similarity 83.3%; Pred. No. 6.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSAL 6  
Db 250 IDMSAL 255

RESULT 9  
AAB63738  
ID AAB63738 standard; Protein; 345 AA.  
XX  
XX AAB63738;  
AC  
XX 26-MAR-2002 (first entry)  
DT  
XX  
XX Drosophila melanogaster polypeptide SEQ ID NO 18006.  
DE  
XX  
XX Drosophila; developmental biology; cell signalling; insecticide;  
KM pharmaceutical.  
XX  
XX Drosophila melanogaster.  
OS  
XX NO200171042-A2.  
PN  
XX  
XX 27-SEP-2001.  
PD  
XX 23-MAR-2001; 2001MO-US09221.  
PF  
XX 23-MAR-2000; 2000US-191637P.  
PR 11-JUL-2000; 2000US-0614150.  
PS  
XX (PEKE ) PE CORP NY.  
PA  
XX Venter JC, Adams M, Li PMD, Myers EW;  
PI WPI; 2001-656860/75.  
DR N-PSDB; ABL07841.  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -  
XX  
XX Disclosure; SEQ ID NO 18006; 21pp + Sequence Listing; English.  
PS  
XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (AB16176-ABL0511), expressed DNA  
CC sequences (AB101840-ABL16175) and the encoded proteins  
CC (AAB57737-AAB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 345 AA;  
Query Match 93.9%; Score 31; DB 22; Length 345;  
Best Local Similarity 83.3%; Pred. No. 6.9e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSAL 6  
Db 136 LDMSAL 141

RESULT 10  
AAB99822  
ID AAB99822 standard; Protein; 385 AA.  
XX  
XX AAB99822;  
AC  
XX 20-SEP-2001 (first entry)  
DT  
XX  
XX AGC protein kinase family member PRK2 protein sequence.  
DE  
XX  
XX Protein kinase; identification; hydrophobic pocket; interacting;  
KM cancer; diabetes; inhibition; apoptosis; tissue injury;  
KM ischaemic injury; stroke.  
XX  
XX Homo sapiens.  
OS  
XX Synthetic.  
OS  
XX WO200144497-A2.  
PN  
XX 21-JUN-2001.  
PD  
XX  
XX 04-DEC-2000; 2000MO-GB04598.  
PF  
XX  
XX 02-DEC-1999; 99US-0168559.  
PR  
XX (UYDU-) UNIV DUNDEE.  
PA  
XX  
XX Alesai D, Blondi R;  
PI WPI; 2001-390252/41.  
DR  
XX  
XX Identifying modulators of protein kinase (PK) activity, useful in  
PT developing drugs for treating cancer or diabetes, by measuring the  
PT ability of the compound to modulate or mimic the interaction of PK with  
PT interacting polypeptides -  
XX  
XX  
XX Disclosure; Fig 15; 180pp; English.  
PS  
XX  
XX The present invention describes a method for identifying a compound that  
CC modulates protein kinase activity. The method comprises measuring the  
CC ability of the compound to inhibit, promote or mimic the interaction of  
CC a hydrophobic pocket-containing protein kinase with an interacting  
CC polypeptide. The interacting polypeptide interacts with the hydrophobic  
CC pocket of the protein kinase and/or comprises the amino acid sequence  
CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays  
CC for developing pharmaceutical compounds or drugs. Compounds, polypeptides  
CC or polynucleotides from the present invention are useful in medicine,  
CC particularly in the manufacture of a medicament for treating a patient  
CC in need of modulation of signalling by a hydrophobic pocket-containing  
CC protein kinase. Specifically, the patient has cancer or diabetes or is  
CC in need of inhibition of apoptosis, e.g. a patient suffering from tissue  
CC injury or ischemic injury, including stroke. The compound or  
CC composition is also useful for inhibiting the degree or rate of  
CC phosphorylation by the protein kinase. The interacting polypeptide or  
CC compound is useful in methods of stabilizing a hydrophobic pocket-  
CC containing protein kinase, where the protein kinase is exposed to the  
CC compound or polypeptide. AAB99786 to AAB99847 represent amino acid  
CC sequences, and AAH44210 and AAH44211 represent oligonucleotide sequences,  
CC used in the exemplification of the present invention.

XX  
XX Sequence 385 AA;  
Query Match 93.9%; Score 31; DB 22; Length 385;  
Best Local Similarity 83.3%; Pred. No. 7.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSAL 6  
:|||||  
Db 320 LDMSAL 325

RESULT 11  
ABBS9094  
ID ABBS9094 standard; Protein: 652 AA.

XX AC ABBS9094;  
XX DT 26-MAR-2002 (first entry)  
XX DE Drosophila melanogaster polypeptide SEQ ID NO 4074.  
XX KM Drosophila; developmental biology; cell signalling; insecticide;  
XX OS pharmaceutical.  
XX OS Drosophila melanogaster.  
XX PN WO200171042-A2.  
XX PD 27-SEP-2001.  
XX PF 23-MAR-2001; 2001WO-US09231.  
XX PR 23-MAR-2000; 2000US-191637P.  
XX PR 11-JUL-2000; 2000US-0614150.  
XX PA (PEKE ) PE CORP NY.  
XX PI Venter JC, Adams M, Li PWD, Myers EW;  
XX DR WPI; 2001-656860/75.  
XX DR N-PSDB; ABL03197.  
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -  
XX PS  
XX PS Disclosure; SEQ ID NO 4074; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (AB16176-ABL30511), expressed DNA  
CC sequences (AB101840-ABL16175) and the encoded proteins  
CC (ABBS7737-ABBS72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX SQ Sequence 652 AA;

OY Query Match 93.9%; Score 31; DB 22; Length 652;  
Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 LDMSAL 6  
:|||||  
447 LDMSAM 452

RESULT 12  
AA94736  
ID AA94736 standard; Protein: 984 AA.  
XX AC AA94736;  
XX DT 29-JAN-2001 (first entry)  
XX

DE Protein kinase C related protein kinase 2.  
XX KM Substrate specificity; phosphoinositide-dependent protein kinase 1;  
XX KM PDK1; protein kinase C related protein kinase 2; PKR2; cancer; apoptosis;  
XX KM mechanical tissue damage; ischemic disease; stroke;  
XX KM myocardial infarction; antigenic peptide.  
XX OS  
XX OS Unidentified.  
XX PN WO200056864-A2.  
XX PD 28-SEP-2000.  
XX PF 17-MAR-2000; 2000WO-GB01004.  
XX PR 19-MAR-1999; 99GB-0006245.  
XX PA (YUDU-) UNIV DUNDEE.  
XX PI Alessi D, Balendran A, Deak M, Currie R, Downes P, Casamayor A;  
XX DR WPI; 2000-647155/62.  
XX PT Altering substrate specificity of phosphoinositide-dependent protein  
PT kinase 1 to phosphorylate Ser473 in addition to Thr308 by exposing to  
XX interacting polypeptide -  
XX PS Disclosure; Fig 11; 103pp; English.

CC This invention relates to a method for altering the substrate  
CC specificity of phosphoinositide-dependent protein kinase 1 (PKI), by  
CC exposing it to an interacting polypeptide. Included in the invention are  
CC a preparation comprising PDK1 and an interacting polypeptide, PDK1 with  
CC altered specificity is useful for phosphorylating a residue corresponding  
CC to the Ser/Thr residue of a substrate with the following peptide  
CC Phe/Tyr-Xaa-Xaa-Phe/Tyr-Ser/Thr-Phe/Tyr. Altered PDK1 is also used for  
CC phosphorylating protein kinase C related protein kinase 2 (PRK2). The  
CC compound identified by methods of the invention that are capable of  
CC altering the substrate specificity of PDK1 are useful for manufacturing a  
CC medicament for treating a patient who is in need of modulation of the  
CC insulin signalling pathway and/or PDK1, PDK2 or PRK2 signalling. A  
CC compound that is capable of reducing the activity (i.e. the PDK1 and/or  
CC the PDK2 activity) of PDK1 may be useful in treating cancer. PDK1, e.g.  
CC via protein kinase B and/or SGK, may be capable of providing a survival  
CC signal that protects cells from apoptosis induced in a variety of ways.  
CC Reduction of the activity of PDK1 may promote apoptosis and may be useful  
CC in treating cancer. Conditions in which aiding apoptosis may be benefit  
CC may also include resolution of inflammation. A compound capable of  
CC increasing the activity of PDK1 may be useful in treating diabetes or  
CC obesity, or may be useful in inhibiting apoptosis. Increased activity of  
CC PDK1 may lead to increased levels of leptin, which may lead to weight  
CC loss. The compounds may suppress apoptosis, which may aid cell survival  
CC during or following cell damaging processes and in treating disease in  
CC which apoptosis is involved. Examples of the diseases include, mechanical  
CC (including heat) tissue injury or ischemic disease, for example stroke  
CC and myocardial infarction, or neural injury. The present sequence  
CC represents a protein kinase C related protein kinase 2 amino acid  
CC sequence, used in the course of the invention.  
XX SQ Sequence 984 AA;

OY Query Match 93.9%; Score 31; DB 21; Length 984;  
Best Local Similarity 83.3%; Pred. No. 2.1e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 LDMSAL 6  
:|||||  
919 LDMSAL 924

RESULT 13  
AA015489  
ID AA015489 standard; Protein: 984 AA.

XX	AAO15489;
AC	
DT	03-OCT-2002 (first entry)
DE	
XX	Human serin-threonin-kinase PRK2.
XX	
KM	Human; DHAM-Kinase inhibitor; guanylate kinase I; PRK2; deregulated in hyperactive macrophage kinase inhibitor; GUKL; serin-threonin-kinase; PAK2; inflammatory condition;
KW	chronic inflammatory airway disease; chronic bronchitis;
XX	chronic obstructive pulmonary disease; COPD.
OS	Homo sapiens.
XX	
PN	MOJ00252036-A2.
XX	
XD	04-JUL-2002.
XX	
PP	15-DEC-2001; 2001WO-BP14844.
PR	22-DEC-2000; 2000US-257854P.
XX	
PA	(BOEH ) BOEHRINGER INGELHEIM PHARMA KG.
P1	Jung B, Mueller S, Kraut N;
XX	
DR	WPI; 2002-583570/62.
DR	N-PSDB; AAL44147.
XX	
PT	Determining activators or inhibitors of 'deregulated in hyperactive macrophage' (DHAM)-kinase for treating chronic inflammatory airway diseases, by measuring DHAM-kinase function after it is contacted with a test substance -
PT	
XX	
PS	Claim 8; Page 41-47; 48pp; English.
XX	
CC	The invention comprises a method for determining whether a substance is an activator or an inhibitor of a DHAM-kinase (deregulated in hyperactive macrophage kinase). DHAM-kinases used in the invention include guanylate kinase I (GUKL), serin-threonin-kinase PAK2 and serin-threonin-kinase PRK2. The method of the invention is useful for identifying substances that influence inflammatory conditions of chronic inflammatory airway diseases (e.g. chronic bronchitis or chronic obstructive pulmonary disease - COPD). The present amino acid sequence represents the human serin-threonin-kinase PRK2.
CC	
CC	
SC	Sequence 984 AA;
QY	
Query Match	93.9%; Score 31; DB 23; Length 984;
Best Local Similarity	83.3%; Pred. No. 2.1e+03;
Matches 5; Conservative	1; Mismatches 0; Indels 0; Gaps 0
DB	1 LDWSAL 6 :      919 IDWSAL 924
RESULT 14	
AAG56197	
ID	AAG56197 standard; Protein; 53 AA.
XX	
AC	AAG56197;
XX	
DT	18-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 72196.
XX	
KM	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
KW	
XX	
OS	Arabidopsis thaliana.

[illegible]

PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
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GenCore version 5.1.6  
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Title: US-09-643-260-12

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APPLICANT: May, Michael J.  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-117CP  
CURRENT APPLICATION NUMBER: US/09/847,940B  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
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GENERAL INFORMATION:  
APPLICANT: May, Michael J

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APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
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PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
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US-09-847-946A-12

Query Match 100.0%; Score 36; DB 11; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7e+05; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;

QY 1 LDYSWL 6  
Db 1 LDYSWL 6

RESULT 3  
US-09-847-946A-95  
Sequence 95; Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 95  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-95

Query Match 100.0%; Score 36; DB 11; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7e+05; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;

QY 1 LDYSWL 6  
Db 1 LDYSWL 6

RESULT 4  
US-09-847-946A-99  
Sequence 99; Application US/09847946A  
Publication No. US20030054999A1

GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 99  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-99

Query Match 100.0%; Score 36; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 7e+05; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;

QY 1 LDYSWL 6  
Db 1 LDYSWL 6

RESULT 5  
US-09-847-946A-92  
Sequence 92; Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 92  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-92

Query Match 100.0%; Score 36; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 7e+05; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;

QY 1 LDYSWL 6  
Db 3 LDYSWL 8

RESULT 6

US-09-847-946A-100  
; Sequence 100, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 100  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-100

Query Match 100.0%; Score 36; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6  
| | | | |  
Db 1 LDYSWL 6

RESULT 7  
US-09-847-946A-91  
; Sequence 91, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 91  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-91

Query Match 100.0%; Score 36; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6  
| | | | |  
Db 1 LDYSWL 6

RESULT 8  
US-09-847-946A-94  
; Sequence 94, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 94  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-94

Query Match 100.0%; Score 36; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6  
| | | | |  
Db 1 LDYSWL 6

RESULT 9  
US-09-847-946A-97  
; Sequence 97, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 97  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-97

Query Match 100.0%; Score 36; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6  
| | | | |  
DB 3 LDYSWL 8

## RESULT 10

US-09-847-946A-98  
; Sequence 98, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 98  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-98

Query Match 100.0%; Score 36; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6  
| | | | |  
DB 2 LDYSWL 7

## RESULT 11

US-09-847-946A-93  
; Sequence 93, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 93  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-93

Query Match 100.0%; Score 36; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 8.2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDYSWL 6  
| | | | |  
DB 2 LDYSWL 7

## RESULT 12

US-09-847-946A-96  
; Sequence 96, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 96  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-96

Query Match 100.0%; Score 36; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6  
| | | | |  
DB 3 LDYSWL 8

## RESULT 13

US-09-847-946A-90  
; Sequence 90, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 90  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-90

US-09-847-946A-90

Query Match 100.0%; Score 36; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.9;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6  
|||||  
DB 3 LDYSWL 8

RESULT 14  
US-10-074-978A-310

/ Sequence 310, Application US/10074978A  
/ Publication No. US20040010119A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Leite, Mario  
/ APPLICANT: Spytek, Kimberly A  
/ APPLICANT: Guo, Xiaojia (Sasha)  
/ APPLICANT: Fernandes, Elma  
/ APPLICANT: Li, Li  
/ APPLICANT: Kekuda, Ramesh  
/ APPLICANT: Liu, Xiahong  
/ APPLICANT: Casman, Stacie  
/ APPLICANT: Boldog, Ferenc  
/ APPLICANT: Patuturajan, Meera  
/ APPLICANT: Bialock, Angela  
/ APPLICANT: Ballinger, Robert  
/ APPLICANT: Verneet, Corine  
/ APPLICANT: Tchernev, Velizar T  
/ APPLICANT: Malyankar, Uriel M  
/ APPLICANT: Gusev, Vladimir  
/ APPLICANT: Rastelli, Luca  
/ APPLICANT: Mezes, Peter S  
/ APPLICANT: Ellerman, Karen  
/ APPLICANT: Heyes, Melvin P  
/ APPLICANT: Herrman, John  
/ APPLICANT: Pena, Carol E A  
/ APPLICANT: Shimkets, Richard A  
/ APPLICANT: Taupler Jr, Raymond J  
/ APPLICANT: Moore, No. US20040010119A111e  
/ APPLICANT: Shenoy, Suresh  
/ APPLICANT: Edinger, Shlomit  
/ APPLICANT: Gunther, Erik  
/ APPLICANT: Stone, Dave  
/ APPLICANT: Millet, Isabelle  
/ APPLICANT: Peyman, John  
/ APPLICANT: Smithson, Glenda  
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
/ FILE REFERENCE: 21402-269  
/ CURRENT APPLICATION NUMBER: US/10/074,978A  
/ CURRENT FILING DATE: 2003-01-07  
/ PRIOR APPLICATION NUMBER: 60/268,221  
/ PRIOR FILING DATE: 2001-02-12  
/ PRIOR APPLICATION NUMBER: 60/335,109  
/ PRIOR FILING DATE: 2001-10-31  
/ PRIOR APPLICATION NUMBER: 60/312,284  
/ PRIOR FILING DATE: 2001-08-14  
/ PRIOR APPLICATION NUMBER: 60/268,496  
/ PRIOR FILING DATE: 2001-02-13  
/ PRIOR APPLICATION NUMBER: 60/276,703  
/ PRIOR FILING DATE: 2001-03-16  
/ PRIOR APPLICATION NUMBER: 60/330,293  
/ PRIOR FILING DATE: 2001-10-18  
/ PRIOR APPLICATION NUMBER: 60/322,127  
/ PRIOR FILING DATE: 2001-11-21  
/ PRIOR APPLICATION NUMBER: 60/280,899  
/ PRIOR FILING DATE: 2001-04-02  
/ PRIOR APPLICATION NUMBER: 60/330,293  
/ PRIOR FILING DATE: 2001-08-08  
/ PRIOR APPLICATION NUMBER: 60/268,646  
/ PRIOR FILING DATE: 2001-02-14  
/ Remaining Prior Application data removed - See File Wrapper or PALM.

/ NUMBER OF SEQ ID NOS: 547  
/ SOFTWARE: Patentin Ver. 2.1  
/ SEQ ID NO 310  
/ LENGTH: 73  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-074-978A-310

Query Match 91.7%; Score 33; DB 12; Length 73;  
Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6  
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DB 46 LDYSWL 51

RESULT 15

US-10-074-978A-66  
/ Sequence 66, Application US/10074978A  
/ Publication No. US20040010119A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Leite, Mario  
/ APPLICANT: Spytek, Kimberly A  
/ APPLICANT: Guo, Xiaojia (Sasha)  
/ APPLICANT: Fernandes, Elma  
/ APPLICANT: Li, Li  
/ APPLICANT: Kekuda, Ramesh  
/ APPLICANT: Liu, Xiahong  
/ APPLICANT: Casman, Stacie  
/ APPLICANT: Boldog, Ferenc  
/ APPLICANT: Patuturajan, Meera  
/ APPLICANT: Bialock, Angela  
/ APPLICANT: Ballinger, Robert  
/ APPLICANT: Verneet, Corine  
/ APPLICANT: Tchernev, Velizar T  
/ APPLICANT: Malyankar, Uriel M  
/ APPLICANT: Gusev, Vladimir  
/ APPLICANT: Rastelli, Luca  
/ APPLICANT: Mezes, Peter S  
/ APPLICANT: Ellerman, Karen  
/ APPLICANT: Heyes, Melvin P  
/ APPLICANT: Herrman, John  
/ APPLICANT: Pena, Carol E A  
/ APPLICANT: Shimkets, Richard A  
/ APPLICANT: Taupler Jr, Raymond J  
/ APPLICANT: Moore, No. US20040010119A111e  
/ APPLICANT: Shenoy, Suresh  
/ APPLICANT: Edinger, Shlomit  
/ APPLICANT: Gunther, Erik  
/ APPLICANT: Stone, Dave  
/ APPLICANT: Millet, Isabelle  
/ APPLICANT: Peyman, John  
/ APPLICANT: Smithson, Glenda  
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
/ FILE REFERENCE: 21402-269  
/ CURRENT APPLICATION NUMBER: US/10/074,978A  
/ CURRENT FILING DATE: 2003-01-07  
/ PRIOR APPLICATION NUMBER: 60/268,221  
/ PRIOR FILING DATE: 2001-02-12  
/ PRIOR APPLICATION NUMBER: 60/335,109  
/ PRIOR FILING DATE: 2001-10-31  
/ PRIOR APPLICATION NUMBER: 60/312,284  
/ PRIOR FILING DATE: 2001-08-14  
/ PRIOR APPLICATION NUMBER: 60/268,496  
/ PRIOR FILING DATE: 2001-02-13  
/ PRIOR APPLICATION NUMBER: 60/276,703  
/ PRIOR FILING DATE: 2001-03-16  
/ PRIOR APPLICATION NUMBER: 60/330,293  
/ PRIOR FILING DATE: 2001-10-18  
/ PRIOR APPLICATION NUMBER: 60/322,127  
/ PRIOR FILING DATE: 2001-11-21  
/ PRIOR APPLICATION NUMBER: 60/280,899

;; PRIOR FILING DATE: 2001-04-02  
;; PRIOR APPLICATION NUMBER: 60/310,797  
;; PRIOR FILING DATE: 2001-08-08  
;; PRIOR APPLICATION NUMBER: 60/268,646  
;; PRIOR FILING DATE: 2001-02-14  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 547  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO: 66  
;; LENGTH: 314  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-074-978A-66

Query Match 91.7%; Score 33; DB 12; Length 314;  
Best Local Similarity 83.3%; Pred. No. 4.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDYSML 6  
Db 116 LDYTWL 121

Search completed: February 18, 2004, 15:41:59  
Job time : 17.7529 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds  
(without alignments)  
41.814 Million cell updates/sec

Title: US-09-643-260-12

Perfect score: 36

Sequence: 1 LDYSWL 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
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12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
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22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
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25: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	6	23	ABB08734
2	36	100.0	6	23	AAW48591
3	36	100.0	6	23	AAW48594
4	36	100.0	6	23	AAW48595
5	36	100.0	6	23	AAW48596
6	36	100.0	6	23	AAW48597
7	36	100.0	6	23	AAW48598
8	36	100.0	6	23	AAW48599
9	36	100.0	6	23	AAW48600

10	36	100.0	9	23	AAW48591	Anti-inflammatory
11	36	100.0	9	23	AAW48594	Anti-inflammatory
12	36	100.0	9	23	AAW48595	Anti-inflammatory
13	36	100.0	10	23	AAW48596	Anti-inflammatory
14	36	100.0	10	23	AAW48597	Anti-inflammatory
15	36	100.0	11	23	AAW48598	Anti-inflammatory
16	36	100.0	11	23	AAW48599	Anti-inflammatory
17	36	100.0	11	23	AAW48600	Anti-inflammatory
18	36	100.0	11	23	AAW48601	Anti-inflammatory
19	36	100.0	11	23	AAW48602	Anti-inflammatory
20	36	100.0	11	23	AAW48603	Anti-inflammatory
21	36	100.0	11	23	AAW48604	Anti-inflammatory
22	36	100.0	11	23	AAW48605	Anti-inflammatory
23	36	100.0	11	23	AAW48606	Anti-inflammatory
24	36	100.0	11	23	AAW48607	Anti-inflammatory
25	36	100.0	11	23	AAW48608	Anti-inflammatory
26	36	100.0	11	23	AAW48609	Anti-inflammatory
27	36	100.0	11	23	AAW48610	Anti-inflammatory
28	36	100.0	11	23	AAW48611	Anti-inflammatory
29	36	100.0	11	23	AAW48612	Anti-inflammatory
30	36	100.0	11	23	AAW48613	Anti-inflammatory
31	36	100.0	11	23	AAW48614	Anti-inflammatory
32	36	100.0	11	23	AAW48615	Anti-inflammatory
33	36	100.0	11	23	AAW48616	Anti-inflammatory
34	36	100.0	11	23	AAW48617	Anti-inflammatory
35	36	100.0	11	23	AAW48618	Anti-inflammatory
36	36	100.0	11	23	AAW48619	Anti-inflammatory
37	36	100.0	11	23	AAW48620	Anti-inflammatory
38	36	100.0	11	23	AAW48621	Anti-inflammatory
39	36	100.0	11	23	AAW48622	Anti-inflammatory
40	36	100.0	11	23	AAW48623	Anti-inflammatory
41	36	100.0	11	23	AAW48624	Anti-inflammatory
42	36	100.0	11	23	AAW48625	Anti-inflammatory
43	36	100.0	11	23	AAW48626	Anti-inflammatory
44	36	100.0	11	23	AAW48627	Anti-inflammatory
45	36	100.0	11	23	AAW48628	Anti-inflammatory

#### ALIGNMENTS

RESULT 1	ABB08734	standard; peptide; 6 AA.
XX	ABB08734	
XX	ABB08734	
DT	14-JUN-2002	(first entry)
XX		
DE	Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 12.	
XX		
XX	IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;	
XX	kinase activation; leukocyte; inflammation; B-selection; osteoclast;	
XX	autoimmune disease; transplant rejection; osteoporosis; cancer;	
XX	Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;	
XX	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;	
XX	corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;	
XX	osteopathic; cytotoxic; nocitopic; neuroprotective; anti-HIV; human;	
XX	antiarteriosclerotic; vincutide; antiasthmatic; antineutrophic;	
XX	dermatological; antibacterial; antiparasitic; antineutrophic;	
XX	antiarthritic; osteopathic; antitumor; mutant; mutain.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
FT	Key	Location/Qualifiers
FT	Misc-difference	3 /note="Wildtype Trp substituted by Tyr"
PN	WO200183547-A2.	
PD	08-NOV-2001.	
XX		



PF 02-MAY-2001; 2001MO-US40654.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S;  
 XX  
 DR WPI; 2002-179350/23.  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorder, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 XX  
 PS Claim 23; Page 45; 82pp; English.  
 XX  
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprising contacting a cell with an anti-inflammatory compound  
 CC (AB808725-AB808742) comprising at least one NEMO binding domain  
 CC (AB877313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of IkbppaB. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC polydactylitis. Also for Crohn's disease, ulcerative colitis,  
 CC spondylarthritis, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
 CC binding domain of IKKbeta.  
 CC  
 SQ Sequence 6 AA;  
 QY  
 DB 1 LDYSWL 6  
 1 LDYSWL 6  
 Query Match 100.0%; Score 36; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 2  
 AAM48517  
 ID AAM48517 standard; Peptide; 6 AA.  
 XX  
 AC AAM48517;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE NBD mutant peptide SEQ ID NO 12.

XX  
 XX Antinflammatory; antiaesthetic; cytostatic; antiproliferative; nootropic;  
 XX antirheumatic; antiallergic; osteopathic; antibacterial; virucide;  
 XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 XX autoimmune disorder; multiple sclerosis; transplant rejection;  
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200183554-A2.  
 XX  
 XX PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001MO-US14346.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 XX May MJ, Ghosh S, Flindels MA, Phillips K;  
 PI  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Example 6; Page 48; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
 CC cytostatic, antiproliferative, antirheumatic, antiallergic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polyomyelitis, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 SQ Sequence 6 AA;  
 QY  
 DB 1 LDYSWL 6  
 1 LDYSWL 6  
 Query Match 100.0%; Score 36; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 3  
 AAM48540  
 ID AAM48540 standard; Peptide; 6 AA.

XX	AA048540;	
AC		
XX	20-MAR-2002 (Elixir entry)	
XX		
DE	Anti-inflammatory peptide SEQ ID NO 43.	
XX		
KM	Anti-inflammatory; antiaesthetic; cyostatic; antipsoriatic; nootropic;	
KM	antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;	
KM	immunopressive; dermatological; neuroprotective; antiatherosclerotic;	
KM	antiallergic; membrane translocation domain; NEMO binding domain; eczema;	
KM	cyclokin; NFkBpab; IkappaB kinase beta; IKKbeta; cancer; psoriasis;	
KM	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;	
KM	autoimmune disorder; multiple sclerosis; transplant rejection;	
KM	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;	
KM	ataxia telangiectasia; allergy; anaphylaxis; arthritis.	
XX		
OS	Synthetic.	
XX		
FN	WO200183554-A2.	
XX		
PD	08-NOV-2001.	
XX		
PE	02-MAY-2001; 2001MO-US14346.	
XX		
PR	02-MAY-2000; 2000US-201261P.	
PR	22-AUG-2000; 2000US-0643260.	
XX		
PA	(PRAE-) PRAECS PHARM INC.	
PA	(UYIA ) UNIV YALE.	
XX		
P1	May MJ, Ghosh S, Fandels MA, Phillips K;	
DR	WPI; 2002-121889/16.	
XX		
PT	Novel anti-inflammatory compound comprising membrane translocation	
PT	domain fused to NEMO binding sequence, useful for blocking nuclear	
PT	factor kappaB activation, and for treating asthma, lung inflammation,	
PT	psoriasis	
XX		
PS	Claim 6; Page 61; 88pp; English.	
XX		
CC	The invention relates to an anti-inflammatory compound (especially	
CC	AA048628-AA048645), comprising a membrane translocation domain	
CC	(AA048620-AA048627 or AA048646-AA048651) which comprises from 6-15	
CC	amino acid residues, fused to a NEMO binding sequence	
CC	(AA048625-AA048619). The anti-inflammatory compounds have antiaesthetic,	
CC	cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,	
CC	antibacterial, immunopressive, dermatological, neuroprotective,	
CC	nootropic, antiatherosclerotic, virucide and antiallergic activity. The	
CC	compounds act as selective inhibitors of cytokine-mediated NFkBpab	
CC	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at	
CC	the NEMO binding domain that results in inhibition of IKKbeta Kinase	
CC	activation and subsequent decreased phosphorylation of IkappaB. The	
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,	
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,	
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,	
CC	bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,	
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;	
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia	
CC	telangiectasia. The compounds are also useful for treating	
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,	
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and	
CC	arthritis.	
XX		
XX	Sequence 6 AA;	
XX		
XX	Query Match 100.0%; Score 36; DB 23; Length 6;	
XX	Best Local Similarity 100.0%; Pred. No. 9.3e+05;	
XX	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
XX	1 LDYSWL 6	
XX		

Db	1 LDYSWL 6
XX	RESULT 4
XX	AA048592
ID	AA048592 standard; Peptide; 6 AA.
XX	
XX	AA048592;
AC	
XX	
DT	20-MAR-2002 (first entry)
XX	
DE	Anti-inflammatory peptide SEQ ID NO 95.
XX	
KW	Anti-inflammatory; antiaesthetic; cyostatic; antipsoriatic; nootropic;
KW	antirheumatic; antiarthritic; osteoprotic; antibacterial; vincidine;
KW	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic
KW	antiallergic; membrane translocation domain; NEMO binding domain; ecze-
KW	cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW	autoimmune disorder; multiple sclerosis; transplant rejection;
KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX	
OS	Synthetic.
XX	
PN	WO200183554-A2.
XX	
PD	08-NOV-2001.
XX	
PF	02-MAY-2001; 2001WO-US14346.
XX	
PR	02-MAY-2000; 2000US-201261P.
XX	
PR	22-AUG-2000; 2000US-0643260.
XX	
PA	(PRAE-) PRAECTIS PHARM INC.
PA	(UYVA ) UNIV YALE.
XX	
PI	May MJ, Ghosh S, Findels MA, Phillips K;
XX	
PI	WPI; 2002-121889/16.
DR	
XX	
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis -
XX	
XX	Claim 6; Page 62; 88pp; English.
PS	
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AA048628-AA048645), comprising a membrane translocation domain
CC	(AA048620-AA048627 or AA048646-AA048651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AA048525-AA048619). The antiinflammatory compounds have antiaesthetic;
CC	cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	nootropic, antihypertensive, vincidine and antiallergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NF-kappaB
CC	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of IkappaB. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	burstitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
XX	Sequence 6 AA;
XX	

Query Match 100.0%; Score 36; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LDYSWL 6  
 Db 1 LDYSWL 6

RESULT 5  
 ABU08427 ID ABU08427 standard; peptide: 6 AA.  
 AC ABU08427;  
 XX  
 DT 12-JUN-2003 (first entry)  
 XX  
 DE Human NEMO binding site (NBD) mutant peptide #10.  
 XX  
 KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;  
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;  
 KW nuclear factor-kappaB induction; inflammatory disorder;  
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;  
 KW atherosclerosis; viral infection; Ataxia telangiectasia;  
 KW translocation detection; immunosuppressive; osteopathic;  
 KW cytosolic; neutrotropic; antiatherosclerotic; virucide;  
 KW vasotropic; antirheumatic; antiarthritic; mutant; muteln.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN US200215600-A1.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PE 02-MAY-2001; 2001US-0847940.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (MAYM/) MAY M J.  
 PA (GHOS/) GHOSH S.  
 XX  
 PI May MJ, Ghosh S;  
 XX  
 DR WPI; 2003-209142/20.  
 XX  
 PT Novel antiinflammatory peptide compounds comprising NEMO binding  
 PT domain, useful for modulating NF-kappaB induction in a cell and for  
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,  
 PT psoriasis, vasculitis -  
 XX  
 PS Claim 22; Page 17; 47pp; English.  
 XX  
 CC The present invention relates to antiinflammatory compounds comprising  
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are  
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha  
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention  
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction  
 CC in a cell, where the compounds are capable of blocking the interaction  
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The  
 CC antiinflammatory compound further comprises at least one membrane  
 CC translocation domain. The compounds are useful for treating  
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia  
 CC telangiectasia, and for translocation detection. The compounds of  
 CC the invention block NF-kappaB induction by IKK but do not inhibit  
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human  
 CC NBD mutant peptides.  
 CC  
 XX Sequence 6 AA;  
 SQ  
 Query Match 100.0%; Score 36; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LDYSWL 6  
 Db 1 LDYSWL 6

RESULT 6  
 AAM48596 ID AAM48596 standard; Peptide: 7 AA.  
 AC AAM48596;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 99.  
 XX  
 KW Antiinflammatory; antiasthmatic; cytosolic; antiproliferic; neutrotropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neutrotropic; antiatherosclerotic;  
 KW allergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 OS  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PE 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Finkelstein MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytosolic, antiproliferic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neutrotropic,  
 CC neutrotropic, antiatherosclerotic, virucide and anti-allergic activity. The  
 CC compound act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursts; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 36; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDYSWL 6  
Db 1 LDYSWL 6  
RESULT 7  
ID AAM48589 standard; Peptide; 8 AA.  
XX  
AC AAM48589;  
XX  
DT 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 92.  
XX  
KM Anti-inflammatory; antiaesthetic; cytosolic; antiproliferative; neurotropic;  
XX  
KM antitumor; antiproliferative; osteoporosis; antibacterial; virucide;  
XX  
KM immunosuppressive; dermatological; neuroprotective; antithrombotic;  
XX  
KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
XX  
KM cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
XX  
KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX  
KM autoimmune disorder; multiple sclerosis; transplant rejection;  
XX  
KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
XX  
KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US14346.  
XX  
PR 02-MAY-2000; 2000US-201261P.  
XX  
PR 22-AUG-2000; 2000US-0643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
XX  
PA (UYVA ) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Firdels MA, Phillips K;  
XX  
DR WPI; 2002-121889/16.  
XX  
PT Novel anti-inflammatory compound comprising membrane translocation  
XX  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
XX  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
XX  
PT psoriasis  
XX  
PS Claim 6; Page 62; 88pp; English.  
XX  
CC The invention relates to an anti-inflammatory compound (especially  
XX  
CC AAM48628-AAM48645), comprising a membrane translocation domain  
XX  
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
XX  
CC amino acid residues, fused to a NEMO binding sequence  
XX  
CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiaesthetic,  
XX  
CC cytosolic, antiproliferative, antithrombotic, antiallergic, osteopathic,  
XX  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
XX  
CC neurotropic, antitumor, antiproliferative, virucide and antiallergic activity. The  
XX  
CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
XX  
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
XX  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
XX  
CC activation and subsequent decreased phosphorylation of IkappaB. The  
XX  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
XX  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
XX  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
XX  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
XX  
CC telangiectasia. The compounds are also useful for treating  
XX  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
XX  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
XX  
CC arthritis.  
XX  
SQ Sequence 8 AA;  
Query Match 100.0%; Score 36; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDYSWL 6  
Db 3 LDYSWL 8  
RESULT 8  
ID AAM48597 standard; Peptide; 8 AA.  
XX  
AC AAM48597;  
XX  
DT 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 100.  
XX  
KM Anti-inflammatory; antiaesthetic; cytosolic; antiproliferative; neurotropic;  
XX  
KM antitumor; antiproliferative; osteoporosis; antibacterial; virucide;  
XX  
KM immunosuppressive; dermatological; neuroprotective; antithrombotic;  
XX  
KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
XX  
KM cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
XX  
KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX  
KM autoimmune disorder; multiple sclerosis; transplant rejection;  
XX  
KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
XX  
KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US14346.  
XX  
PR 02-MAY-2000; 2000US-201261P.  
XX  
PR 22-AUG-2000; 2000US-0643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
XX  
PA (UYVA ) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Firdels MA, Phillips K;  
XX  
DR WPI; 2002-121889/16.  
XX  
PT Novel anti-inflammatory compound comprising membrane translocation  
XX  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
XX  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
XX  
PT psoriasis  
XX  
PS Claim 6; Page 62; 88pp; English.  
XX  
CC The invention relates to an anti-inflammatory compound (especially  
XX  
CC AAM48628-AAM48645), comprising a membrane translocation domain  
XX  
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
XX  
CC amino acid residues, fused to a NEMO binding sequence  
XX  
CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiaesthetic,  
XX  
CC cytosolic, antiproliferative, antithrombotic, antiallergic, osteopathic,  
XX  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
XX  
CC neurotropic, antitumor, antiproliferative, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.

CC Sequence 8 AA;  
 SQ

Query Match 100.0%; Score 36; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6  
 |||||  
 Db 1 LDYSWL 6

RESULT 9  
 AAM48588  
 ID AAM48588 standard; Peptide; 9 AA.  
 XX  
 AC AAM48588;  
 DT 20-MAR-2002 (first entry)  
 DE Anti-inflammatory peptide SEQ ID NO 91.  
 XX

XX Antinflammatory; antiasthmatic; cytoskeletal; antiapoptotic; neurotropic;  
 XX antineuritic; antiarthritic; osteopathic; antibacterial; vitruide;  
 XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 XX autoimmune disorder; multiple sclerosis; transplant rejection;  
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 PD 08-NOV-2001.  
 PP 02-MAY-2001; 2001WO-US14346.  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 PI May MJ, Ghosh S, Flindeis MA, Phillips K;  
 DR WPI, 2002-121889/16.  
 XX  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 XX Claim 6; Page 62; 88pp; English.  
 XX  
 XX The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytoskeletal, antiapoptotic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC neurotropic, antiatherosclerotic, vitruide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.

CC Sequence 9 AA;  
 SQ

Query Match 100.0%; Score 36; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6  
 |||||  
 Db 1 LDYSWL 6

RESULT 10  
 AAM48591  
 ID AAM48591 standard; Peptide; 9 AA.  
 XX  
 AC AAM48591;  
 DT 20-MAR-2002 (first entry)  
 DE Anti-inflammatory peptide SEQ ID NO 94.  
 XX

XX Antinflammatory; antiasthmatic; cytoskeletal; antiapoptotic; neurotropic;  
 XX antineuritic; antiarthritic; osteopathic; antibacterial; vitruide;  
 XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 XX autoimmune disorder; multiple sclerosis; transplant rejection;  
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 PD 08-NOV-2001.  
 PP 02-MAY-2001; 2001WO-US14346.  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 PI May MJ, Ghosh S, Flindeis MA, Phillips K;  
 DR WPI, 2002-121889/16.  
 XX  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -

PT		psoriasis -
PS		Claim 6; page 62; 8pp; English.
XX		
CC	The invention relates to an antiinflammatory compound (especially	
CC	AAW48628-AAW48645), comprising a membrane translocation domain	
CC	(AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15	
CC	amino acid residues, fused to a NEMO binding sequence	
CC	(AAW48525-AAW48619). The antiinflammatory compounds have antiaesthetic,	
CC	cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteoprotective,	
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,	
CC	nocotropic, antihistosclerotic, virucide and antiallergic activity. The	
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB	
CC	activation by blocking interaction of Ikappab kinase beta (IKKbeta) at	
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase	
CC	activation and subsequent decreased phosphorylation of Ikappab. The	
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,	
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,	
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,	
CC	bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,	
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;	
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia	
CC	relangiectasia. The compounds are also useful for treating	
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,	
CC	dry eye food sensitivity, eczema, dermatitis, sunburn, aging and	
CC	arthritis.	
SQ	Sequence 9 AA:	
Query Match	100.0%; Score 36; DB 23; Length 9;	
Best Local Similarity	100.0%; Pred. No. 9.3e+05;	
Matches 6; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 LDYSWL 6 	
Ds	1 LDYSWL 6	
RESULT 11		
AAW48594		
ID	AAW48594 standard; Peptide; 9 AA.	
XX		
AC	AAW48594;	
XX		
DT	20-MAR-2002 (first entry)	
XX		
DE	Anti-inflammatory peptide SEQ ID NO 97.	
XX		
KW	Antinflammatory; antiaesthetic; cytostatic; antipsoriatic; nocotropic;	
KW	antirheumatic; antiarthritic; osteoprotic; antibacterial; virucide;	
KW	immunosuppressive; dermatological; neuroprotective; antihistosclerotic;	
KW	antiallergic; membrane translocation domain; NEMO binding domain; eczema;	
KW	cyclokin; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;	
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;	
KW	autoimmune disorder; multiple sclerosis; transplant rejection;	
KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;	
KW	ataxia telangiectasia; allergy; anaphylaxis; arthritis.	
XX		
OS	Synthetic.	
XX		
PN	WO200183554-A2.	
XX		
PD	08-NOV-2001.	
XX		
PF	02-MAY-2001; 2001WO-US14346.	
XX		
PR	02-MAY-2000; 2000US-201261P.	
XX		
PR	22-AUG-2000; 2000US-0643260.	
XX		
PA	(PRAE-) PRAECTIS PHARM INC.	
XX		
PA	(UYTA ) UNIV YALE.	
XX		
PI	May MJ, Ghosh S, Rindels MA, Phillips K;	

XX	WP1; 2002-121889/16.
DR	
XX	
PT	Novel anti-inflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis -
XX	
PS	Claim 6; Page 62; 88pp; English.
XX	
CC	The invention relates to an anti-inflammatory compound (especially
CC	AAW48628-AAW48645), comprising a membrane translocation domain
CC	(AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AAW48625-AAW48619). The anti-inflammatory compounds have antiasthmatic,
CC	cytostatic, antipsoriatic, antirheumatic, antiallergic, osteoprotic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	neurotrophic, antihypertensive, virocidic and anti-allergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of IkkappaB kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IkkappaB kinase
CC	activation and subsequent decreased phosphorylation of IkkappaB. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
SO	Sequence 9 AA:
XX	
QY	1 LDVSWL 6
DB	3 LDVSWL 8
XX	
XX	RESULT 12
ID	AAW48595 standard; Peptide; 9 AA.
XX	
AC	AAW48595;
XX	
DT	20-MAR-2002 (first entry)
XX	
DE	Anti-inflammatory peptide SEQ ID NO 98.
XX	
KM	Anti-inflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotrophic;
KM	antirheumatic; antiallergic; osteoprotic; antibacterial; virocidic;
KM	immunosuppressive; dermatological; neuroprotective; antihypertensive;
KM	antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KM	cytokine; NFkappaB; IkkappaB Kinase Beta; IKKbeta; cancer; psoriasis;
KM	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KM	autoimmune disorder; multiple sclerosis; transplant rejection;
KM	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KM	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS	Synthetic.
XX	
PN	WO200183554-A2.
XX	
PD	08-NOV-2001.
XX	
PF	02-MAY-2001; 2001WO-US14346.
XX	
PR	02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.  
 XX (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 XX WPI; 2002-121889/16.  
 DR  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AA48628-AA48645), comprising a membrane translocation domain  
 CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytoskeletal, antipneumonia, antirheumatic, antiarthritic, osteoprotective,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virocidic and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 SQ Sequence 9'AA;  
 XX  
 XX  
 Query Match 100.0%; Score 36; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6  
 |||||  
 Db 2 LDYSWL 7

RESULT 13  
 AA48590  
 ID AA48590 standard; Peptide: 10 AA.  
 XX  
 AC AA48590;  
 XX  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 93.  
 XX  
 KW Antiinflammatory; antiasthmatic; cytoskeletal; antipneumonia; nootropic;  
 KW antirheumatic; antiarthritic; osteoprotective; antibacterial; virocidic;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 KW  
 OS Synthetic.  
 XX  
 XX WO200183554-A2.

XX 08-NOV-2001.  
 PD  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 PF  
 XX  
 PR 03-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 XX WPI; 2002-121889/16.  
 DR  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AA48628-AA48645), comprising a membrane translocation domain  
 CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytoskeletal, antipneumonia, antirheumatic, antiarthritic, osteoprotective,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virocidic and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 SQ Sequence 10 AA;  
 XX  
 XX  
 Query Match 100.0%; Score 36; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.9;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6  
 |||||  
 Db 2 LDYSWL 7

RESULT 14  
 AA48593  
 ID AA48593 standard; Peptide: 10 AA.  
 XX  
 AC AA48593;  
 XX  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 96.  
 XX  
 KW Antiinflammatory; antiasthmatic; cytoskeletal; antipneumonia; nootropic;  
 KW antirheumatic; antiarthritic; osteoprotective; antibacterial; virocidic;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;

KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 OS Synthetic.  
 XX WO200183554-A2.  
 PN XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRACIS PHARM INC.  
 PA (UYTA) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytostatic, antiproliferative, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virocidic and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 36; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.9; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDYSWL 6  
 Db 3 LDYSWL 8  
 RESULT 15  
 AAM48587  
 ID AAM48587 standard; Peptide; 11 AA.  
 XX  
 AC AAM48587;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 90.  
 XX  
 KM Antiinflammatory; antiasthmatic; cytostatic; antiproliferative; nootropic;

KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 OS Synthetic.  
 XX WO200183554-A2.  
 PN XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRACIS PHARM INC.  
 PA (UYTA) UNIV YALE.  
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 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
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 PT psoriasis -  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
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 CC nootropic, antiatherosclerotic, virocidic and antiallergic activity. The  
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 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
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 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX  
 SQ Sequence 11 AA;  
 Query Match 100.0%; Score 36; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. NO. 4.3; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDYSWL 6  
 Db 3 LDYSWL 8  
 Search completed: February 18, 2004, 14:26:23  
 Job time : 23.7763 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 / Search time 17.3684 Seconds  
(without alignments)  
89.145 Million cell updates/sec

Title: US-09-643-260-11

Perfect score: 35

Sequence: 1 LDPSWL 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp Vertebrate:\*
- 14: sp Unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	179	11	Q8BZUS
2	35	100.0	315	13	Q91838
3	35	100.0	391	16	P95247
4	35	100.0	407	2	Q55047
5	35	100.0	414	2	Q950Y1
6	35	100.0	414	2	Q950Y1
7	35	100.0	415	16	Q8VJK7
8	35	100.0	1115	10	Q942A0
9	33	94.3	61	16	Q9PEJ5
10	33	94.3	144	16	Q826L9
11	33	94.3	144	16	Q84950
12	33	94.3	253	16	Q24927
13	33	94.3	253	16	Q92MX2
14	33	94.3	518	16	Q9JYP7
15	33	94.3	518	16	Q9JYN9
16	33	94.3	1227	5	Q20129

17	32	91.4	208	17	Q28570	Q28570 archaeoglob
18	32	91.4	355	10	Q8RWE1	Q8RWE1 arabidopsis
19	32	91.4	371	10	Q81871	Q81871 arabidopsis
20	32	91.4	449	16	Q910V1	Q910V1 pseudomonas
21	32	91.4	467	16	Q92X93	Q92X93 rhizobium m
22	32	91.4	490	16	P96442	P96442 rhizobium m
23	31	88.6	44	4	Q96PA0	Q96PA0 homo sapien
24	31	88.6	54	16	Q8E977	Q8E977 shewanella
25	31	88.6	56	8	Q8WFM8	Q8WFM8 diadema pau
26	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema pau
27	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema set
28	31	88.6	56	8	Q8WFM7	Q8WFM7 diadema pal
29	31	88.6	56	8	Q8WFM7	Q8WFM7 diadema set
30	31	88.6	56	8	Q8WFM2	Q8WFM2 diadema sav
31	31	88.6	56	8	Q8WFM2	Q8WFM2 diadema set
32	31	88.6	56	8	Q8WFM1	Q8WFM1 diadema sav
33	31	88.6	56	8	Q8WFM2	Q8WFM2 echinorrix
34	31	88.6	56	8	Q8WFM9	Q8WFM9 diadema pal
35	31	88.6	56	8	Q8WFM8	Q8WFM8 diadema sav
36	31	88.6	56	8	Q8WFM4	Q8WFM4 diadema pau
37	31	88.6	56	8	Q8WFM4	Q8WFM4 diadema pau
38	31	88.6	56	8	Q8WFM4	Q8WFM4 diadema pau
39	31	88.6	56	8	Q8WFM4	Q8WFM4 diadema ant
40	31	88.6	56	8	Q8WFM6	Q8WFM6 diadema sav
41	31	88.6	56	8	Q8WFM9	Q8WFM9 diadema ant
42	31	88.6	56	8	Q8WFM5	Q8WFM5 diadema max
43	31	88.6	56	8	Q8WFM2	Q8WFM2 diadema pau
44	31	88.6	56	8	Q8WFM4	Q8WFM4 diadema set
45	31	88.6	56	8	Q952H7	Q952H7 diadema ant

## ALIGNMENTS

### RESULT 1

Q8BZUS PRELIMINARY; PRT; 179 AA.  
ID Q8BZUS  
AC Q8BZUS  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Hypothetical membrane all-alpha structure containing protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Colon;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RT Nature 420:563-573 (2002).  
DR EMBL; AK033531; BAC28343.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 179 AA; 21321 MW; CBF710227B0CDB18 CRC64;

Query Match 100.0%; Score 35; DB 11; Length 179;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6  
Db 5 LDPSWL 10

### RESULT 2

Q91838 PRELIMINARY; PRT; 315 AA.  
ID Q91838  
AC Q91838  
DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)  
 DE Interferon regulatory factor 1 (interferon regulatory factor-1).  
 GN IRF-1.  
 OS *Coturnix coturnix* (Common quail), and  
 OS *Coturnix coturnix japonica* (Japanese quail).  
 OC *Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix*.  
 NCBI\_TaxID=9091, 93934;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=C.coturnix;  
 RA Zoeller B., Mueller I., Nanda I., Gutenbach M., Doseh E., Schmid M., Jungwirth C.;  
 RT "Sequence analysis of avian interferon regulatory factors (IRF) reveals close relation of the chicken and quail interferon induced transcriptional apparatus. Cytogenetic studies and sequence comparison of the avian IRF-1, ISBP and a MHC class II gene reveals that the avian cell line C-32 is derived from quail.";  
 RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=C.coturnix japonica; STRAIN=BREED.FRANZOSISCHE MASTWACHTEL;  
 RA Zoeller B., Ingold R.M., Nanda I., Gutenbach M.;  
 RT "Sequence comparison of avian interferon regulatory factors and identification of the avian CEC-32 cell as a quail cell line.";  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ2771052; CAC01088.1; -.  
 DR EMBL; AJ277745; CAB91630.1; -.  
 DR HSP; PI5314; 11F1.  
 DR InterPro; IPR001346; IRF.  
 DR Pfam; PF00605; IRF; 1.  
 DR PRINTS; PR00267; INTERFERGCT.  
 DR ProDom; PD002355; IRF; 1.  
 DR SMART; SM00348; IRF; 1.  
 DR PROSITE; PS00601; IRF; 1.  
 SQ SEQUENCE 315 AA; 36257 MW; 7E32521A2D2D62D0 CRC64;  
 Query Match 100.0%; Score 35; DB 13; Length 315;  
 Best Local Similarity 100.0%; Pred. No. 66;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDPSWL 6  
 Db 297 LDPSWL 302  
 RESULT 3  
 ID P95247 PRELIMINARY; PRT; 391 AA.  
 AC P95247;  
 DT 01-MAY-1997 (TReMBLrel. 03, Created)  
 DT 01-MAY-1997 (TReMBLrel. 03, last sequence update)  
 DT 01-OCT-2002 (TReMBLrel. 22, last annotation update)  
 DE Hypothetical 37.4 kDa protein (PPE family protein).  
 GN RY2352C OR MTCY98.21C OR MT2419.  
 OS *Mycobacterium tuberculosis*.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 NCBI\_TaxID=11773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Broesch R., Parkhill J., Garnier T., Church C., Harris D., Gordon S.V., Eiglmeyer K., Gao S., Barry C.E. III, Tekala F., Baccoc K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Ketchum A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

RT "Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence.";  
 RL Nature 393:537-544 (1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Ralston J., Ubertack T., Weidman J., Khouri H., Gill J., Mikula A., Bhat W.;  
 RT "Whole genome comparison of *Mycobacterium tuberculosis* clinical and laboratory strains.";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z83860; CAB06149.1; -.  
 DR EMBL; AE007082; AAK46712.1; -.  
 DR TIGR; MT2419; -.  
 DR R2352C; -.  
 DR InterPro; IPR000030; Microbac\_PPE.  
 DR Pfam; PF00823; PPE; 1.  
 DR Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 391 AA; 37355 MW; 360B67EEF6CB46A CRC64;  
 Query Match 100.0%; Score 35; DB 16; Length 391;  
 Best Local Similarity 100.0%; Pred. No. 83;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDPSWL 6  
 Db 3 LDPSWL 8  
 RESULT 4  
 ID Q55047 PRELIMINARY; PRT; 407 AA.  
 AC Q55047;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)  
 DE Form I operon ORF protein genes, insertion sequence IS630 protein.  
 OS *Shigella sonnei*.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Shigella.  
 NCBI\_TaxID=624;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=53G;  
 RA Hough H-S.;  
 RT "Genetic analysis and identification of an IS630 element in the form I operon of *Shigella sonnei* 53G.";  
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U34305; AA84874.1; -.  
 SQ SEQUENCE 407 AA; 47980 MW; 23BPAF09EBBD5D7 CRC64;  
 Query Match 100.0%; Score 35; DB 2; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 86;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDPSWL 6  
 Db 175 LDPSWL 180  
 RESULT 5  
 ID Q9S0Y1 PRELIMINARY; PRT; 414 AA.  
 AC Q9S0Y1;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)  
 DE ORF5P (MBGV) (ORF5G).  
 GN MBGV OR ORF5G.

OS *Plesiomonas shigelloides* (*Aeromonas shigelloides*), and  
 OS *Shigella sonnei*.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; *Plesiomonas*.  
 RN NCBI\_TaxID=703, 624;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=*P.shigelloides*; STRAIN=SEROTYPE O17;  
 RA Child T., Okamura N., Yoshida Y., Ohtani K., Arakawa E., Watanabe H.;  
 RT "Complete DNA sequence of the O-antigen (rfb) gene cluster in  
 RT *Plesiomonas shigelloides* serotype O17 having the same O-antigen as  
 RT *Shigella sonnei*: comparison with that of *S. sonnei*.";  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=*P.shigelloides*; STRAIN=SEROTYPE O17;  
 RX MEDLINE=99036814; PubMed=9817819;  
 RA Houng H.H., Venkatesan M.M.;  
 RT "Genetic analysis of *Shigella sonnei* form I antigen: identification of  
 RT novel 16S30 as an essential element for the form I expression.";  
 RL Microb. Pathog. 25:165-173(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=*P.shigelloides*; STRAIN=C27;  
 RX PubMed=10992522;  
 RA Shepherd J., Wang L., Reeves P.R.;  
 RT "Comparison of the O antigen gene clusters of *Escherichia coli*  
 RT (*Shigella*) *sonnei* and *Plesiomonas shigelloides* O17: *Sonnei* gained its  
 RT current plasmid borne O antigen genes from *Plesiomonas shigelloides* in  
 RT a recent event.";  
 RL Infect. Immun. 68:6056-6061(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=*S.sonnei*;  
 RA Xu D.Q., Clear J.O., Ambrose N. Jr., Burr D., Kopecko D.J.;  
 RT "Molecular cloning and characterization of the O-antigen gene cluster  
 RT of *Shigella sonnei*: genetic stability, proposed biosynthetic pathway  
 RT and essential genes for expression of form I O polysaccharide in  
 RT *Salmonella* vaccine vector strain.";  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB025970; BAA85010.1; -;  
 DR EMBL; AF285970; AAG17412.1; -;  
 DR EMBL; AF294823; AAK85169.1; -;  
 SO SEQUENCE 414 AA; 49038 MW; E92985FE7F19D953 CRC64;  
 Query Match 100.0%; Score 35; DB 2; Length 414;  
 Best Local Similarity 100.0%; Pred. No. 88;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDPSWL 6  
 DB 175 LDPSWL 180  
 RESULT 6  
 ID Q9F738 PRELIMINARY; PRT; 414 AA.  
 AC Q9F738;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE WbGV.  
 GN *Shigella sonnei*.  
 OG *Shigella sonnei*.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; *Shigella*.  
 OK NCBI\_TaxID=624;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=53G1;  
 RX MEDLINE=20448976; PubMed=10992522;  
 RA Shepherd J., Wang L., Reeves P.R.;

RT "Comparison of the O antigen gene clusters of *Escherichia coli*  
 RT (*Shigella*) *sonnei* and *Plesiomonas shigelloides* O17: *Sonnei* gained its  
 RT current plasmid borne O antigen genes from *Plesiomonas shigelloides* in  
 RT a recent event.";  
 RL Infect. Immun. 68:6056-6061(2000).  
 DR EMBL; AF285971; AAG17422.1; -;  
 KW Plasmid.  
 SO SEQUENCE 414 AA; 49034 MW; EA6CA44A19ACD8CD CRC64;  
 Query Match 100.0%; Score 35; DB 2; Length 414;  
 Best Local Similarity 100.0%; Pred. No. 88;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDPSWL 6  
 DB 175 LDPSWL 180  
 RESULT 7  
 ID Q8VJK7 PRELIMINARY; PRT; 415 AA.  
 AC Q8VJK7;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE PPE family protein.  
 GN MT2422.  
 OS *Mycobacterium tuberculosis*.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacteriaceae; *Mycobacterium*.  
 OK NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / OshKosh;  
 RA Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Knouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of *Mycobacterium tuberculosis* clinical and  
 RT laboratory strains.";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE007082; AAK46715.1; -;  
 DR TIGR; MT2422; -;  
 DR InterPro; IPR000030; Microbac\_PPE.  
 DR Pfam; PF00823; PPE; 1.  
 SO SEQUENCE 415 AA; 40093 MW; 8B48C7671BFA521 CRC64;  
 Query Match 100.0%; Score 35; DB 16; Length 415;  
 Best Local Similarity 100.0%; Pred. No. 88;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDPSWL 6  
 DB 34 LDPSWL 39  
 RESULT 8  
 ID Q942A0 PRELIMINARY; PRT; 1115 AA.  
 AC Q942A0;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Beta galactosidase-like protein.  
 GN P0431G06.9.  
 OS *Oryza sativa* (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; *Oryza*.  
 OK NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=cv. Nipponbare;  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nippobare (GA3) genomic DNA, chromosome 1, PAC  
 clone: P043106.";  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP003683; BAB64698.1; -.  
 DR Gramene; Q942A0; -.  
 DR InterPro: IPR006101; Glyco\_hydro\_2.  
 DR InterPro: IPR006102; Glyco\_hydro\_21g.  
 DR InterPro: IPR006104; Glyco\_hydro\_25b.  
 DR InterPro: IPR006103; Glyco\_hydro\_27tm.  
 DR InterPro: IPR004200; Glyco\_hydro\_42c.  
 DR InterPro: IPR004199; Glyco\_hydro\_42n.  
 DR Pfam; PF02930; Bgal\_small\_1; 1.  
 DR Pfam; PF02929; Bgal\_small\_N; 1.  
 DR Pfam; PF00703; Glyco\_hydro\_2; 1.  
 DR Pfam; PF02836; Glyco\_hydro\_2\_C; 1.  
 DR Pfam; PF02837; Glyco\_hydro\_2\_N; 1.  
 DR PRINTS; PR00132; GLHYDRLASE2.  
 DR PROSITE; PS00719; GLYCOSYL\_HYDROL\_F2\_1; 1.  
 DR PROSITE; PS00608; GLYCOSYL\_HYDROL\_F2\_2; 1.  
 SQ SEQUENCE 1115 AA; 126078 MW; 1AABF6AA305CA85 CRC64;

Query Match 100.0%; Score 35; DB 10; Length 1115;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6  
 DB 697 LDPSWL 702

RESULT 9  
 OPEP35 PRELIMINARY; PRT; 61 AA.  
 ID OPEP35  
 AC OPEP35  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical protein Xf1033.  
 GN Xf1033.  
 OS Xylella fastidiosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 CC Xanthomonadaceae; Xylella.  
 OX NCBI\_TaxID=2371;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=965C;  
 RX MEDLINE=20365717; PubMed=10910347;  
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,  
 RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,  
 RA Barroo M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,  
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carrero D.M., Carter H.,  
 RA Colaço N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,  
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,  
 RA Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,  
 RA Frega J.S., Franca S.C., Franco M.C., Frohne M., Furlan L.R.,  
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,  
 RA Ho P.L., Hohnselt J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,  
 RA Krieger J.E., Kuramae E.B., Laigret F., Lambais M.R., Leite L.C.C.,  
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,  
 RA Machado M.V., Madelira A.M.B.N., Madelira H.M.F., Martino C.L.,  
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,  
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,  
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,  
 RA Nhani A., Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,  
 RA Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,  
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A., Jr., Pesquero J.B.,  
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,  
 RA de Rosa V.E., Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,  
 RA da Silva A.C.R., da Silva A.M., da Silva P.R., Silva W.A., Jr.,  
 RA da Silveira J.F., Silveira M.L.Z., Silveira W.J., de Souza A.A.,  
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuchioka M.H.,

RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,  
 RA Zago M.A., Zacz M., Melandri J., Setubal J.C.;  
 RT "The genome sequence of the plant pathogen Xylella fastidiosa.";  
 RL Nature 406:151-159(2000).  
 DR EMBL; AE003940; AA083843.1; -.  
 DR Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 61 AA; 6849 MW; 6CD0800BD7B8E107 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 61;  
 Best Local Similarity 83.3%; Pred. No. 30;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6  
 DB 2 MDPSWL 7

RESULT 10  
 ID O826L9 PRELIMINARY; PRT; 144 AA.  
 AC O826L9;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Putative pathogenicity island protein.  
 GN SSCB OR STY1717.  
 OS Salmonella typhi.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=601;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CT18;  
 RX MEDLINE=21534947; PubMed=11677608;  
 RA Barkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,  
 RA Churcher C., Kung'u K.L., Bentley S.D., Holden M.T.G., Sebatina M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Fellwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,  
 RA Krogan A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrett B.G.,  
 RT "Complete genome sequence of a multiple drug resistant Salmonella  
 RT enterica serovar Typhi CT18.";  
 RL Nature 413:848-852(2001).  
 DR EMBL; AL627271; CAD01962.1; -.  
 DR InterPro: IPR001440; TPR.  
 DR Pfam; PF00515; TPR; 2.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 144 AA; 16390 MW; ECD0DA7F0B325B08 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 144;  
 Best Local Similarity 83.3%; Pred. No. 72;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6  
 DB 45 IDPSWL 50

RESULT 11  
 ID O84950 PRELIMINARY; PRT; 144 AA.  
 AC O84950;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE SSCB (Secretion system chaparone).  
 GN SSCB OR STY1403.  
 OS Salmonella typhimurium.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=602;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SL1344;
RA Cirillo D.M., Valdivia R.H., Monack D., Falkow S.;
RT "Macrophage-dependent induction of the Salmonella pathogenicity island
RL 2 type III secretion system and its role in intracellular survival.";
RM Mol. Microbiol. 0:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RA MEDLINE=99000132; PubMed=9786193;
RA Hensel M., Shea J.E., Waterman R., Mundy R., Nikolaus T., Banke G.,
RA Vazquez-Torres A., Gleason C., Fang F.C., Holden D.W.;
RT "Genes encoding putative effector proteins of the type III secretion
RT system of Salmonella pathogenicity island 2 are required for bacterial
RL virulence and proliferation in macrophages.";
RM Mol. Microbiol. 30:163-174(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RA MEDLINE=21534948; PubMed=11677609;
RA McClelland W., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Portnoiiik S., Ali J., Dante M., Du P., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan B., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
DR EMBL; AF020808; AAC28884.1; -
DR EMBL; AJ224892; CA112190.1; -
DR EMBL; AB008761; AL20327.1; -
DR InterPro; IPR01440; TPR.
DR Pfam; PF00515; TPR.
KM Complete proteome.
SQ SEQUENCE 144 AA; 16375 MW; B60EDA7F0E325B0B CRC64;

Query Match 94.3%; Score 33; DB 16; Length 144;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDPSWL 6
Db 45 IDPSWL 50

RESULT 12
O24927
ID O24927 PRELIMINARY; PRT; 253 AA.
AC O24927;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein HP0101.
GN HP0101.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteriaceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RA MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirnes E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watney L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter

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RT pylori.";
RL Nature 388:539-547(1997).
DR EMBL; AB000532; AAD07180.1; -
DR TIGR; HP0101; -
DR InterPro; IPR002718; HP OMP.
DR Pfam; PF01856; HP OMP; I.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 253 AA; 29463 MW; C9A6BBE2C5A90003 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 253;
Best Local Similarity 83.3%; Pred. No. 1,3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDPSWL 6
Db 149 LDPSWI 154

RESULT 13
O92MX2
ID O92MX2 PRELIMINARY; PRT; 253 AA.
AC O92MX2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Putative.
GN JHP0093.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteriaceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Dolg P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.B., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
DR EMBL; AB001448; AAD05674.1; -
KM Complete proteome.
SQ SEQUENCE 253 AA; 29526 MW; 5C5F5239737B90AB CRC64;

Query Match 94.3%; Score 33; DB 16; Length 253;
Best Local Similarity 83.3%; Pred. No. 1,3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDPSWL 6
Db 149 LDPSWI 154

RESULT 14
O9JYP7
ID O9JYP7 PRELIMINARY; PRT; 518 AA.
AC O9JYP7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein NMB1485.
GN NMB1485.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RA MEDLINE=2017575; PubMed=10710307;
RA Tetelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

```

RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,  
 RA Nelson W.C., Gwin M.L., DeBoy R., Peterson J.D., Hickey E.K.,  
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,  
 RA Mason T., Ciecko A., Parksey D.S., Blair E., Citron H., Clark E.B.,  
 RA Cotton M.D., Utterback T.R., Kouri H., Qin H., Vamadevan J.,  
 RA Gill J., Scariato V., Maignant V., Piza M., Grandi G., Sun L.,  
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;  
 RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain  
 MC58";  
 RL Science 287:1809-1815(2000).  
 DR EMBL: AE002498; AAF41841.1; -.  
 DR TIGR: NMB1485; -.  
 DR InterPro: IPR000644; CBS\_domain.  
 DR InterPro: IPR005170; CorC\_H1YC.  
 DR InterPro: IPR005496; Terc.  
 DR Pfam: PF00571; CBS; 2.  
 DR Pfam: PF03471; CorC\_H1YC; 1.  
 DR Pfam: PF03741; Terc; 1.  
 DR SMART: SM00116; CBS; 2.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 518 AA; 57342 MW; CFP9324DA672DC96 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 518;  
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDPSWL 6  
 :|||||  
 Db 1 MDPSWL 6

## RESULT 15

O9JTN9 PRELIMINARY; PRT; 518 AA.  
 AC O9JTN9;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Conserved hypothetical integral membrane protein.  
 GN NMA1694.  
 OS *Neisseria meningitidis* (serogroup A).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=65699;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=22491 / Serogroup A / Serotype 4A;  
 RX MEDLINE=2022556; PubMed=10761919;  
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,  
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,  
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holtroyd S.,  
 RA Jagsis K., Leachter S., Moule S., Mungall K., Quail M.A.,  
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,  
 RA Whitehead S., Spratt B.G., Barrall B.G.;  
 RT "Complete DNA sequence of a serogroup A strain of *Neisseria*  
 RT *meningitidis* Z2491";  
 RL Nature 404:502-506(2000).  
 RL EMBL: AL162756; CAB84922.1; -.  
 DR InterPro: IPR000644; CBS\_domain.  
 DR InterPro: IPR005170; CorC\_H1YC.  
 DR InterPro: IPR005496; Terc.  
 DR Pfam: PF00571; CBS; 2.  
 DR Pfam: PF03471; CorC\_H1YC; 1.  
 DR Pfam: PF03741; Terc; 1.  
 DR SMART: SM00116; CBS; 2.  
 KW Complete proteome.  
 SQ SEQUENCE 518 AA; 57358 MW; 47FBC652664E3B80 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 518;  
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDPSWL 6

Db :|||||  
 1 MDPSWL 6

Search completed: February 18, 2004, 14:35:50  
 Job time : 19.3684 secs



Db 295 LDFSWL 300

RESULT 2

NI80 YEAST STANDARD; PRT; 866 AA.

AC P33420: 008917; 866 AA.

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE NIP80 protein (NIP100 protein).

GN NIP80 OR NIP100 OR YPL174C.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes;

OC Baktaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI\_TaxID=4932;

RA SEQUENCE FROM N.A.

RA Schlenker G., Silver P.A.

RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.

RN REVISIONS.

RA Silver P.A.

RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=5286C / AB972;

RX MEDLINE=97313271; PubMed=9169875;

RA Bussey H., Storm R.K., Ahmed A., Albermann K., Allen E., Ansgore W.,

RA Arujo R., Aparicio A., Barrell B.G., Badcock K., Barnes V.,

RA Bockstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,

RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,

RA Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesthoeft A.,

RA Duncan M., Floeth W., Fortin N., Friesen J.D., Fritz C., Goffeau A.,

RA Hall J., Hebling S., Hyman R., Johnston M., Kallman S., Klein K.,

RA Hunnicke-Smith S., Hyman R., Johnston M., Kallman S., Klein K.,

RA Komp C., Kurdi O., Laehkari D., Lew H., Lin A., Lin D., Louis E.J.,

RA Marathe R., Messenguy F., Mewes H.-W., Miripati S., Moestl D.,

RA Mueller-Auer S., Namath A., Newtich U., Oefner P., Pearson D.,

RA Petel F.X., Pohl T.M., Purnelle D., Schaefer M., Schaefer M.,

RA Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tetteil H.,

RA Uresatrasu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,

RA Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,

RA Zhong W.W., Zollner A., Vo D.H., Hart J.,

RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI."

RL Nature 387:103-105 (1997).

CC -1- SIMILARITY: Contains 1 CAP-Gly domain.

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CC -----

DR EMBL: X72227; CAAS1030.1; -

DR EMBL: Z73330; CA97881.1; -

DR PIR: S65186; S65186.

DR SGD: S0006095; NIP100.

DR GO: GO:0005869; C:cytoskeleton; IDA.

DR GO: GO:0000992; P:mitotic anaphase B; IGI.

DR InterPro: IPR000938; CAP-Gly.

DR Pfam: PF01302; CAP\_Gly; 1.

DR PROSITE: PS00845; CAP\_Gly\_1; 1.

DR PROSITE: PS50245; CAP\_Gly\_2; 1.

KM Cytoskeleton; Coiled coil.

FT DOMAIN 34 84 CAP-Gly.

FT DOMAIN 101 175 COILED COIL (POTENTIAL).

FT DOMAIN 207 375 COILED COIL (POTENTIAL).

FT DOMAIN 645 776 COILED COIL (POTENTIAL).

SO SEQUENCE 866 AA; 100289 MW; A72EA9E38845081 CRC64;

Query Match 94.3%; Score 33; DB 1; Length 868;

Best Local Similarity 83.3%; Pred. No. 54;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6

Db 782 LDFSWL 787

RESULT 3

YGD4 YEAST STANDARD; PRT; 121 AA.

AC P33186;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Hypothetical 13.6 kDa protein in MIG1-AGA2 intergenic region.

GN YGL034C.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Baktaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI\_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RA Hedling U., Hofmann B., Delius H.

RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

RN [3]

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CC -----

DR EMBL: Z72556; CA96735.1; -

DR PIR: S64036; S64036.

DR SGD: S0003002; YGL034C.

KM Hypothetical protein; ATP-binding.

FT NP BIND 77 84 ATP (POTENTIAL).

SO SEQUENCE 121 AA; 13573 MW; 88D46FF50B67000F CRC64;

Query Match 88.6%; Score 31; DB 1; Length 121;

Best Local Similarity 83.3%; Pred. No. 17;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6

Db 40 LDFSWL 45

RESULT 4

PDXH MYCTU STANDARD; PRT; 224 AA.

ID PDXH MYCTU

AC O06207;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5) (PNP/PMP oxidase)

DE (PNPOX)

GN PDXH OR RV2607 OR MT2682 OR MTCV1A10.26C.

OS Mycobacterium tuberculosis.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI\_TaxID=1773;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H37Rv;

RX MEDLINE=98255987; PubMed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

RA Gordon S.V., Eigler K., Gao S., Barry C.B. III, Tekale F.,

RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,



RA Hornaby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajendram M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sullivan J.E., Taylor K., Whitehead S., Barrett B.G.,  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence.",  
 RL Nature 393:537-544(1998).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,  
 RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Blaisel W.,  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains.",  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: OXIDIZE PNP AND PNP INTO PYRIDOXAL 5'-PHOSPHATE (PLP)  
 CC (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Pyridoxamine 5'-phosphate + H(2)O + O(2) =  
 CC -1- COFACTOR: FMN (BY SIMILARITY).  
 CC -1- PATHWAY: De novo synthesis of pyridoxine (vitamin B6) and  
 CC -1- SIMILARITY: BELONGS TO THE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE  
 CC FAMILY.  
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 CC -----  
 CC DR EMBL: Z95387; CAB08633.1; -  
 CC DR EMBL: AE007101; AA046998.1; -  
 CC DR F1R: F70570; F70570.  
 CC DR HSSP: P28225; 1DNL.  
 CC DR TIGR: MT2682; -  
 CC DR TubercuList: RV2607; -  
 CC DR InterPro: IPR000659; Pyridox\_oxidase.  
 CC DR Pfam: PF01243; Pyridox\_oxidase; 1.  
 CC DR ProDom: PD006312; Pyridox\_oxidase; 1.  
 CC DR TIGRFAmE: TIGR00558; pdkH; 1.  
 CC DR PROSITE: PS01064; PYRIDOX OXIDASE; 1.  
 CC KM Pyridoxine biosynthesis; Oxidoreductase; Flavoprotein; FMN;  
 CC KW Complete proteome.  
 CC SQ SEQUENCE 224 AA; 25186 MW; 66ABCOAAACE90DC1 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 224;  
 Best Local Similarity 83.3%; Pred. No. 32;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDPSTL 6  
 DB 32 LDPDWL 37

RESULT 5  
 BCL2\_BOVIN STANDARD; PRT; 229 AA.  
 AC 002718;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 GN Apoptosis regulator Bcl-2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Holstein; Tissue=Thymus;  
 RA Reyes R.A., Cockerell G.L.,  
 RT "Bovine leukemia virus associated-leukemogenesis is correlated  
 RT with suppression of programmed cell death and increased expression  
 RT of Bcl-2.",  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (Apaf-1) (By similarity).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(L). Heterodimerization with BAX requires intrac BH1 and BH2  
 CC domains, and is necessary for anti-apoptotic activity (By  
 CC similarity). Also interacts with Apaf-1 and Raf-1 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intercellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum (By  
 CC similarity).  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 CC for interaction with Raf-1 (By similarity).  
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
 CC occurs during the G2/M phase of the cell cycle (By similarity). In  
 CC the absence of growth factors, Bcl2 appears to be phosphorylated  
 CC by other protein kinases such as ERKs and stress-activated  
 CC kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By  
 CC similarity).  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity (By similarity).  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC DR EMBL: U92434; AAB53319.1; -  
 CC DR HSSP: Q07817; 1MAZ.  
 CC DR InterPro: IPR000712; Bcl2\_BH.  
 CC DR InterPro: IPR003093; Bcl2\_BH4.  
 CC DR InterPro: IPR002475; BCL2\_FAMILY.  
 CC DR InterPro: IPR004725; Bcl2\_reg.  
 CC DR Pfam: PF00452; Bcl-2; 1.  
 CC DR Pfam: PF02180; BH4; 1.  
 CC DR SMART: SM00337; BCL; 1.  
 CC DR SMART: SM00265; BH4; 1.  
 CC DR TIGRFAmE: TIGR00865; Bcl-2; 1.  
 CC DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 CC DR PROSITE: PS01080; BH1; 1.  
 CC DR PROSITE: PS01258; BH2; 1.  
 CC DR PROSITE: PS01259; BH3; 1.  
 CC DR PROSITE: PS01260; BH4; 1.  
 CC DR PROSITE: PS50063; BH4\_2; 1.  
 CC KM Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
 KW DOMAIN 10 30 BH4.  
 FT DOMAIN 64 68 POLY-PRO.  
 FT DOMAIN 69 72 POLY-ALA.  
 FT DOMAIN 83 97 BH3.

FT DOMAIN 126 145 BH1.  
 FT DOMAIN 177 192 BH2.  
 FT TRANSMEM 202 223 POTENTIAL.  
 FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
 FT MOD RES 63 63 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
 SQ SEQUENCE 229 AA; 25099 MW; ADID0AF98FF1D CRC64;  
 Query Match 88.6%; Score 31; DB 1; Length 229;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DFSWL 6  
 DB 201 DFSWL 205  
 RESULT 6  
 BCL2\_CRILIO STANDARD; PRT; 236 AA.  
 ID BCL2\_CRILIO  
 AC Q9JVB8;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2.  
 OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Criceulidae.  
 ON NCBI\_TaxID=10030;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=20431763; PubMed=10973819;  
 RA Tomicic M.T., Christmann M., Kaina B.;  
 RT "Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein."  
 RL Biochem. Biophys. Res. Commun. 275:899-903(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A. AND CLEAVAGE BY CASPASES.  
 RX MEDLINE=21092839; PubMed=1181062;  
 RA Tomicic M.T., Kaina B.;  
 RT "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9 and caspase-3."  
 RL Biochem. Biophys. Res. Commun. 281:404-408(2001).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1) (By similarity).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAIF-1 (By similarity).  
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptotic activity and occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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 CC EMBL; AJ271720; CAB92245.1; -  
 CC PIR; JC7383; JC7383.  
 DR HSSP; 007817; 1MAZ.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR InterPro; IPR004725; Bcl2\_reg.  
 DR Pfam; PF00452; Bcl-2\_1.  
 DR Pfam; PF02180; BH4\_1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR TIGRFAMs; TIGR00865; bcl-2\_1.  
 DR PROSITE; PS0062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4\_1; 1.  
 DR PROSITE; PS0063; BH4\_2; 1.  
 KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
 FT DOMAIN 10 30 BH4.  
 FT DOMAIN 90 104 BH3.  
 FT DOMAIN 133 152 BH1.  
 FT DOMAIN 184 199 BH2.  
 FT TRANSMEM 209 230 POTENTIAL.  
 FT SITE 64 65 CLEAVAGE (BY CASPASE-3 AND CASPASE-9).  
 FT MOD RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
 SQ SEQUENCE 236 AA; 26491 MW; BECADFIEF337228 CRC64;  
 Query Match 88.6%; Score 31; DB 1; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DFSWL 6  
 DB 208 DFSWL 212  
 RESULT 7  
 BCL2\_MOUSE STANDARD; PRT; 236 AA.  
 ID BCL2\_MOUSE  
 AC P10417; P10418;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2 OR BCL-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RX [1]  
 RP SEQUENCE FROM N.A. (ISOPFORMS ALPHA AND BETA).  
 RC STRAIN=BA1B/C; TISSUE=Liver;  
 RX MEDLINE=87187643; PubMed=3032455;  
 RA Negrint M., Siliu E., Kozak C., Tsujimoto Y., Croce C.M.;  
 RT "Molecular analysis of mbcl-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma."  
 RL Cell 49:455-463(1987).  
 RN [2]  
 RP REVISIONS TO 221-222.

RA MEDLINE=92375724; PubMed=1508712;  
 RA Eguuchi Y., Ewert D.L., Teufelmo Y.;  
 RT "Isolation and characterization of the chicken bcl-2 gene: expression  
 RT in a variety of tissues including lymphoid and neuronal organs in  
 RT adult and embryo.";  
 RL Nucleic Acids Res. 20:4187-4192(1992).  
 CC [3]  
 RP PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.  
 RX MEDLINE=97277291; PubMed=9115213;  
 RA Ito T., Deng X., Carr B., May W.S. Jr.;  
 RT "Bcl-2 phosphorylation required for anti-apoptosis function.";  
 RL J. Biol. Chem. 272:11671-11673(1997).  
 CC [4]  
 RP DEPHOSPHORYLATION BY PP2A.  
 RX MEDLINE=99069407; PubMed=9852076;  
 RA Deng X., Ito T., Carr B., Mundy M., May W.S. Jr.;  
 RT "Reversible phosphorylation of Bcl-2 following interleukin 3 or  
 RT bryostatin 1 is mediated by direct interaction with protein  
 RT phosphatase 2A.";  
 RL J. Biol. Chem. 273:34157-34163(1998).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (APAF-1).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
 CC domains, and is necessary for anti-apoptotic activity (By  
 CC similarity). Also interacts with APAF-1 and RAF-1.  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Alpha;  
 CC IsoId=PI0417-1; Sequence=Displayed;  
 CC Name=Beta;  
 CC IsoId=PI0417-2; Sequence=VSP 000513;  
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 CC for interaction with RAF-1.  
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
 CC occurs during the G2/M phase of the cell cycle. In the absence of  
 CC growth factors, Bcl2 appears to be phosphorylated by other protein  
 CC kinases such as ERKs and stress-activated kinases.  
 CC Dephosphorylated by protein phosphatase 2A (PP2A).  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: L31532; AAA37282.1; -;  
 DR EMBL: M16506; AAA37282.1; JOINED.  
 DR EMBL: M16506; AAA37281.1; -;  
 DR PIR: B25960; TMSB1.  
 DR HSSP: Q07817; IMAZ.  
 DR MGI: 88138; Bcl2.

DR GO: GO:0008189; F:apoptosis inhibitor activity; IDA.  
 DR GO: GO:0005515; F:protein binding activity; IPI.  
 DR GO: GO:0006915; F:apoptosis; IDA.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR InterPro: IPR002475; Bcl2\_family.  
 DR InterPro: IPR004725; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRfam: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 KW Apoptosis; Alternative splicing; Transmembrane; Mitochondrion;  
 KW Phosphorylation.  
 KM DOMAIN 10 30 BH4.  
 FT DOMAIN 90 104 BH3.  
 FT DOMAIN 133 152 BH1.  
 FT DOMAIN 184 199 BH2.  
 FT TRANSMEM 209 230 POTENTIAL.  
 FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
 FT MOD\_RBS 70 70 PHOSPHORYLATION (BY PKC).  
 FT VASPLIC 193 236 DAPFLYGPSRPLPDPSPSLKTLSTALVGACITLGAYL  
 FT GHK -> VGACTIVE (in isoform Beta).  
 FT /FTId=VSP 000513.  
 SQ SEQUENCE 236 AA; 26425 MW; AA85EP6B0766BBE0A CRC64;  
 Query Match 88.6%; Score 31; DB 1; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Cy 2 DFWL 6  
 Db 208 DFWL 212  
 RESULT 8  
 ID\_BCL2\_RAT STANDARD; PRT; 236 AA.  
 AC P49950; Q62837; Q64032;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2 OR BCL-2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=94193015; PubMed=8144041;  
 RA Sato T., Irie S., Krajewski S., Reed J.C.;  
 RT "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";  
 RL Gene 140:291-292(1994).  
 CC [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Ovary;  
 RX MEDLINE=95129487; PubMed=7828536;  
 RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;  
 RT "Expression of members of the bcl-2 gene family in the immature rat  
 RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa  
 RT cell apoptosis is associated with decreased bax and constitutive  
 RT bcl-2 and bcl-x-long messenger ribonucleic acid levels.";  
 RL Endocrinology 136:232-241(1995).  
 CC [3]  
 RP SEQUENCE OF 19-172 FROM N.A.

RX MEDLINE=9505917; PubMed=7969891;  
 RA Castrén E., Ohga Y., Berzagli M.P., Tzimagiorgis G., Thoenen H.,  
 RA Lindholm D.;  
 RT "bcl-2 messenger RNA is localized in neurons of the developing and  
 adult rat brain."  
 RL Neuroscience 61:165-177(1994).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 permeability. Appears to function in a feedback loop system with  
 caspases. Inhibits caspase activity either by preventing the  
 release of cytochrome c from the mitochondria and/or by binding to  
 the apoptosis-activating factor (Apaf-1).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
 domains, and is necessary for anti-apoptotic activity (By  
 similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues, with  
 highest levels in reproductive tissues. In the adult brain,  
 expression is localized in mitral cells of the olfactory bulb,  
 granule and pyramidal neurons of hippocampus, pontine nuclei,  
 cerebellar granule neurons, and in ependymal cells. In prenatal  
 brain, expression is higher and localized in the neuroepithelium  
 and in the cortical plate.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 for interaction with RAIF-1 (By similarity).  
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 on Ser-70 by PKC is required for the anti-apoptotic activity and  
 occurs during the G2/M phase of the cell cycle. In the absence of  
 growth factors, Bcl2 appears to be phosphorylated by other protein  
 kinases such as ERKs and stress-activated kinases.  
 CC -1- PTM: Phosphorylated by protein phosphatase 2A (PP2A) (By similarity).  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 activity, causes the release of cytochrome c into the cytosol  
 promoting further caspase activity (By similarity).  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U14680; AAA53662.1; -;  
 DR EMBL: U14680; AAA53662.1; -;  
 DR EMBL: 874122; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: I53744; I53744.  
 DR PIR: I67432; I67432.  
 DR HSP: Q07817; IMAZ.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR002475; Bcl2\_family.  
 DR InterPro: IPR004725; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; Bcl-2; 1.  
 DR SMART: SMO0337; BCL; 1.  
 DR SMART: SMO0265; BH4; 1.  
 DR TIGRfam: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS00062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1; 1.

DR PROSITE: PS00063; BH4\_2; 1.  
 KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
 FT DOMAIN 10 30  
 FT DOMAIN 90 104 BH4.  
 FT DOMAIN 133 152 BH1.  
 FT DOMAIN 184 199 BH2.  
 FT TRANSMEM 209 230  
 FT SITE 34 35  
 FT MOD RES 70 72  
 FT CONFLICT 42 42  
 FT CONFLICT 157 157 A -> R (IN REF. 2).  
 FT CONFLICT 164 164 S -> Y (IN REF. 1).  
 FT CONFLICT 212 212 L -> Q (IN REF. 2).  
 SQ SEQUENCE 236 AA; 26622 MW; E7688CB9071A872A CRC64;  
 Query Match 88.6%; Score 31; DB 1; Length 236;  
 Best local Similarity 100.0%; Pred. No. 34;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DFSWL 6  
 Db 208 DFSWL 212  
 RESULT 9  
 BCL2 HUMAN STANDARD; PRT; 239 AA.  
 ID BCL2 HUMAN  
 AC P10415; P10416; Q13842; Q16197;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).  
 RA MEDLINE=86259760; PubMed=3523487;  
 RA Tsujimoto Y., Croce C.M.;  
 RT "Analysis of the structure, transcripts, and protein products of  
 bcl-2, the gene involved in human follicular lymphoma."  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).  
 RN [2]  
 RP REVISIONS TO 96; 110 AND 237.  
 RA MEDLINE=92375724; PubMed=1508712;  
 RA Buchli Y., Ewert D.L., Tsujimoto Y.;  
 RT "Isolation and characterization of the chicken bcl-2 gene: expression  
 in a variety of tissues including lymphoid and neuronal organs in  
 adult and embryo."  
 RL Nucleic Acids Res. 20:4187-4192(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
 RA MEDLINE=87002488; PubMed=2875799;  
 RA Cleary M.L., Smith S.D., Sklar J.;  
 RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-  
 2/immunoglobulin transcript resulting from the t(14;18)  
 translocation."  
 RL Cell 47:19-28(1986).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
 RA MEDLINE=88196071; PubMed=2834197;  
 RA Seto M., Jaeger U., Hockett R.D., Gruninger W., Bennett S.,  
 RA Goldman P., Korsmeyer S.J.;  
 RT "Alternative promoters and exons, somatic mutation and deregulation  
 of the bcl-2 gene in lymphoma."  
 RL EMBO J. 7:123-131(1988).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
 RA TISSUE=Testis;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klauener R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Tohilyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mallary S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywiński M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]  
 RP SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS  
 RP NON-HODGKIN'S LYMPHOMA SER-59 AND ILE-93.  
 RX MEDLINE=92096610; PubMed=1339299;  
 RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.,  
 RT "Frequent incidence of somatic mutations in translocated BCL2  
 RT oncogenes of non-Hodgkin's lymphomas.";  
 RL Blood 79:229-237(1992).  
 RN [7]  
 RP SUBCELLULAR LOCATION.  
 RX MEDLINE=91066924; PubMed=2250705;  
 RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.,  
 RT "Bcl-2 is an inner mitochondrial membrane protein that blocks  
 RT programmed cell death.";  
 RL Nature 348:334-336(1990).  
 RN [8]  
 RP MUTAGENESIS.  
 RX MEDLINE=94239528; PubMed=8183370;  
 RA Yin X.-M., Olvera Z.N., Korsmeyer S.J.,  
 RT "Bhl and Bhl domains of Bcl-2 are required for inhibition of  
 RT apoptosis and heterodimerization with Bax.";  
 RL Science 269:321-323(1994).  
 RN [9]  
 RP CLEAVAGE BY CASPASES, AND MUTAGENESIS.  
 RX MEDLINE=98057466; PubMed=9395403;  
 RA Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,  
 RT "Conversion of Bcl-2 to a Bax-like death effector by caspases.";  
 RL Science 278:1966-1988(1997).  
 RN [10]  
 RP REVIEW ON PHOSPHORYLATION.  
 RX MEDLINE=21260650; PubMed=11368354;  
 RA Ruvoio P.P., Deng X., May W.S.,  
 RT "Phosphorylation of Bcl2 and regulation of apoptosis.";  
 RL Leukemia 15:515-522(2001).  
 RN [11]  
 RP PHOSPHORYLATION BY ASK1/JNK1.  
 RX MEDLINE=20036804; PubMed=10567572;  
 RA Yamamoto K., Ichijo H., Korsmeyer S.J.,  
 RT "BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal  
 RT protein kinase pathway normally activated at G(2)/M.";  
 RL Mol. Cell. Biol. 19:8469-8478(1999).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (Apaf-1).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC domain, and is necessary for anti-apoptotic activity (By  
 CC similarity). Also interacts with Apaf-1 and Raf-1.  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular

CC membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named Isoforms=2;  
 CC Name=Alpha;  
 CC IsoId=PI0415-1; Sequence=Displayed;  
 CC Name=Beta;  
 CC IsoId=PI0415-2; Sequence=VSP 000512;  
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.  
 CC -1- DOMAIN: The Bhl domain is required for anti-apoptotic activity and  
 CC for interaction with Raf-1.  
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
 CC occurs during the G2/M phase of the cell cycle. In the absence of  
 CC growth factors, Bcl2 appears to be phosphorylated by other protein  
 CC kinases such as ERKs and stress-activated kinases.  
 CC Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the Bhl domain, has pro-apoptotic  
 CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity.  
 CC -1- DISEASE: Involved in follicular lymphoma (FL) (also known as type  
 CC II chronic lymphocytic leukemia) by a chromosomal translocation  
 CC t(14;18)(q32;q21) which involves BCL2 and immunoglobulin gene  
 CC regions. BCL2 mutations found in non-Hodgkin's lymphomas carrying  
 CC the chromosomal translocation could be attributed to the Ig  
 CC somatic hypermutation mechanism resulting in nucleotide  
 CC translocations.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
 CC -1- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -1- DATABASE: NAME=Alfa Gene. Cytogene. Oncol. Haematol.;  
 CC WWW="http://www.infobiogen.fr/services/chromcancer/Genes/BCL2ID9.html".  
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 CC -----  
 CC DR EMBL, M13994; AAAS181.1; ALT\_SEQ.  
 CC DR EMBL, M13995; AAAS181.1; ALT\_SEQ.  
 CC DR EMBL, M14745; AAAS591.1; -.  
 CC DR EMBL, X06487; CAA29778.1; -.  
 CC DR EMBL, BC027258; AAH27258.1; -.  
 CC DR EMBL, S72602; AAD14111.1; ALT\_SEQ.  
 CC DR PIR, C37332; TVHUAL.  
 CC DR PDB, 1GSM; 21-MAR-01.  
 CC DR PDB, 1GCH; 13-JUN-01.  
 CC DR GeneW; HGNC:990; BCL2.  
 CC MIM; 151430; -.  
 CC DR GO; GO:0005743; C:mitochondrial inner membrane; TAS.  
 CC DR GO; GO:0008189; F:apoptosis inhibitor activity; TAS.  
 CC DR GO; GO:0006916; P:anti-apoptosis; TAS.  
 CC DR GO; GO:0006959; P:humoral immune response; TAS.  
 CC DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.  
 CC DR GO; GO:0007049; P:oncogenesis; TAS.  
 CC DR GO; GO:0000074; P:regulation of cell cycle; TAS.  
 CC DR InterPro; IPR007072; Bcl2 BH.  
 CC DR InterPro; IPR003093; Bcl2 BH4.  
 CC DR InterPro; IPR00475; Bcl2\_Family.  
 CC DR InterPro; IPR004725; Bcl2\_Reg.  
 CC DR Pfam; PF00452; Bcl-2; 1.  
 CC DR Pfam; PF02180; BH4; 1.  
 CC DR SMART; SM00337; BCL; 1.  
 CC DR SMART; SM00265; BH4; 1.  
 CC DR TIGRFAMs; TIGR00865; bcl-2; 1.  
 CC DR PROSITE; PS5062; BCL2\_FAMILY; 1.  
 CC DR PROSITE; PS01080; BH1; 1.

DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4; 1.  
 DR PROSITE; PS50063; BH4\_2; 1.  
 KM Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane;  
 KM Mitochondrion; Phosphorylation; Chromosomal translocation;  
 KM Polymorphism; Disease mutation; 3D-structure.

Query Match 88.6%; Score 31; DB 1; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DFWL 6  
 DB 211 DFWL 215

## RESULT 10

GLGA\_DEIRA STANDARD; PRT; 444 AA.

AC Q9RWS1;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Glycogen synthase (EC 2.4.1.21) (Starch [bacterial glycogen]  
 DE synthase).  
 GN GLGA OR DRO594.  
 OS Deinococcus radiodurans.  
 OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;  
 OC Deinococcaceae; Deinococcus.  
 OX NCBI\_TaxId=1299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;  
 RX MEDLINE=20036896; PubMed=10567266;  
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
 RA Dodson R.J., Haft D.H., Gwim M.L., Nelson W.C., Richardson D.L.,  
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,  
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,  
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,  
 RA Fraser C.M.;  
 RT "Genome sequence of the radioresistant bacterium Deinococcus  
 RT radiodurans R1";  
 RL Science 286:1571-1577(1999).

CC -1- FUNCTION: Synthesizes alpha-1,4-glucan chains using ADP-glucose.  
 CC -1- CATALYTIC ACTIVITY: ADP-glucose + (1,4)-alpha-D-glucosyl(N) =  
 CC ADP + (1,4)-alpha-D-glucosyl(N+1).  
 CC -1- PATHWAY: Glycogen biosynthesis; second step.  
 CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1.  
 CC Bacterial/plant glycogen synthase subfamily.  
 CC -----  
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CC EMBL; AE001917; AAF10170.1; ALT\_INT.  
 DR TIGR; DR0594; -; 1.  
 DR HAMAP; MF\_00484; -; 1.  
 DR InterPro; IPR001296; Glyco\_trans\_1.  
 DR Pfam; PF00534; Glycos\_transf\_1; 1.  
 KM Glycogen biosynthesis; transferase; Glycosyltransferase;  
 KM Complete proteome.  
 FT BINDING 15 ADP-GLUCOSE (BY SIMILARITY).  
 SO SEQUENCE 444 AA; 48457 MW; 767605781A915302 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 444;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSW 5  
 DB 426 LDFSW 430

## RESULT 11

STC\_AQUAE STANDARD; PRT; 495 AA.

AC O67163;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Cysteineyl-cRNA synthetase (EC 6.1.1.16) (Cysteine--cRNA ligase)  
 DE (CysKs).  
 GN CYS OR AQ\_1068.  
 OS Aquifex aeolicus.  
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.  
 OX NCBI\_TaxId=63363;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VF5;  
 RX MEDLINE=98196666; PubMed=9537320;  
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Anjey M., Huber R.,  
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;  
 RT "The complete genome of the hyperthermophilic bacterium Aquifex  
 RT aeolicus";  
 RL Nature 392:353-358(1998).

CC -1- CATALYTIC ACTIVITY: ATP + L-cysteine + cRNA(Cys) = AMP +  
 CC diphosphate + L-cysteineyl-cRNA(Cys).  
 CC -1- SUBUNIT: Monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to class-I aminoacyl-cRNA synthetase family.  
 CC Strong, to methionyl-cRNA synthetase.  
 CC -----  
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CC EMBL; AE000721; AAC07125.1; -;  
 DR PIR; H70391; H70391.  
 DR HAMAP; MF\_00041; -; 1.  
 DR InterPro; IPR002308; Cys\_cRNA-synt\_1a.  
 DR InterPro; IPR001412; cRNA-synt\_1.  
 DR Pfam; PF01406; cRNA-synt\_1e; 1.  
 DR PRINTS; PR00963; TRANSYNTHCS.  
 DR TIGRPFAM; TIGR00435; CysKs; 1.  
 DR PROSITE; PS00178; AA TRNA\_LIGASE\_I; PALSE NEG.  
 KM Aminoacyl-cRNA synthetase; Protein biosynthesis; ligase; ATP-binding;  
 KM Complete proteome.  
 FT SITE 31 "HIGH" REGION.  
 FT SITE 266 "RMSK" REGION.  
 FT BINDING 269 ATP (BY SIMILARITY).  
 SO SEQUENCE 495 AA; 57135 MW; A454658B2BBA8BA4 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 495;  
 Best Local Similarity 100.0%; Pred. No. 75;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSW 5  
 DB 302 LDFSW 306

## RESULT 12

YNB8\_YEAST STANDARD; PRT; 612 AA.  
 AC P53976;

DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Hypothetical 69.6 kDa protein in HDAL-FUBI intergenic region.  
 GN YNL018C OR N2831.  
 OS Saccharomyces cerevisiae (Baker's Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Andre B., Iraqi Housaini I., Urrestazu L.A., Vlasers S.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO YEAST YNL034W.  
 CC -----  
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 CC -----  
 DR EMBL: Z71294; CAA95880.1; -.  
 DR PIR: S62930; S62930.  
 DR SGD: S0004963; YNL018C.  
 KW Hypothetical protein.  
 SQ SEQUENCE 612 AA; 69551 MW; E655B2D96317FC62 CRC64;  
 Query Match 88.6%; Score 31; DB 1; Length 612;  
 Best Local Similarity 83.3%; Pred. No. 94;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LDPSWL 6  
 Db 17 LDPSWL 22

RESULT 13  
 YND4 YEAST STANDARD; PRT; 612 AA.  
 AC P53963;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Hypothetical 69.4 kDa protein in NCE3-HRT2 intergenic region.  
 GN YNL034W OR N2740.  
 OS Saccharomyces cerevisiae (Baker's Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Duesterhoef A., Floeth M., Fritz C., Heuss-Neitzel D.,  
 RA Hilbert H., Moestl D.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO YEAST YNL018C.  
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 CC -----  
 DR EMBL: Z71310; CAA95897.1; -.  
 DR PIR: S62956; S62956.  
 DR SGD: S0004979; YNL034W.  
 KW Hypothetical protein.  
 SQ SEQUENCE 612 AA; 69373 MW; E39B7080BDE0285 CRC64;  
 Query Match 88.6%; Score 31; DB 1; Length 612;

Best Local Similarity 83.3%; Pred. No. 94;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LDPSWL 6  
 Db 17 LDPSWL 22

RESULT 14  
 VID3 AGRH STANDARD; PRT; 678 AA.  
 ID VID3 AGRH  
 AC P13463;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Protein VID3.  
 GN VID3.  
 OS Agrobacterium rhizogenes.  
 OC Plasmid pRiA4b.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.  
 NCBI\_TaxID=359;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A4;  
 RX MEDLINE=89039712; PubMed=3185501;  
 RA Hirayama T., Muranaka T., Ohkawa H., Oka A.;  
 RT "Organization and characterization of the vircD genes from  
 RT Agrobacterium rhizogenes."  
 RL Mol. Gen. Genet. 213:225-237 (1988).  
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 CC -----  
 DR EMBL: X12867; CAA1352.1; -.  
 DR PIR: S12456; S12456.  
 DR Crown gall tumor; Plasmid.  
 SQ SEQUENCE 678 AA; 72777 MW; A5BCBA58AC25532 CRC64;  
 Query Match 88.6%; Score 31; DB 1; Length 678;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DPSWL 6  
 Db 418 DPSWL 422

RESULT 15  
 VGR2 RAT STANDARD; PRT; 1343 AA.  
 ID VGR2 RAT  
 AC O08775;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)  
 DE (VEGFR-2) (Protein-tyrosine kinase receptor f1k-1) (Fetal liver kinase  
 DE 1).  
 GN KDR OR FLK1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Retina;  
 RA Wen Y., Edelman J.L., De Vries G.W., Sachs G.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.





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OM protein - protein search, using SW model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds

(without alignments)  
87.531 Million cell updates/sec

Title: US-09-643-260-11

Perfect score: 35

Sequence: 1 LDPSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96166682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR76:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	391	2 A70663	probable PPE prote
2	35	100.0	414	2 T44513	hypothetical prote
3	33	94.3	61	2 D82732	hypothetical prote
4	33	94.3	144	2 A10698	probable pathogeni
5	33	94.3	253	2 D71975	hypothetical prote
6	33	94.3	253	2 E64532	hypothetical prote
7	33	94.3	518	2 A81865	conserved hypotet
8	33	94.3	518	2 C81077	conserved hypotet
9	33	94.3	868	2 S65186	NIP80 protein - ye
10	33	94.3	1214	2 T21915	hypothetical prote
11	32	91.4	208	1 F69462	hypothetical prote
12	32	91.4	371	2 T04971	hypothetical prote
13	32	91.4	449	2 F83328	hypothetical prote
14	32	91.4	467	2 E95850	probable sodium/AI
15	32	91.4	490	2 G95953	probable amino aci
16	31	88.6	121	2 S64036	probable membrane
17	31	88.6	150	2 S74754	hypothetical prote
18	31	88.6	199	2 F82836	hypothetical prote
19	31	88.6	219	2 T30439	hypothetical prote
20	31	88.6	224	2 F70570	transforming pdkH prot
21	31	88.6	236	1 TVMSA1	transforming prote
22	31	88.6	236	2 I53744	gene bel-2 protein
23	31	88.6	236	2 JC7383	B-cell lymphoma 2
24	31	88.6	239	1 TVYUAI	transforming prote
25	31	88.6	247	2 C96594	unknown protein, 7
26	31	88.6	253	2 S65170	hypothetical prote
27	31	88.6	262	2 G72694	hypothetical prote
28	31	88.6	262	2 T31582	hypothetical prote
29	31	88.6	331	2 B95880	conserved hypotet

30	31	88.6	338	2 A82890	hypothetical prote
31	31	88.6	387	2 D88968	protein T27B7.3 (1
32	31	88.6	401	2 T44831	probable emulsan r
33	31	88.6	440	2 B71153	hypothetical prote
34	31	88.6	461	2 B83601	probable transport
35	31	88.6	467	2 A81892	hypothetical prote
36	31	88.6	472	2 B75501	glycogen synthase
37	31	88.6	484	2 T33504	hypothetical prote
38	31	88.6	495	2 H70391	cyteline-cRNA 11ga
39	31	88.6	516	2 AC1892	hypothetical prote
40	31	88.6	544	2 T45498	hypothetical prote
41	31	88.6	611	2 G83177	probable sodium/hy
42	31	88.6	612	2 S62930	hypothetical prote
43	31	88.6	612	2 S62956	hypothetical prote
44	31	88.6	641	2 A62794	hypothetical prote
45	31	88.6	641	2 F97573	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

A70663 probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999

C:Accession: A70663

R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, J.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentile, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: A70663

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-391 <COL>

A:Cross-references: GB:283860; GB:AL133456; NID:93261661; PIDN:CAB06149.1; PID:e290759;

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: PPE

Query Match	100.0%	Score 35;	DB 2;	Length 391;
Best Local Similarity	100.0%;	Pred. No. 21;		
Matches	6;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;

##### RESULT 2

T44513 hypothetical protein 5P [imported] - Pleistomonas shigelloides

C:Species: Pleistomonas shigelloides

C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jan-2000

C:Accession: T44513

R:Chida, T.; Okamura, N.; Yoshida, Y.; Ohtani, K.; Arakawa, E.; Watanabe, H.

submitted to the EMBL Data Library, April 1999

A:Description: Complete DNA sequence of the O-antigen (rfb) gene cluster in Pleistomonas

A:Reference number: Z22786

A:Accession: T44513

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-414 <CHI>

A:Cross-references: EMBL:AB025970; PIDN:BA085010.1

A:Experimental source: ATCC 14029

Query Match	100.0%	Score 35;	DB 2;	Length 414;
Best Local Similarity	100.0%;	Pred. No. 22;		
Matches	6;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;

QY 1 LDPSWL 6  
 DB 175 LDPSWL 180

## RESULT 3

D82732  
 hypothetical protein XP1033 [imported] - *Xylella fastidiosa* (strain 945c)  
 C/Species: *Xylella fastidiosa*  
 C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C/Accession: D82732  
 R:Anonymous. The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing  
 Nature 406, 151-157, 2000  
 A/Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.  
 A/Reference number: A82515; PMID:20365717; PMID:10910347  
 A/Note: for a complete list of authors see reference number A59328 below  
 A/Accession: D82732  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-61 <STM>  
 A/Cross-references: GB:AE003940; GB:AE003849; NID:99105966; PIDN:AA83843.1; GSPDB:GN001  
 A/Experimental source: strain 945c  
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Agencio, M.; Alvarenga, R.; A  
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, H  
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.F.; Ferreira, A.J.S.  
 submitted to Genbank, June 2000  
 A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm  
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.B.; Laizy  
 Chado, M.A.; Madeira, A.M.B.N.; Madeira, M.F.; Marino, C.L.; Marques, M.V.; Martins, E  
 A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
 R.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A  
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawaasak  
 M.; Teuhako, M.H.; Vallada, H.; Van Sluyk, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
 A/Reference number: A59328  
 A/Content: annotation  
 C/Genetic: 8  
 A/Genes: XP1033

Query Match 94.3%; Score 33; DB 2; Length 61;  
 Best Local Similarity 83.3%; Pred. No. 6.9;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

## RESULT 4

A10698  
 probable pathogenicity island protein sscB [imported] - *Salmonella enterica* subsp. enter  
 C/Species: *Salmonella enterica* subsp. *enterica* serovar Typh  
 A/Note: this species has also been called *Salmonella typhi*  
 C/Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
 C/Accession: A10698  
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
 Ch, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
 S.; Moule, S.; O'Garra, P.  
 Nature 413, 848-852, 2001  
 A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skellton, J.; Stevens, K.;  
 A/Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov  
 A/Reference number: AB0502; MUID:21534947; PMID:11677608  
 A/Accession: A10698  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-144 <PAR>  
 A/Cross-references: GB:AL513382; PIDN:CAD01962.1; PID:G16502804; GSPDB:GN00176  
 C/Genetic: 8  
 A/Genes: sscB

Query Match 94.3%; Score 33; DB 2; Length 144;  
 Best Local Similarity 83.3%; Pred. No. 17;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6  
 DB 45 LDPSWL 50

## RESULT 5

D71975  
 hypothetical protein jhp0093 - *Helicobacter pylori* (strain J99)  
 C/Species: *Helicobacter pylori*  
 A/Variety: strain J99  
 C/Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 08-Oct-1999  
 C/Accession: D71975  
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Dolg, P.C.; Smith, D.R  
 i Ives, C.; Gibson, R.; Merberg, D.; Miller, S.D.; Jlang, Q.; Taylor, D.B.; Vovis, G.F.;  
 Nature 397, 176-180, 1999  
 A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric pa  
 A/Reference number: A71800; MUID:99120557; PMID:9923682  
 A/Accession: D71975  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-253 <ARN>  
 A/Cross-references: GB:AE001448; GB:AE001439; NID:94154594; PIDN:AA05674.1; PID:94154  
 A/Experimental source: strain J99  
 C/Genetic: 8  
 A/Genes: jhp0093

Query Match 94.3%; Score 33; DB 2; Length 253;  
 Best Local Similarity 83.3%; Pred. No. 32;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

## RESULT 6

B64532  
 hypothetical protein HP0101 - *Helicobacter pylori* (strain 26695)  
 C/Species: *Helicobacter pylori*  
 C/Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 08-Oct-1999  
 C/Accession: B64532  
 R:omb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.  
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khajak, H.G.; Glodek, A.; McKen  
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Welden, J.M.; Fujii, C.; Bowman, C.; Watney, J  
 Nature 388, 539-547, 1997  
 A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C  
 A/Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.  
 A/Reference number: A64520; MUID:97394467; PMID:9252185  
 A/Accession: B64532  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Genetic: 8  
 A/Molecule type: DNA  
 A/Residues: 1-253 <TOM>  
 A/Cross-references: GB:AE000532; GB:AE000511; NID:92313184; PIDN:AA07180.1; PID:92313;  
 C/Genetic: 8  
 A/Start codon: TTG

Query Match 94.3%; Score 33; DB 2; Length 253;  
 Best Local Similarity 83.3%; Pred. No. 32;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

## RESULT 7

AB1865  
 conserved hypothetical integral membrane protein NMA1694 [imported] - *Neisseria mening*;  
 C/Species: *Neisseria meningitidis*  
 C/Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
 C/Accession: AB1865  
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mori

Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000  
 A>Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.  
 A:Reference number: AB1775; UID:2022556; PMID:10761919  
 A:Accession: AB1865  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-518 <PAR>  
 A:Cross-references: GB:AL62756; GB:AL57959; NID:G7380091; PIDN:CA864922.1; PID:G738033  
 A:Experimental source: serogroup A, strain Z2491  
 A:Genetics:  
 A:Gene: NMB1694

Query Match 94.3%; Score 33; DB 2; Length 518;  
 Best Local Similarity 83.3%; Pred. No. 70;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6  
 Db 1 MDPSWL 6

## RESULT 8

conserved hypothetical protein NMB1485 (imported) - *Neisseria meningitidis* (strain MC58  
 C:Species: *Neisseria meningitidis*  
 C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
 C:Accession: C81077  
 R:Retcelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
 Hickey, B.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
 Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizsa, M.  
 Science 287, 1889-1815, 2000  
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Frazer, C.M.; Moxon, E.R.; Rappuoli, R.; VE  
 A>Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.  
 A:Reference number: AB1000; UID:20175755; PMID:10710307  
 A:Accession: C81077  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-518 <RET>  
 A:Cross-references: GB:AE002498; GB:AE002098; NID:G7226724; PIDN:AAFA1841.1; PID:G722672  
 A:Experimental source: serogroup B, strain MC58  
 A:Genetics:  
 A:Gene: NMB1485

Query Match 94.3%; Score 33; DB 2; Length 518;  
 Best Local Similarity 83.3%; Pred. No. 70;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6  
 Db 1 MDPSWL 6

## RESULT 9

NIP80 protein - yeast (*Saccharomyces cerevisiae*)  
 N:Alternate names: protein P2279; protein YPL174c  
 C:Species: *Saccharomyces cerevisiae*  
 C>Date: 10-Dec-1994 #sequence\_revision 31-May-1996 #text\_change 05-Dec-1997  
 C:Accession: S65186; S34343  
 R:Beneš, V.; Reehmann, S.; Nentwich, U.; Vogt, H.; Ansozge, W.  
 submitted to the Protein Sequence Database, May 1996  
 A:Reference number: S65183  
 A:Accession: S65186  
 A:Molecule type: DNA  
 A:Residues: 1-868 <BEN>  
 A:Cross-references: EMBL:Z73530; NID:G1370366; PID:G246907; PID:G1370367; MIPS:YPL174c  
 A:Experimental source: strain S288C (AB872)  
 R:Schlueder, G.; Silver, P.A.  
 submitted to the EMBL Data Library, May 1993  
 A:Reference number: S34342  
 A:Accession: S34343  
 A:Molecule type: DNA

A:Residues: 169-429, 'V', 431-868 <SCH>  
 A:Cross-references: EMBL:X72227  
 A:Genetics:  
 A:Gene: SGD:NIP100; NIP80  
 A:Cross-references: MIPS:YPL174c; SGD:S0006095  
 A:Map position: 16L  
 C:Keywords: transmembrane protein  
 F:574-590/Domain: transmembrane #status predicted <TM>

Query Match 94.3%; Score 33; DB 2; Length 868;  
 Best Local Similarity 83.3%; Pred. No. 1,2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6  
 Db 782 IDPSWL 787

## RESULT 10

hypothetical protein F37D6.1 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T21915  
 R:McMurray, A.  
 submitted to the EMBL Data Library, June 1996  
 A:Reference number: Z19487  
 A:Accession: T21915  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1214 <WIL>  
 A:Cross-references: EMBL:Z75540; PIDN:CAA99847.1; GSPDB:GN00019; CESP:F37D6.1  
 A:Experimental source: clone F37D6  
 A:Genetics:  
 A:Gene: CESP:F37D6.1  
 A:Map position: 1  
 A:Intons: 43/1; 59/3; 103/3; 149/2; 230/3; 278/3; 313/1; 439/2; 489/3; 571/1; 625/2; 6

Query Match 94.3%; Score 33; DB 2; Length 1214;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6  
 Db 772 LDPSWI 777

## RESULT 11

hypothetical protein AF1703 - *Archaeoglobus fulgidus*  
 C:Species: *Archaeoglobus fulgidus*  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: F69462  
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
 Glodok, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
 Nature 390, 364-370, 1997  
 A:Authors: Uteback, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S  
 Smith, H.O.; Moese, C.R.; Venter, J.C.  
 A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae  
 A:Reference number: A69250; UID:98049343; PMID:9389475  
 A:Accession: F69462  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-208 <KLE>  
 A:Cross-references: GB:AE000986; GB:AE000782; NID:G2689309; PIDN:AA89558.1; PID:G26488  
 C:Superfamily: Mechanobacterium thermoautotrophicum conserved hypothetical protein MTH1

Query Match 91.4%; Score 32; DB 1; Length 208;  
 Best Local Similarity 83.3%; Pred. No. 41;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPSWL 6

Db 155 LDPFAML 160

## RESULT 12

hypothetical protein T16L1.30 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 04-Mar-2000  
C/Accession: T04971

R/Author: M. Obermaier, B. Deutschenbaue, S. Piravandi, E. Hohetzel, J. Mewes, H.W. ;  
submitted to the Protein Sequence Database, November 1998

A/Reference number: 215393

A/Accession: T04971

A/Molecule type: DNA

A/Residues: 1-371 <BEV>

A/Cross-references: EMBL:AL031394

A/Genetics:

A/Map position: 4

A/Intons: 69/1; 83/3; 123/3; 176/2; 201/2; 224/3; 275/3; 312/1; 333/1

A/Note: T16L1.30

C/Superfamily: Arabidopsis thaliana hypothetical protein T16L1.30

## Query Match

Best Local Similarity 91.4%; Score 32; DB 2; Length 371;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPFAML 6  
Db 325 LDPFAML 330

## RESULT 13

probable sodium/alanine symporter PA2533 [imported] - Pseudomonas aeruginosa (strain PAO C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C/Accession: F83328

R/Author: C.K. Pham, X.Q. Erwin, A.L. Misoguchi, S.D. Warren, P. Hickey, M.J. Bradman, S. Yuan, Y. Brody, L.L. Coulter, S.N. Folger, K.R. Kas, A. Larbig, K. Lam, ; Lory, S. Olson, M.V.

A/Residues: 1-449 <STO>

A/Cross-references: GB:AE004681; GB:AE004091; NID:99948587; PIDN:AA005921.1; GSPDB:GN001

A/Genetics:

A/Map position: 4

A/Intons: 69/1; 83/3; 123/3; 176/2; 201/2; 224/3; 275/3; 312/1; 333/1

A/Note: T16L1.30

C/Superfamily: Arabidopsis thaliana hypothetical protein T16L1.30

## Query Match

Best Local Similarity 91.4%; Score 32; DB 2; Length 449;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPFAML 6  
Db 407 LDPFAML 412

## RESULT 14

probable amino acid carrier protein [imported] - Sinorhizobium meliloti (strain 1021) me C/Species: Sinorhizobium meliloti

C/Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
C/Accession: E95850

R/Author: T.M. Weidner, S. Wong, K. Buhmester, J. Chain, P. Vorholter, F.J. Hernandez, Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A/Residues: 1-449 <STO>

A/Cross-references: GB:AE004681; GB:AE004091; NID:99948587; PIDN:AA005921.1; GSPDB:GN001

A/Genetics:

A/Map position: 4

A/Intons: 69/1; 83/3; 123/3; 176/2; 201/2; 224/3; 275/3; 312/1; 333/1

A/Note: T16L1.30

C/Superfamily: Arabidopsis thaliana hypothetical protein T16L1.30

## Query Match

Best Local Similarity 91.4%; Score 32; DB 2; Length 449;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPFAML 6  
Db 407 LDPFAML 412

A/Reference number: A95842; MUID:21396508; PMID:11461431

A/Accession: E95850

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-467 <KUR>

A/Cross-references: GB:AL591985; PIDN:CA048469.1; PID:G15139941; GSPDB:GN00167

A/Experimental source: strain 1021, megaplasmid pSymb

R/Author: F. Finan, T.M. Long, S.R. Puhler, A. Abola, P. Ampe, F. Barloy-Hubler, D. J. Chain, P. Cowie, A. Davis, R.W. Dreano, S. Federpiet, N.A. Fisher, R.F. L. Hymn, R.W. Jones, T.

A/Residues: 1-467 <KUR>

A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kise, E.; Komp, C.; Lelaure, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, I.

A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A/Reference number: A96039; MUID:21368234; PMID:11474104

A/Contents: annotation

A/Genetics:

A/Map position: 4

A/Intons: 69/1; 83/3; 123/3; 176/2; 201/2; 224/3; 275/3; 312/1; 333/1

A/Note: T16L1.30

C/Superfamily: Arabidopsis thaliana hypothetical protein T16L1.30

## Query Match

Best Local Similarity 91.4%; Score 32; DB 2; Length 467;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPFAML 6  
Db 407 LDPFAML 412

## RESULT 15

probable membrane-anchored protein [imported] - Sinorhizobium meliloti (strain 1021) me C/Species: Sinorhizobium meliloti

C/Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
C/Accession: G95953

R/Author: T.M. Weidner, S. Wong, K. Buhmester, J. Chain, P. Vorholter, F.J. Hernandez, Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A/Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing end

A/Reference number: A95842; MUID:21396508; PMID:11461431

A/Accession: G95953

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-490 <KUR>

A/Cross-references: GB:AL591985; PIDN:CA049295.1; PID:G15140781; GSPDB:GN00167

A/Experimental source: strain 1021, megaplasmid pSymb

R/Author: F. Finan, T.M. Long, S.R. Puhler, A. Abola, P. Ampe, F. Barloy-Hubler, D. J. Chain, P. Cowie, A. Davis, R.W. Dreano, S. Federpiet, N.A. Fisher, R.F. L. Hymn, R.W. Jones, T.

A/Residues: 1-467 <KUR>

A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kise, E.; Komp, C.; Lelaure, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, I.

A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A/Reference number: A96039; MUID:21368234; PMID:11474104

A/Contents: annotation

A/Genetics:

A/Map position: 4

A/Intons: 69/1; 83/3; 123/3; 176/2; 201/2; 224/3; 275/3; 312/1; 333/1

A/Note: T16L1.30

C/Superfamily: Arabidopsis thaliana hypothetical protein T16L1.30

## Query Match

Best Local Similarity 91.4%; Score 32; DB 2; Length 490;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDPFAML 6  
Db 466 VDFPAML 471

Search completed: February 18, 2004, 14:38:46

Job time : 8.5921 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds  
(without alignments)  
75.239 Million cell updates/sec

Title: US-09-643-260-11

Perfect score: 35

Sequence: 1 LDFSWL 6

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

801455

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	6	10	US-09-847-940B-11
2	35	100.0	6	11	US-09-847-946A-11
3	35	100.0	6	11	US-09-847-946A-42
4	35	100.0	6	11	US-09-847-946A-84
5	35	100.0	7	11	US-09-847-946A-88
6	35	100.0	8	11	US-09-847-946A-81
7	35	100.0	8	11	US-09-847-946A-89
8	35	100.0	9	11	US-09-847-946A-80
9	35	100.0	9	11	US-09-847-946A-83
10	35	100.0	9	11	US-09-847-946A-86
11	35	100.0	9	11	US-09-847-946A-87
12	35	100.0	10	11	US-09-847-946A-82
13	35	100.0	10	11	US-09-847-946A-85
14	35	100.0	11	11	US-09-847-946A-79
15	33	94.3	265	10	US-09-881-752A-368

16	33	94.3	868	12	US-10-369-493-22465	Sequence 22465, A
17	32	91.4	6	10	US-09-847-940B-12	Sequence 12, Appl
18	32	91.4	6	11	US-09-847-946A-12	Sequence 12, Appl
19	32	91.4	6	11	US-09-847-946A-95	Sequence 95, Appl
20	32	91.4	7	11	US-09-847-946A-99	Sequence 99, Appl
21	32	91.4	8	11	US-09-847-946A-92	Sequence 92, Appl
22	32	91.4	8	11	US-09-847-946A-100	Sequence 100, Appl
23	32	91.4	9	11	US-09-847-946A-91	Sequence 91, Appl
24	32	91.4	9	11	US-09-847-946A-94	Sequence 94, Appl
25	32	91.4	9	11	US-09-847-946A-97	Sequence 97, Appl
26	32	91.4	9	11	US-09-847-946A-98	Sequence 98, Appl
27	32	91.4	10	11	US-09-847-946A-93	Sequence 93, Appl
28	32	91.4	10	11	US-09-847-946A-96	Sequence 96, Appl
29	32	91.4	11	11	US-09-847-946A-90	Sequence 90, Appl
30	31	88.6	106	12	US-09-864-408A-5624	Sequence 5624, Ap
31	31	88.6	236	15	US-10-277-693A-11	Sequence 11, Appl
32	31	88.6	239	8	US-08-726-211-5	Sequence 5, Appl
33	31	88.6	239	12	US-10-141-618-12	Sequence 12, Appl
34	31	88.6	239	12	US-10-053-645A-21	Sequence 21, Appl
35	31	88.6	239	12	US-10-387-961A-5	Sequence 5, Appl
36	31	88.6	239	15	US-10-101-482-12	Sequence 12, Appl
37	31	88.6	239	15	US-10-277-693A-10	Sequence 10, Appl
38	31	88.6	239	15	US-10-072-830-2	Sequence 2, Appl
39	31	88.6	472	12	US-10-369-493-23432	Sequence 23432, A
40	31	88.6	662	10	US-09-924-358-11	Sequence 11, Appl
41	31	88.6	662	12	US-10-410-764-11	Sequence 11, Appl
42	31	88.6	1398	12	US-10-021-571-6	Sequence 6, Appl
43	30	85.7	6	10	US-09-847-940B-2	Sequence 2, Appl
44	30	85.7	6	11	US-09-847-946A-2	Sequence 2, Appl
45	30	85.7	6	11	US-09-847-946A-33	Sequence 33, Appl

#### ALIGNMENTS

RESULT 1  
US-09-847-940B-11  
; Sequence 11, Application US/09847940B  
; Patent No. US2002015600A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J.  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-117CP  
; CURRENT APPLICATION NUMBER: US/09/847, 940B  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-11

Query Match 100.0%; Score 35; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6  
|||||  
Db 1 LDFSWL 6

RESULT 2  
US-09-847-946A-11  
; Sequence 11, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J

```
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-11
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Query Match          100.0%; Score 35; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LDFSWL 6
Db 1 LDFSWL 6
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RESULT 3
US-09-847-946A-42
Sequence 42, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
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```
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 42
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-42
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Query Match          100.0%; Score 35; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 LDFSWL 6
Db 1 LDFSWL 6
```

```
RESULT 4
US-09-847-946A-84
Sequence 84, Application US/09847946A
Publication No. US20030054999A1
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GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 84
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-84
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Query Match          100.0%; Score 35; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 LDFSWL 6
Db 1 LDFSWL 6
```

```
RESULT 5
US-09-847-946A-88
Sequence 88, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 88
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-88
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Query Match          100.0%; Score 35; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 LDFSWL 6
Db 1 LDFSWL 6
```

```
RESULT 6
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US-09-847-946A-81  
; Sequence 81, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 81  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-81

Query Match 100.0%; Score 35; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6  
Db 3 LDFSWL 8

RESULT 7  
US-09-847-946A-89  
; Sequence 89, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 89  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-89

Query Match 100.0%; Score 35; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6  
Db 1 LDFSWL 6

RESULT 8  
US-09-847-946A-80  
; Sequence 80, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 80  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-80

Query Match 100.0%; Score 35; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6  
Db 1 LDFSWL 6

RESULT 9  
US-09-847-946A-83  
; Sequence 83, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 83  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-83

Query Match 100.0%; Score 35; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6  
| | | | |  
Db 1 LDFSWL 6

## RESULT 10

US-09-847-946A-86  
; Sequence 86, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 86  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-86

Query Match Best Local Similarity 100.0%; Score 35; DB 11; Length 9;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6  
| | | | |  
Db 3 LDFSWL 8

## RESULT 11

US-09-847-946A-87  
; Sequence 87, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 87  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-87

Query Match 100.0%; Score 35; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6  
| | | | |  
Db 2 LDFSWL 7

## RESULT 12

US-09-847-946A-82  
; Sequence 82, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 82  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-82

Query Match Best Local Similarity 100.0%; Score 35; DB 11; Length 10;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDFSWL 6  
| | | | |  
Db 2 LDFSWL 7

## RESULT 13

US-09-847-946A-85  
; Sequence 85, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 85  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-85



US-09-847-946A-85

Query Match 100.0%; Score 35; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6  
 |||||  
 DB 3 LDFSWL 8

RESULT 14

US-09-847-946A-79  
 ; Sequence 79, Application US/09847946A  
 ; Publication No. US2003005499A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: May, Michael J  
 ; APPLICANT: Ghosh, Sanjay  
 ; APPLICANT: Pindels, Mark A  
 ; APPLICANT: Phillips, Kathryn  
 ; APPLICANT: Hannig, Gerhard  
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
 ; FILE REFERENCE: PPI-119  
 ; CURRENT APPLICATION NUMBER: US/09/847,946A  
 ; PRIOR FILING DATE: 2001-05-02  
 ; PRIOR APPLICATION NUMBER: 60/201,261  
 ; PRIOR FILING DATE: 2000-05-02  
 ; PRIOR APPLICATION NUMBER: 09/643,260  
 ; PRIOR FILING DATE: 2000-08-22  
 ; NUMBER OF SEQ ID NOS: 160  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 79  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: MEMO binding  
 ; OTHER INFORMATION: sequence  
 US-09-847-946A-79

Query Match 100.0%; Score 35; DB 11; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6  
 |||||  
 DB 3 LDFSWL 8

RESULT 15

US-09-881-752A-368  
 ; Sequence 368, Application US/09881752A  
 ; Patent No. US20020115078A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kleantous, Harold  
 ; APPLICANT: Al-Garawi, Amal  
 ; APPLICANT: Miller, Charles  
 ; APPLICANT: Tomb, Jean-Francois  
 ; APPLICANT: Oomen, Raymond P.  
 ; TITLE OF INVENTION: Identification of Polynucleotides  
 ; TITLE OF INVENTION: Encoding No. US20020115078A1 Helicobacter Polypeptides in the  
 ; TITLE OF INVENTION: Genome  
 ; FILE REFERENCE: 06132/041002  
 ; CURRENT APPLICATION NUMBER: US/09/881,752A  
 ; CURRENT FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: US 08/833,457  
 ; PRIOR FILING DATE: 1997-04-01  
 ; NUMBER OF SEQ ID NOS: 370  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 368  
 ; LENGTH: 265  
 ; TYPE: PRT  
 ; ORGANISM: Helicobacter pylori

US-09-881-752A-368

Query Match 94.3%; Score 33; DB 10; Length 265;  
 Best Local Similarity 83.3%; Pred. No. 3.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6  
 |||||  
 DB 161 LDFSWI 166

Search completed: February 18, 2004, 15:41:58  
 Job time : 16.7529 secs



FF	02-MAY--2001; 2001WO-US40654.
XX	
PR	02-MAY--2000; 2000US-201261P.
PR	22-AUG--2000; 2000US-0643260.
XX	
PA	(UYVA ) UNIV YALE.
XX	
PI	May MJ, Ghosh S;
DR	WPI, 2002-179350/23.
XX	
PT	Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT	inflammatory disorders, osteoporosis and cancer, comprising contacting a
PT	cell with an anti-inflammatory compound comprising at least one NEMO
XX	binding domain -
PS	Claim 23; Page 44; 82pp; English.
XX	
CC	The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC	comprising contacting a cell with an anti-inflammatory compound
CC	(ABB087125-ABB08742) comprising at least one NEMO binding domain
CC	(ABB877113). The compound has acts through selective inhibition of
CC	cytokine-mediated NF-kB activation by blocking the interaction of NEMO
CC	with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC	interaction results in inhibition of IKKbeta kinase activation and
CC	subsequent decreased phosphorylation of IkappaB. The compound may also
CC	act (directly or indirectly) by blocking the recruitment of leukocytes
CC	into sites of acute and chronic inflammation, by down-regulating the
CC	expression of E-selectin on leukocytes or by blocking osteoclast
CC	differentiation. The compound is useful in treating NF-kB mediated
CC	conditions, where the condition is an inflammatory disorder, an
CC	autoimmune disease, transplant rejection, osteoporosis, cancer, an
CC	Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC	telangiectasia. The inflammatory disorder is asthma, allergies,
CC	urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
CC	rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
CC	bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC	burns. The inflammatory disorder may also be dermatitis, eczema,
CC	psoriasis, osteoarthritis, psoriatic arthritis, lupus and
CC	spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC	polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC	cryoglobulinaemia or multiple sclerosis. For chronic viral infections
CC	caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
CC	diseases include HIV and influenza. The compound may also be useful for
CC	treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC	sunburn or aging. The compound may be used to replace corticosteroids in
CC	any application in which corticosteroids are used, including
CC	immunosuppression in transplants and cancer therapy. Also for identifying
CC	anti-inflammatory compounds and for diagnosis of an inflammatory disorder.
CC	The compound may be administered alone or in combination with other known
CC	anti-inflammatory agents. The present sequence is that of a mutated NEMO
CC	binding domain of IKKbeta.
XX	
XX	Sequence 6 AA;
QY	Query Match 100.0%; Score 35; DB 23; Length 6;
DB	Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 LDFSWL 6
DB	1 LDFSWL 6
XX	
RESULT 2	
AA048516	
ID	AA048516 standard; Peptide; 6 AA.
XX	
AA048516;	
XX	
DT	20-MAR--2002 (first entry)
DE	NBD mutant peptide SEQ ID NO 11.

XX Antinflammatory; antiaesthetic; cytosarctic; antiporiatic; nootropic;  
 KW antineumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW anti-allergy; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NKkappa; Ikappa kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 PF 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRACTIS PHARM INC.  
 PA (UYTA ) UNIV YALE.  
 PI May MJ, Ghosh S, Findeis MA, Phillips K,  
 DR WPL; 2002-121889/16.  
 XX  
 PT Novel antinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 PT  
 XX  
 PS Example 6; Page 47; 88pp; English.  
 CC The invention relates to an antinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antinflammatory compounds have antiaesthetic,  
 CC cytosarctic, antiporiatic, antineumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX  
 XX Sequence 6 AA:  
 SQ  
 Query Match 100.0%; Score 35; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9,3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDPSWT 6  
 |||||  
 D6 1 LDPSWT 6  
 |||||

XX AC AAM48539;  
 XX DT 20-MAR-2002 (first entry)  
 XX DE Anti-inflammatory peptide SEQ ID NO 42.  
 XX KM Antiinflammatory; antiasthmatic; cytoskeletal; antiporiatic; nootropic;  
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX OS Synthetic.  
 XX PN WO200183554-A2.  
 XX PD 08-NOV-2001.  
 XX PF 02-MAY-2001; 2001WO-US14346.  
 XX PR 02-MAY-2000; 2000US-201261P.  
 XX PR 22-AUG-2000; 2000US-0643260.  
 XX PA (PRAE-) PRAECIS PHARM INC.  
 XX PA (UYVA ) UNIV YALE.  
 XX PI May MJ, Ghosh S, Pindels MA, Phillips K;  
 XX DR WPI; 2002-121889/16.  
 XX PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX PS Claim 6; Page 61; 88pp; English.  
 XX CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48519). The antiinflammatory compounds have antiasthmatic,  
 CC cytoskeletal, antiporiatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX SQ Sequence 6 AA;  
 Query Match 100.0%; Score 35; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 LDFSWL 6  
 |||||

DB 1 LDFSWL 6  
 RESULT 4  
 ID AAM48581  
 ID AAM48581 standard; Peptide; 6 AA.  
 XX AC AAM48581;  
 XX DT 20-MAR-2002 (first entry)  
 XX DE Anti-inflammatory peptide SEQ ID NO 84.  
 XX KM Antiinflammatory; antiasthmatic; cytoskeletal; antiporiatic; nootropic;  
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX OS Synthetic.  
 XX PN WO200183554-A2.  
 XX PD 08-NOV-2001.  
 XX PF 02-MAY-2001; 2001WO-US14346.  
 XX PR 02-MAY-2000; 2000US-201261P.  
 XX PR 22-AUG-2000; 2000US-0643260.  
 XX PA (PRAE-) PRAECIS PHARM INC.  
 XX PA (UYVA ) UNIV YALE.  
 XX PI May MJ, Ghosh S, Pindels MA, Phillips K;  
 XX DR WPI; 2002-121889/16.  
 XX PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX PS Claim 6; Page 62; 88pp; English.  
 XX CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48519). The antiinflammatory compounds have antiasthmatic,  
 CC cytoskeletal, antiporiatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDPFWL 6  
 1 LDPFWL 6  
 Db 1 LDPFWL 6

RESULT 5  
 ABU08426  
 ID ABU08426 standard; peptide; 6 AA.  
 XX  
 AC ABU08426;  
 XX  
 DT 12-JUN-2003 (first entry)  
 XX  
 DE Human NEMO binding site (NBD) mutant peptide #9.  
 KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;  
 KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;  
 KW nuclear factor-kappaB induction; inflammatory disorder;  
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;  
 KW atherosclerosis; viral infection; Ataxia telangiectasia;  
 KW translocation detection; immunosuppressive; osteopathic;  
 KW cytostatic; neuroprotective; antiatherosclerotic; virucide;  
 KW vasotropic; antirheumatic; antiarthritic; mutant; mutein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN US2002156000-A1.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 02-MAY-2001; 2001US-0847940.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (MAYM/) MAY M J.  
 PA (GHOSH/) GHOSH S.  
 XX  
 PI May MJ, Ghosh S;  
 XX  
 DR WPI; 2003-209142/20.  
 XX  
 PT Novel antiinflammatory peptide compounds comprising NEMO binding  
 PT domain, useful for modulating NF-kappaB induction in a cell and for  
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,  
 PT psoriasis, vasculitis -  
 XX  
 PS Claim 22; Page 17; 47pp; English.  
 XX  
 CC The present invention relates to antiinflammatory compounds comprising  
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are  
 CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha  
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention  
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction  
 CC in a cell, where the compounds are capable of blocking the interaction  
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The  
 CC antiinflammatory compound further comprises at least one membrane  
 CC translocation domain. The compounds are useful for treating  
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia  
 CC telangiectasia, and for translocation detection. The compounds of  
 CC the invention block NF-kappaB induction by IKK but do not inhibit  
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human  
 CC NBD mutant peptides.  
 CC  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 35; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDPFWL 6  
 1 LDPFWL 6  
 Db 1 LDPFWL 6

RESULT 6  
 AAM48585  
 ID AAM48585 standard; Peptide; 7 AA.  
 XX  
 AC AAM48585;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 88.  
 KW Antiinflammatory; antirheumatic; cytostatic; antipsoriatic; neurotropic;  
 KW antirheumatic; antirheumatic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA-) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Finkel MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48585-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antirheumatic,  
 CC cytostatic, antipsoriatic, antirheumatic, antirheumatic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC neurotropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC psoriasis, autoimmune diseases such as lupus, polyarthritis, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 100.0%; Score 35; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSWL 6  
 |||||  
 Db 1 LDFSWL 6

RESULT 7  
 AAM48578  
 ID AAM48578 standard; Peptide; 8 AA.  
 XX  
 AC AAM48578;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 81.  
 XX  
 KM Antiinflammatory; antiaesthetic; cytostatic; antiporiatic; nootropic;  
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
 CC cytostatic, antiporiatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 35; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSWL 6  
 |||||  
 Db 3 LDFSWL 8

RESULT 8  
 AAM48586  
 ID AAM48586 standard; Peptide; 8 AA.  
 XX  
 AC AAM48586;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 89.  
 XX  
 KM Antiinflammatory; antiaesthetic; cytostatic; antiporiatic; nootropic;  
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
 CC cytostatic, antiporiatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The



PT psoriasis -  
 XX Claim 6; Page 62; 88pp; English.  
 XX  
 XX The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytostatic, antiproliferative, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX SQ Sequence 9 AA;  
 XX  
 XX Query Match 100.0%; Score 35; DB 23; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 LDPSWL 6  
 XX |||||  
 Db 1 LDPSWL 6  
 XX  
 XX RESULT 11  
 XX AAM48583  
 XX ID AAM48583 standard; Peptide; 9 AA.  
 XX  
 AC AAM48583;  
 XX  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 86.  
 XX  
 KW Antiinflammatory; antiasthmatic; cytostatic; antiproliferative; neurotropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 XX Synthetic.  
 XX  
 XX PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 XX  
 XX 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 XX (UYVA ) UNIV YALE.  
 XX  
 XX May MJ, Ghosh S, Fandels MA, Phillips K,  
 PI

XX DR WPI; 2002-121889/16.  
 XX  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 XX Claim 6; Page 62; 88pp; English.  
 XX  
 XX The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM4645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytostatic, antiproliferative, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX SQ Sequence 9 AA;  
 XX  
 XX Query Match 100.0%; Score 35; DB 23; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 LDPSWL 6  
 XX |||||  
 Db 3 LDPSWL 8  
 XX  
 XX RESULT 12  
 XX AAM48584  
 XX ID AAM48584 standard; Peptide; 9 AA.  
 XX  
 AC AAM48584;  
 XX  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 87.  
 XX  
 KW Antiinflammatory; antiasthmatic; cytostatic; antiproliferative; neurotropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 XX Synthetic.  
 XX  
 XX PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 XX (UYVA ) UNIV YALE.  
 XX  
 XX May MJ, Ghosh S, Fandels MA, Phillips K,  
 PI



PR 22-AUG-2000; 2000US-0643260.  
 XX (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 XX  
 PI May MJ, Ghosh S, Findels MA, Phillips K,  
 XX WPI; 2002-121889/16.  
 XX  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 XX The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytostatic, antipsoriatic, antiinflammatory, antiarthritic, osteoprotective,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 CC  
 SQ Sequence 9 AA;  
 XX  
 XX  
 Query Match 100.0%; Score 35; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6  
 |||||  
 Db 2 LDFSWL 7

RESULT 13  
 AAM48579  
 ID AAM48579 standard; Peptide; 10 AA.  
 XX  
 AC AAM48579;  
 XX  
 XX 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 82.  
 XX  
 XX Antiinflammatory; antiasthmatic; cytostatic; antibacterial; nootropic;  
 KM antirheumatic; antiarthritic; osteoprotective; antiatherosclerotic;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 KM  
 XX  
 OS Synthetic.  
 XX  
 XX  
 PN W0200183554-A2.

XX 08-NOV-2001.  
 PD  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 PF  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findels MA, Phillips K,  
 XX WPI; 2002-121889/16.  
 XX  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 XX The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytostatic, antipsoriatic, antiinflammatory, antiarthritic, osteoprotective,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 CC  
 SQ Sequence 10 AA;  
 XX  
 XX  
 Query Match 100.0%; Score 35; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6  
 |||||  
 Db 2 LDFSWL 7

RESULT 14  
 AAM48582  
 ID AAM48582 standard; Peptide; 10 AA.  
 XX  
 AC AAM48582;  
 XX  
 XX 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 85.  
 XX  
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;  
 KM antirheumatic; antiarthritic; osteoprotective; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM

KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KV	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX	Synthetic.
OS	
XX	WO200183554-A2.
PN	
PD	08-NOV-2001.
XX	
PP	02-MAY-2001; 2001WO-US14346.
XX	
XX	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-0643260.
XX	
PA	(PRAE-) PRAECIS PHARM INC.
PA	(UYTA ) UNIV YALE.
XX	
PI	May MJ, Ghosh S, Findels MA, Phillips K;
XX	
DR	WPI: 2002-121889/16.
XX	
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis
PS	
PS	Claim 6; Page 62; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AAW48628-AAW48645), comprising a membrane translocation domain
CC	(AAW48620-AAW48637 or AAW48646-AAW48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AAW48523-AAW48619). The antiinflammatory compounds have antiaesthetic,
CC	cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	nocotropic, antiatherosclerotic, virucide and anti allergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of IkappaB. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	burstitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
XX	Sequence 10 AA;
XX	
Query Match	100.0%; Score 35; DB 23; Length 10;
Best Local Similarity	100.0%; Pred. NO. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 LDFSWL 6
Db	3 LDFSWL 8
XX	
RESULT 15	
ID	AAW48576
XX	AAW48576 standard; Peptide; 11 AA.
AC	AAW48576;
XX	
DT	20-MAR-2002 (first entry)
XX	
DE	Anti-inflammatory peptide SEQ ID NO 79.
XX	
KW	Antiinflammatory; antiaesthetic; cytostatic; antipsoriatic; nocotropic;

KW antiinflammatory; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antithrombotic;  
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cyclokinin; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
XX Synthetic.  
XX  
PN WO200183554-A2.  
XX  
XX 08-NOV-2001.  
XX  
PP 02-MAY-2001; 2001WO-US14346.  
XX  
PR 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
PA (UYVA ) UNIV YALE.  
PI May MJ, Ghosh S, Findeis MA, Phillips K;  
XX  
XX WPI, 2002-121899/16.  
XX  
XX Novel antiinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis -  
XX  
XX Claim 6; Page 62; 8pp; English.  
PS  
SS The invention relates to an antiinflammatory compound (especially  
CC AA48638-AA48645), comprising a membrane translocation domain  
CC (AA48638-AA48645) or AA48646-AA48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AA48652-AA48619). The antiinflammatory compounds have antiaesthetic,  
CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC nootropic, antithrombotic, virucide and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
CC activation by blocking interaction of Ikappab kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of Ikappab. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursts; autoimmune diseases such as lupus, polyarthritis, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
XX  
SQ Sequence 11 AA;

Query Match 100.0%; Score 35; DB 23; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.6;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 LDFSMI 6  
|||  
Db 3 LDFSMI 8

Search completed: February 18, 2004, 14:26:22  
Job time : 22.7763 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds  
(without alignments)  
89.145 Million cell updates/sec

Title: US-09-643-260-10

Perfect score: 33  
Sequence: 1 LDASWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mmc:\*
- 8: sp\_organella:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriophage:\*
- 17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	518	5	Q968Y8
2	33	100.0	521	11	Q8C4D5
3	33	100.0	535	5	Q968Y7
4	31	93.9	908	16	Q8ZAJ4
5	31	93.9	535	17	Q27987
6	31	93.9	763	10	Q96U25
7	30	90.9	187	2	Q9JRL8
8	30	90.9	187	2	Q9JRL9
9	30	90.9	187	2	Q9JRL5
10	30	90.9	187	2	Q9JRL7
11	30	90.9	187	2	Q9JRL7
12	30	90.9	205	16	Q8BBG1
13	30	90.9	221	16	Q9A120
14	30	90.9	221	16	Q8B239
15	30	90.9	225	17	Q8BTR10
16	30	90.9	245	2	Q68096

17	30	90.9	261	4	Q9P012	Q9P012 homo sapien
18	30	90.9	261	11	Q99K13	Q99K13 mus musculus
19	30	90.9	290	2	Q9F238	Q9F238 xanthomonas
20	30	90.9	290	2	Q9RBQ2	Q9RBQ2 xanthomonas
21	30	90.9	290	2	Q9RBQ2	Q9RBQ2 xanthomonas
22	30	90.9	290	2	Q9RBQ2	Q9RBQ2 xanthomonas
23	30	90.9	293	16	Q8PFR8	Q8PFR8 xanthomonas
24	30	90.9	307	11	Q9CXJ5	Q9CXJ5 mus musculus
25	30	90.9	316	16	Q9BIR6	Q9BIR6 rhizobium 1
26	30	90.9	317	4	Q9BRA3	Q9BRA3 homo sapien
27	30	90.9	332	2	Q9RA30	Q9RA30 vibrio mari
28	30	90.9	344	11	Q8R306	Q8R306 mus musculus
29	30	90.9	442	10	Q9S232	Q9S232 arabidopsis
30	30	90.9	461	10	Q9M0J8	Q9M0J8 arabidopsis
31	30	90.9	500	11	Q8CHX7	Q8CHX7 mus musculus
32	30	90.9	563	4	Q8B510	Q8B510 homo sapien
33	30	90.9	688	9	Q9PRZ2	Q9PRZ2 mycoplasma
34	30	90.9	810	16	Q8ZKN4	Q8ZKN4 salmoneilla
35	30	90.9	810	16	Q8Z226	Q8Z226 salmoneilla
36	30	90.9	906	16	Q8YXK2	Q8YXK2 anabaena sp
37	30	90.9	997	2	Q68533	Q68533 pseudomonas
38	29	87.9	69	10	Q43289	Q43289 arabidopsis
39	29	87.9	125	16	Q8DUJ9	Q8DUJ9 streptococc
40	29	87.9	150	16	Q9HTX9	Q9HTX9 pseudomonas
41	29	87.9	151	5	Q77003	Q77003 biophila
42	29	87.9	156	4	Q96G14	Q96G14 homo sapien
43	29	87.9	162	8	Q94Z49	Q94Z49 neolepidape
44	29	87.9	162	8	Q94Z27	Q94Z27 profundiver
45	29	87.9	175	16	Q8PQ4	Q8PQ4 xanthomonas

## ALIGNMENTS

RESULT 1	Q968Y8	PRELIMINARY	PRT	518 AA.
AC	Q968Y8	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Hypothetical protein T28B4.1b.			
GN	T28B4.1 OR T28B4.1b.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;			
OC	Rhabditidae; Pelodierinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RX	MEDLINE=99069613; PubMed=9851916;			
RA	None;			
RT	"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.",			
RL	Science 282:2012-2018 (1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RA	Wilson R., Greco T., Sansone J.;			
RT	"The sequence of C. elegans cosmid T28B4.",			
RL	Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RA	Waterston R.;			
RT	Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.			
RL	EMBL, AF026206; AK39308.1; --			
DR	WormSep; T28B4.1b; CR27216.			
DR	InterPro; IPR001810; F-box.			
DR	Pfam; PF00646; F-box; 1.			
DR	SMART; SM00256; FBOX; 1.			
DR	PROSITE; PSS0181; FBOX; 1.			
SO	SEQUENCE 518 AA, 60125 MW; A8A30C911618BD47 CRC64;			

Query Match 100.0%; Score 33; DB 5; Length 518;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
 DB 323 LDASWL 328

## RESULT 2

08C4D5 PRELIMINARY; PRT; 521 AA.

AC 08C4D5; 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA the FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK082517; BAC38515.1; -.  
 KW Hypothetical protein.  
 FT NON TR

SO SEQUENCE 521 AA; 57719 MW; D4C2F39CB2512D5 CRC64;

Query Match 100.0%; Score 33; DB 11; Length 521;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
 DB 283 LDASWL 288

## RESULT 3

0968Y7 PRELIMINARY; PRT; 535 AA.

AC 0968Y7; 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE T28B4.1a protein.  
 GN T28B4.1 OR T28B4.1A.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditicoidea;  
 OC Rhabditidae; Pseudocercariae; Caenorhabditis.  
 CX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium."  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;  
 RA Wilson R., Greco T., Sansone J.,  
 RT "The sequence of C. elegans cosmid T28B4."  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 [3]

RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Waterston R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF026206; AAK39309.1; -.  
 DR WormRep; T28B4.1a; CE27215.  
 DR InterPro; IPR001810; F-box.  
 DR Pfam; PF00646; F-box; 1.  
 DR SMART; SM00256; FBOX; 1.  
 DR PROSITE; PSS0181; FBOX; 1.

SO SEQUENCE 535 AA; 62557 MW; CFEA8794E188C104 CRC64;

Query Match 100.0%; Score 33; DB 5; Length 535;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
 DB 340 LDASWL 345

## RESULT 4

08ZAJ4 PRELIMINARY; PRT; 308 AA.

AC 08ZAJ4; 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE High-affinity branched-chain amino acid transport system,  
 DE protein (High-affinity branched-chain amino acid ABC transport system  
 DE membrane permease).  
 GN LIVH OR YPO3807 OR Y0423.  
 OS Yersinia pestis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Yersinia.

NCBI\_TaxID=632;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=CO-92 / Biovar Orientalis;  
 RX MEDLINE=21470413; PubMed=11586360;  
 RA Parkhill J., Wren B.W., Thomson N.R., Tiplall R.W., Holden M.T.G.,  
 RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,  
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Rarraga A.M.,  
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
 RA Felwell T., Hamlin N., Holtroyd S., Jegerle K., Karyshev A.V.,  
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,  
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,  
 RT "Genome sequence of Yersinia pestis, the causative agent of plague."  
 RL Nature 413:523-527(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN=KIMS / Biovar Mediaevalis;  
 RX MEDLINE=22137863; PubMed=12142430;  
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Lise P.,  
 RA Perna N.T., Rose D.J., Muu B., Zhou S., Schwartz D.C.,  
 RA Retherston J.D., Lindler L.B., Brubaker R.R., Plano G.V.,  
 RA Straley S.C., McDonough K.A., Niles M.L., Watson J.S., Blattner F.R.,  
 RA Perry R.D.;  
 RT "Genome sequence of Yersinia pestis KIM."

RT J. Bacteriol. 184:4601-4611(2002).  
 DR EMBL; AJ614159; CAC93274.1; -.  
 DR EMBL; AB013643; AAM84012.1; -.  
 DR InterPro; IPR001851; BAC\_inmem\_transp.  
 DR Pfam; PF02653; BPD\_transp\_2; 1.  
 KW Complete proteome.

SO SEQUENCE 308 AA; 33042 MW; 9C2527B553063A7 CRC64;

Query Match 93.9%; Score 31; DB 16; Length 308;  
 Best Local Similarity 83.3%; Pred. No. 4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
 :|||||

Db 66 IDASWL 71

RESULT 5  
027987 PRELIMINARY; PRT; 535 AA.

AC 027987;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Cytochrome oxidase, subunit I (CYDA-2).  
GN AF2297.  
OS Archaeoglobus fulgidus.  
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;  
OC Archaeoglobaceae; Archaeoglobus.  
OX NCBI\_TaxID=2234;  
[1] IDASWL 2234;  
RP SEQUENCE FROM N.A.  
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
RX MEDLINE=98049343; PubMed=9389475;  
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
Richardson D.L., Kierkegaard A.R., Graham D.E., Kyriakides N.C.,  
Rieschmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,  
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterback T.,  
Cotton M.D., Spriggs T., Arlrich P., Kaine B.P., Sykes S.M.,  
Sadov P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
Venter J.C.,  
RT "The complete genome sequence of the hyperthermophilic, sulphate-  
reducing archaeon Archaeoglobus fulgidus.";  
RL Nature 390:364-370(1997).  
DR EMBL; AE000946; AAB8960.1; -  
DR TIGR; AF2297; -  
DR InterPro; IPR002585; Bac\_Ubq\_Cox.  
DR InterPro; IPR000515; BPD\_transp.  
DR Pfam; PF01654; Bac\_Ubq\_Cox; 1.  
DR PROSITE; PS00402; BPD\_TRANSF\_INN\_MEMBER; 1.  
KM Hypothetical protein; Complete proteome.  
SQ SEQUENCE 535 AA; 57605 MW; 68C82D58A11EE96 CRC64;

Query Match 93.9%; Score 31; DB 17; Length 535;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDASWL 6  
Db 8 IDASWL 13

RESULT 6  
09SUZ5 PRELIMINARY; PRT; 763 AA.

AC 09SUZ5;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Hypothetical 85.2 kDa protein.  
GN F4F15.210.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC euroside II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
[1] IDASWL 3702;  
RP SEQUENCE FROM N.A.  
RA Alcaraz J.P., Clabault G., Cottet A., Mache R., Mewes H.W., Lemcke K.,  
Mayer K.F.X., Quelet F., Salanoubat M.,  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL049711; CAB41330.1; -  
DR InterPro; IPR001965; Znf\_PHD.  
DR InterPro; IPR001941; Znf\_PHD.  
DR SMART; SM00249; PHD; 2.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS50016; ZF\_PHD\_2; 1.  
DR PROSITE; PS50089; ZF\_RING\_2; 1.  
KM Hypothetical protein.  
SQ SEQUENCE 763 AA; 85199 MW; 92BB47843D5314F9 CRC64;

Query Match 93.9%; Score 31; DB 10; Length 763;  
Best Local Similarity 83.3%; Pred. No. 1e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDASWL 6  
Db 613 IDASWL 618

RESULT 7  
09JRL8 PRELIMINARY; PRT; 187 AA.

AC 09JRL8;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Metallo-beta-lactamase 3 (Fragment).  
GN MBL3.  
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
OC Xanthomonadaceae; Stenotrophomonas.  
OX NCBI\_TaxID=40324;  
[1] IDASWL 40324;  
RP SEQUENCE FROM N.A.  
RC STRAIN=U152;  
RA Walker R.A., Higgins P., Payne D.J., Ames S.G.,  
RT "A biochemical and molecular assessment of the heterogeneity of the  
metallo-beta-lactamases from clinical Stenotrophomonas maltophilia  
isolates.";  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ289083; CAB94702.1; -  
DR HSP; P52700; ISML.  
DR InterPro; IPR001018; Beta\_lactamase\_B.  
DR InterPro; IPR001279; Blactamase-like.  
DR Pfam; PF00753; lactamase\_B; 1.  
DR PROSITE; PS00743; BETA\_LACTAMASE\_B\_1; 1.  
FT NON\_TER 187  
FT TER 187  
SQ SEQUENCE 187 AA; 19931 MW; F07D49B4C88043 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 187;  
Best Local Similarity 83.3%; Pred. No. 3.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDASWL 6  
Db 12 IDASWL 17

RESULT 8  
09JRL9 PRELIMINARY; PRT; 187 AA.

AC 09JRL9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Metallo-beta-lactamase 2 (Fragment).  
GN MBL2.  
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).

```
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Stenotrophomonas.
OX NCBI_TaxID=40324;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=0062;
RA Walker R.A., Higgins P., Payne D.J., Ames S.G.;
RT "A biochemical and molecular assessment of the heterogeneity of the
RT metallo-beta-lactamases from clinical Stenotrophomonas maltophilia
RT isolates."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ289082; CAB94701.1; -.
DR HSSP; P52700; ISML.
DR InterPro; IPR001018; Beta_lactamase_B.
DR InterPro; IPR001279; Blactamase-1like.
DR Pfam; PF00753; lactamase_B; 1.
DR PROSITE; PS00743; BETA_LACTAMASE_B_1; 1.
FT NON_TER 1
FT NON_TER 187
SQ SEQUENCE 187 AA; 19960 MW; 877D49E4B4C898F4 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 187;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 12 VDASWL 17

RESULT 9
Q9JRL5 PRELIMINARY; PRT; 187 AA.
ID Q9JRL5;
AC Q9JRL5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Metallo-beta-lactamase 511 (Fragment).
GN MBL511 OR MBL5.
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas
OS maltophilia).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Stenotrophomonas.
OX NCBI_TaxID=40324;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=511, and 37;
RA Walker R.A., Higgins P., Payne D.J., Ames S.G.;
RT "A biochemical and molecular assessment of the heterogeneity of the
RT metallo-beta-lactamases from clinical Stenotrophomonas maltophilia
RT isolates."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ289086; CAB94705.1; -.
DR EMBL; AJ289085; CAB94704.1; -.
DR HSSP; P52700; ISML.
DR InterPro; IPR001018; Beta_lactamase_B.
DR InterPro; IPR001279; Blactamase-1like.
DR Pfam; PF00753; lactamase_B; 1.
DR PROSITE; PS00743; BETA_LACTAMASE_B_1; 1.
FT NON_TER 1
FT NON_TER 187
SQ SEQUENCE 187 AA; 19811 MW; 7A2B11372028E5FE CRC64;

Query Match 90.9%; Score 30; DB 2; Length 187;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 12 VDASWL 17

RESULT 10
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```
Q9JRM0 PRELIMINARY; PRT; 187 AA.
ID Q9JRM0;
AC Q9JRM0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Metallo-beta-lactamase 1 (Fragment).
GN MBL1.
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas
OS maltophilia).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Stenotrophomonas.
OX NCBI_TaxID=40324;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GEL;
RA Walker R.A., Higgins P., Payne D.J., Ames S.G.;
RT "A biochemical and molecular assessment of the heterogeneity of the
RT metallo-beta-lactamases from clinical Stenotrophomonas maltophilia
RT isolates."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ289081; CAB94700.1; -.
DR HSSP; P52700; ISML.
DR InterPro; IPR001018; Beta_lactamase_B.
DR InterPro; IPR001279; Blactamase-1like.
DR Pfam; PF00753; lactamase_B; 1.
DR PROSITE; PS00743; BETA_LACTAMASE_B_1; 1.
FT NON_TER 1
FT NON_TER 187
SQ SEQUENCE 187 AA; 19901 MW; 72B8515412892A08 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 187;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6
Db 12 VDASWL 17

RESULT 11
Q9JRL7 PRELIMINARY; PRT; 187 AA.
ID Q9JRL7;
AC Q9JRL7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Metallo-beta-lactamase 4 (Fragment).
GN MBL4.
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas
OS maltophilia).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Stenotrophomonas.
OX NCBI_TaxID=40324;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Q2323;
RA Walker R.A., Higgins P., Payne D.J., Ames S.G.;
RT "A biochemical and molecular assessment of the heterogeneity of the
RT metallo-beta-lactamases from clinical Stenotrophomonas maltophilia
RT isolates."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ289084; CAB94703.1; -.
DR HSSP; P52700; ISML.
DR InterPro; IPR001018; Beta_lactamase_B.
DR InterPro; IPR001279; Blactamase-1like.
DR Pfam; PF00753; lactamase_B; 1.
DR PROSITE; PS00743; BETA_LACTAMASE_B_1; 1.
FT NON_TER 1
FT NON_TER 187
SQ SEQUENCE 187 AA; 19900 MW; D3C749B4B60C3F18 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 187;
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Best Local Similarity 83.3%; Pred. No. 3.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6  
12 VDASWL 17

Db 12 VDASWL 17

RESULT 12

Q8EBG1 PRELIMINARY; PRT; 205 AA.

AC Q8EBG1, 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Conserved hypothetical protein.  
GN S03557.  
OS Shewanella oneidensis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
OC Alteromonadaceae; Shewanella.  
CX NCBI\_TaxID=70863;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MR-1;  
RX MEDLINE=22297686; PubMed=12368813;  
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,  
Reed I.D., Eilen J.A., Sehnadi R., Ward N., Meche B., Clayton R.A.,  
Meyer T., Tsapin A., Scott J., Beaman M., Brinac L.H., Daugherty S.,  
Deboy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,  
Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,  
Vamathevan J., Weidman J., Impram M., Lee K., Berry K., Lee C.,  
Muller J., Khouri H., Gill U., Utterback T.R., McDonald L.A.,  
Feilblyum T.V., Smith H.O., Venter J.C., Neilson K.H., Fraser C.M.,  
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium  
Shewanella oneidensis.";  
RL Nat. Biotechnol. 20:1118-1123(2002).  
DR EMBL; AB015792; AAN56548.1; -  
DR TIGR; S03557; -  
KM Hypothetical protein; Complete proteome.  
SQ SEQUENCE 205 AA; 23686 MW; 3A301AC03E782334 CRC64;

Query Match 90.9%; Score 30; DB 16; Length 205;  
Best Local Similarity 83.3%; Pred. No. 4.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6  
194 LDSSWL 199

Db 194 LDSSWL 199

RESULT 13

Q9A120 PRELIMINARY; PRT; 221 AA.

AC Q9A120, 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Putative NAD(P)H-flavin oxidoreductase.  
GN SPY0512.  
OS Streptococcus pyogenes.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus  
CX NCBI\_TaxID=1314;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;  
RX MEDLINE=21192684; PubMed=11296296;  
RA Ferrer J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,  
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,  
Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,  
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.,  
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";  
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

DR EMBL; AE006509; AAJ33511.1; -  
DR InterPro; IPR000415; Nitroreductase.  
DR Pfam; PF00881; Nitroreductase; 1.  
KM Complete proteome.  
SQ SEQUENCE 221 AA; 25283 MW; 724C1A54FC72C85 CRC64;

Query Match 90.9%; Score 30; DB 16; Length 221;  
Best Local Similarity 83.3%; Pred. No. 4.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6  
36 LDAAWL 41

Db 36 LDAAWL 41

RESULT 14

Q8P239 PRELIMINARY; PRT; 221 AA.

AC Q8P239, 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE Putative NAD(P)H-flavin oxidoreductase.  
GN SPY18 0570 OR SPY13 0360.  
OS Streptococcus pyogenes (serotype M18), and  
OS Streptococcus pyogenes (serotype M3).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
CX NCBI\_TaxID=186103, 198466;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=S.pyogenes; STRAIN=MGAS8232 / Serotype M18;  
RX MEDLINE=21927593; PubMed=11917108;  
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,  
RA Sylva G.L., Sturdevant D.B., Ricklefs S.M., Porcella S.F.,  
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,  
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.,  
RT "Genome sequence and comparative microarray analysis of serotype M18  
group A Streptococcus strains associated with acute rheumatic fever  
outbreaks.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES=S.pyogenes; STRAIN=MGAS315 / Serotype M3;  
RX MEDLINE=22133806; PubMed=12122206;  
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,  
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,  
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,  
RA Schlivert P.M., Musser J.M.,  
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:  
RT phage-encoded toxins, the high-virulence phenotype, and clone  
RT emergence.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).  
DR EMBL; AB009993; AAL97264.1; -  
DR NCBI\_TaxID=14143; AAL78967.1; -  
DR InterPro; IPR000415; Nitroreductase.  
DR Pfam; PF00881; Nitroreductase; 1.  
KM Hypothetical protein; Complete proteome.  
SQ SEQUENCE 221 AA; 25269 MW; A929A147EB0027D6 CRC64;

Query Match 90.9%; Score 30; DB 16; Length 221;  
Best Local Similarity 83.3%; Pred. No. 4.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6  
36 LDAAWL 41

Db 36 LDAAWL 41

RESULT 15

Q8TR10 PRELIMINARY; PRT; 225 AA.

AC Q8TR10, 08TR10;

DT 01-JUN-2002 (T-EMBLrel. 21, Created)  
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
 DE Hypothetical protein MA1374.  
 GN MA1374.  
 OS Methanosarcina acetivorans.  
 OC Archaea: Euryarchaeota: Methanococci: Methanosarcinales;  
 OC Methanosarcinaceae: Methanosarcina.  
 OC NCBI\_TaxID=2214;  
 RX MEDLINE=21929760; PubMed=11932238;  
 RA Galagan J.E., Nussbaum C., Roy A., Endrizzi M.G., MacDonald P.,  
 Fitzhugh W., Calvo S., Engels R., Smitrov S., Alnoor D., Brown A.,  
 Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,  
 Lincon L., McEwan P., McKernan K., Talamas J., Tixrell A., Ye W.,  
 Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,  
 Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,  
 Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,  
 Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,  
 Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,  
 Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,  
 Metcalf W.W., Birren B.;  
 RA "The genome of Methanosarcina acetivorans reveals extensive metabolic  
 RT and physiological diversity.";  
 RL Genome Res. 12:532-542(2002).  
 DR EMBL: AB010807; AM04790.1; -;  
 DR InterPro: IPR005237; Cons. hypoth289.  
 DR InterPro: IPR002761; DUF71.  
 DR Pfam: PF01902; DUF71.1.  
 DR TIGRPM: TIGR00289; MJ0570\_dom; 1.  
 DR TIGRPM: TIGR00289; TIGR00289; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 225 AA; 25146 MW; A573D46D1DDFB9D1 CRC64;

Query Match 90.9%; Score 30; DB 17; Length 225;  
 Best Local Similarity 83.3%; Pred. NO. 4.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDASWL 6  
 Db 149 LDSSWL 154

Search completed: February 18, 2004, 14:35:48  
 Job time : 19.3684 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds  
(without alignments)  
87.531 Million cell updates/sec

Title: US-09-643-260-10

Perfect score: 33

Sequence: 1 LDASWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing filter 45 summaries

Database :  
1: p1r1:  
2: p1r2:  
3: p1r3:  
4: p1r4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	419	T32441	hypothetical prote
2	31	93.9	308	AF0463	high-affinity bran
3	31	93.9	535	A69537	cytochrome oxidase
4	31	93.9	763	T49089	hypothetical prote
5	30	90.9	245	T03533	probable precorrin
6	30	90.9	290	T48880	beta-lactamase (EC
7	30	90.9	290	S45349	L1 metallo-beta-la
8	30	90.9	332	T44337	aminooxychromium
9	30	90.9	442	T04815	hypothetical prote
10	30	90.9	461	D85312	probable homeodoma
11	30	90.9	810	AH0937	bifunctional aspar
12	30	90.9	906	AG1957	hypothetical prote
13	30	90.9	919	OYFKG	phosphoenolpyruvat
14	29	87.9	150	C82994	conserved hypochet
15	29	87.9	177	B41377	cytochrome c-L pre
16	29	87.9	243	C83450	hypothetical prote
17	29	87.9	252	C83837	hypothetical prote
18	29	87.9	255	G75626	probable 3-alpha-h
19	29	87.9	256	F84612	hypothetical prote
20	29	87.9	264	D84504	probable VSF-1-like
21	29	87.9	269	A75397	probable signal pe
22	29	87.9	274	B83444	probable transcrip
23	29	87.9	277	T29979	hypothetical prote
24	29	87.9	278	H82759	cell division prot
25	29	87.9	282	E70890	hypothetical prote
26	29	87.9	286	A48399	probable oxidoredu
27	29	87.9	286	A85739	probable dehydroge
28	29	87.9	286	H90879	probable dehydroge
29	29	87.9	289	A37209	thiosulfate sulfur

30	29	87.9	295	2	G15081	thiosulfate sulfur
31	29	87.9	296	1	ROHU	thiosulfate sulfur
32	29	87.9	296	2	AH2327	hypothetical prote
33	29	87.9	297	1	ROBO	thiosulfate sulfur
34	29	87.9	297	2	JC4398	thiosulfate sulfur
35	29	87.9	297	2	UC5286	thiosulfate sulfur
36	29	87.9	301	2	G83182	hypothetical prote
37	29	87.9	316	2	P89791	peptidoglycan hyd
38	29	87.9	318	2	T52663	thiosulfate sulfur
39	29	87.9	326	2	B99790	hypothetical prote
40	29	87.9	329	2	A86300	hypothetical prote
41	29	87.9	333	2	F70678	probable transpos
42	29	87.9	359	2	S15305	rt6g protein - Sal
43	29	87.9	359	2	AH0766	CDPglucose 4,6-deh
44	29	87.9	360	2	T26037	hypothetical prote
45	29	87.9	360	2	S32695	mtc-2 protein - Ca

## ALIGNMENTS

RESULT 1  
T32441  
hypothetical protein T2884.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T32441  
R:Wilson, R.; Greco, T.; Sansone, J.  
submitted to the EMBL Data Library, September 1997  
A:Description: The sequence of C. elegans cosmid T28B4.  
A:Reference number: Z21168  
A:Accession: T32441  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Cross-references: EMBL:AF026206; PIDN:ABJ71262.1; GSPDB:GN00028; CESP:T28B4.1  
A:Experimental source: strain Bristol N2; clone T28B4  
A:Gene: CESP:T28B4.1  
A:Map position: X  
A:Introns: 47/3; 68/3; 102/3; 153/1; 207/1; 296/1

Query Match  
Best Local Similarity 100.0%; Score 33; DB 2; Length 419;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASWL 6  
Db 340 LDASWL 345

RESULT 2  
AF0463  
high-affinity branched-chain amino acid transport system, permease protein 11vH (import  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Nov-2001  
C:Accession: AF0463  
R:Parthill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.E  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;  
Jl, M.; Rutherford, K.; Stimpson, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,  
Nature 413, 523-527, 2001  
A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AF0463  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-308 <KUR>  
A:Cross-references: GB:AU590842; PIDN:CA93274.1; PID:G15981721; GSPDB:GN00175  
A:Gene: 11vH  
C:Superfamily: leucine transport protein 11vH

Query Match 93.9%; Score 31; DB 2; Length 308;

Best Local Similarity 83.3%; Pred. No. 93;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LDASWL 6  
:|||||  
Db 66 LDASWL 71

## RESULT 3

A69537

Cytochrome oxidase, subunit I (cydA-2) homolog - Archaeoglobus fulgidus  
C/Species: Archaeoglobus fulgidus  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 17-Mar-2000

C/Accession: A69537  
R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A/Authors: Overbeek, R.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A/Reference number: A69537; MUID:98049343; PMID:9389475  
A/Accession: A69537  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-535 <KE>

A/Cross-references: GB:AE000946; GB:AE000782; NID:92689269; PIDN:AA88960.1; PID:9264822  
C/Superfamily: cytochrome d complex terminal oxidase chain I

Query Match  
Best Local Similarity 83.3%; Score 31; DB 2; Length 535;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6  
:|||||  
Db 8 LDASWL 13

## RESULT 4

T49089

Hypothetical protein F4F15.210 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000

C/Accession: T49089  
R/Altman, J.P.; Clabault, G.; Cortez, A.; Maché, R.; Mewes, H.W.; Rudd, S.; Lemcke, K.;  
Submitted to the Protein Sequence Database, April 2000  
A/Reference number: 225015  
A/Accession: T49089  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-763 <ALC>

A/Cross-references: EMBL:AL049711; GSPDB:GN00061; ATSP:F4F15.210  
A/Experimental source: cultivar Columbia; BAC clone F4F15  
C/Genetics:  
A/Gene: ATSP:F4F15.210  
A/Map position: 3  
A/Intons: 11/2; 124/3; 183/1; 199/3; 230/3; 274/1; 297/3; 325/2; 351/3; 478/1; 641/2; 6

Query Match  
Best Local Similarity 83.3%; Score 31; DB 2; Length 763;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6  
:|||||  
Db 613 LDASWL 618

## RESULT 5

T03533

probable precorrin-2 methyltransferase (BC 2.1.1.-) - Rhodobacter capsulatus  
C/Species: Rhodobacter capsulatus  
C/Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 18-Feb-2000

C/Accession: T03533

R/Vlcek, C.; Paces, V.; Matveev, N.; Paces, J.; Hasek, R.; Fomstein, M.  
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997  
A/Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB101

A/Reference number: Z14955; MUID:97404404; PMID:9256491  
A/Accession: T03533  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-245 <VLC>  
A/Cross-references: EMBL:AF010496; NID:93128256; PIDN:AA016186.1; PID:93128334  
C/Genetics:  
A/Map position: 1  
C/Superfamily: precorrin-3 methylase  
C/Keywords: methyltransferase

Query Match  
Best Local Similarity 83.3%; Score 30; DB 2; Length 245;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6  
:|||||  
Db 197 LDASWL 202

## RESULT 6

T48880

Beta-lactamase (EC 3.5.2.6) L-1 precursor (validated) - Pseudomonas maltophilia  
N/Alternate names: L-1 metallo-beta-lactamase  
C/Species: Pseudomonas maltophilia

C/Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000

C/Accession: T48880

R/Sanchez, R.; Dufresne, J.; Levesque, R.C.  
Antimicrob. Agents Chemother. 42, 1245-1248, 1998

A/Title: Molecular heterogeneity of the L-1 metallo-beta-lactamase family from Stenotr

A/Reference number: Z24841; MUID:98253390; PMID:9593158

A/Accession: T48880  
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA  
A/Residues: 1-290 <SAN>

A/Cross-references: EMBL:AF010282; PIDN:AA021590.1

A/Experimental source: strain GNI2873

C/Genetics:  
A/Gene: bias

C/Function:  
A/Description: catalyzes the hydrolysis of an amide bond in the beta-lactam ring of the

C/Keywords: antibiotic resistance; hydrolase  
F/1-33/Domain: signal sequence #status predicted <SIG>

F/34-290/Product: L-1 metallo-beta-lactamase #status predicted <MAT>

Query Match  
Best Local Similarity 83.3%; Score 30; DB 2; Length 290;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6  
:|||||  
Db 34 VDAWML 39

## RESULT 7

S45349

L1 metallo-beta-lactamase - Xanthomonas maltophilia  
C/Species: Xanthomonas maltophilia  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Aug-1997

C/Accession: S45349  
R/Walsh, T.R.; Hall, L.; Absinder, S.J.; Nichols, W.W.; Cartwright, S.J.; MacGowan, A.I

Biochim. Biophys. Acta 1218, 199-201, 1994

A/Title: Sequence analysis of the L1 metallo-beta-lactamase from Xanthomonas maltophil

A/Reference number: S45349; MUID:94289479; PMID:8018721

A/Accession: S45349

A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-290 <WAL>

Query Match  
Best Local Similarity 83.3%; Score 30; DB 2; Length 290;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
:|||||  
Db 34 VDASWL 39

## RESULT 8

T44437

aminoacyl-tRNA synthetase [imported] - Moritella marina  
C:Species: Moritella marina  
C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 18-Feb-2000

C:Accession: T44437  
R:Morita, N.; Ueno, A.; Tanaka, M.; Ohgita, S.; Hoshino, T.; Kawasaki, K.; Yumoto, I.; I  
Biotechnol. Lett. 21, 641-646, 1999  
A>Title: Cloning and sequencing of clustered genes involved in fatty acid biosynthesis  
A:Reference number: 222768  
A:Accession: T44437  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-332 <MOR>  
A:Cross-references: EMBL:AB021978; PIR:BAAB5259.1  
A:Experimental source: ATCC 15381  
C:Genetics:  
A>Note: pabc  
C:Superfamily: yceg protein

Query Match 90.9%; Score 30; DB 2; Length 332;  
Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
:|||||  
Db 187 LDASWL 192

## RESULT 9

T04815

hypothetical protein F10M23.260 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 11-Jun-1999

C:Accession: T04815  
R:Bevan, M.; Lecharny, A.; Chafador, F.; Krivitzky, M.; Kreis, M.; Hohnel, J.; Mewes, H  
submitted to the Protein Sequence Database, February 1999  
A:Reference number: 215385  
A:Accession: T04815  
A:Molecule type: DNA  
A:Residues: 1-442 <BEV>  
A:Cross-references: EMBL:AL035440  
A:Experimental source: cultivar Columbia; BAC clone F10M23  
C:Genetics:  
A/Map position: 4  
A:Introns: 140/3; 165/3; 236/1; 358/3  
A>Note: F10M23.260

Query Match 90.9%; Score 30; DB 2; Length 442;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
:|||||  
Db 128 VDASWL 133

## RESULT 10

D85312

probable homeodomain protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001

C:Accession: D85312  
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
Nature 402, 769-777, 1999

A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A:Reference number: AB5001; MUID:20083488; PMID:10617198  
A:Accession: D85312  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-461 <STO>  
A:Cross-references: GB:NC\_001268; NID:g7269545; PIR:CA879547.1; GSPDB:GN00140  
C:Genetics:  
A:Gene: AT4G26920  
A/Map position: 4

Query Match 90.9%; Score 30; DB 2; Length 461;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
:|||||  
Db 128 VDASWL 133

## RESULT 11

AH0937

bifunctional aspartokinase II/homoserine dehydrogenase Iican I write [imported] - Salmo  
C:Species: Salmonella enterica subsp. enterica serovar Typh  
A>Note: This species has also been called Salmonella typh  
C>Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002

C:Accession: AH0937  
R:Parthill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church  
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davie, R.M.; Dowd, L.; White, N.; Farrar  
S.; Moulle, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.  
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serc  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AH0937  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-810 <PAR>  
A:Cross-references: GB:AL513382; PIR:CA09522.1; PIR:g16504639; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY3768  
C:Superfamily: thra bifunctional enzyme; aspartate kinase homology; homoserine dehydrog

Query Match 90.9%; Score 30; DB 2; Length 810;  
Best Local Similarity 83.3%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
:|||||  
Db 146 LDASWL 151

## RESULT 12

AG1957

hypothetical protein all1210 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120  
C:Accession: AG1957  
C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002

C:Accession: AG1957  
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kurita, T.; Sasamoto, S.; Matsumoto, A.; Iritani  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takasawa, M.; Yamada, M.; Yasuda, M.; Tabata,  
DNA Res. 8, 205-213, 2001  
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AG1957  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-906 <KUN>  
A:Cross-references: GB:BA000019; PIR:BA873167.1; PIR:g17130557; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: all1210

Query Match 90.9%; Score 30; DB 2; Length 906;  
 Best Local Similarity 83.3%; Pred. No. 4.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
 |||||  
 DB 225 LDSSWL 230

## RESULT 13

OYFKG

phosphoenolpyruvate carboxylase (EC 4.1.1.31) - Corynebacterium glutamicum  
 C/Species: Corynebacterium glutamicum

C/Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 18-Jun-1999

C/Accession: S05512; JSD183

R/Elkman, B.J.; Follett, M.T.; Griot, M.U.; Slneskey, A.J.

Mol. Gen. Genet. 218, 330-339, 1989

A/Title: The phosphoenolpyruvate carboxylase gene of Corynebacterium glutamicum: molecu

A/Reference number: S05511; PMID:89384460; PMID:2779518

A/Accession: S05512

A/Molecule type: DNA

A/Residues: 1-919 <EIK>

A/Cross-references: GB:X14234; NID:948688; PIDN:CA32450.1; PID:948689

A/Note: the authors translated the codon ATT for residue 387 as Gln, AAA for residue 553

R/O'Regan, M.; Thierbach, G.; Bachmann, B.; Villevall, D.; Lepage, P.; Viret, J.F.; Lemot

Gene 77, 237-251, 1989

A/Title: Cloning and nucleotide sequence of the phosphoenolpyruvate carboxylase-coding g

A/Reference number: JSD183; PMID:89326141; PMID:2662624

A/Accession: JSD183

A/Molecule type: DNA

A/Residues: 1-606; 'KV', 609-799, 'FT', 802-914, 'L', 916-919 <ORE>

A/Cross-references: GB:M25819; NID:9144984; PIDN:AAA83537.1; PID:9144985

A/Experimental source: ATCC 13032

A/Note: residues 2-15 were confirmed by protein sequencing

C/Comment: This enzyme catalyzes the carboxylation (by carbon dioxide) of phosphoenolpy

C/Comment: The activity of this protein is not stimulated by acetyl-CoA in the absence o

C/Genetics:

A/Genes: ppc

C/Superfamily: phosphoenolpyruvate carboxylase

C/Keywords: allosteric regulation; carbon dioxide fixation; carbon-carbon lyase; carboxy

F/2-919/Product: phosphoenolpyruvate carboxylase #status predicted <MAT>

F/611-664/Region: substrate binding #status predicted

Query Match 90.9%; Score 30; DB 1; Length 919;  
 Best Local Similarity 83.3%; Pred. No. 4.4e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
 |||||  
 DB 105 LDATWL 110

## RESULT 14

C82994 conserved hypothetical protein PA5211 (Imported) - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C/Accession: C82994

R/Stover, C.K.; Pham, X.Q.; Eryin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path

A/Reference number: A82950; PMID:20437337; PMID:10984043

A/Accession: C82994

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-150 <STO>

A/Cross-references: GB:AE004934; GB:AE004091; NID:9951515; PIDN:AA08596.1; GSPDB:GN001

A/Experimental source: strain PA01

C/Genetics:

A/Genes: PA5211

Query Match 87.9%; Score 29; DB 2; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DASWL 6  
 |||||  
 DB 117 DASWL 121

## RESULT 15

B41377

cytochrome c-L precursor [validated] - Paracoccus denitrificans  
 N/Alternate names: cytochrome c511; cytochrome c552; moxG protein

C/Species: Paracoccus denitrificans

C/Date: 28-May-1992 #sequence\_revision 02-Jul-1996 #text\_change 15-Sep-2000

C/Accession: B41377

R/Van Spanning, R.J.M.; Wansell, C.W.; De Boer, T.; Hazelaar, M.J.; Anazawa, H.; Harms,

J. Bacteriol. 173, 6948-6961, 1991

A/Title: Isolation and characterization of the moxJ, moxG, moxI, and moxR genes of Par

A/Reference number: A41377; PMID:92041581; PMID:1657871

A/Accession: B41377

A/Molecule type: DNA

A/Residues: 1-177 <VAN>

A/Cross-references: GB:M57684; NID:9150589; PIDN:AAA25583.1; PID:9150591

R/Chen, L.; Durlley, R.C.B.; Matthews, F.S.; Davidson, V.L.

Science 264, 86-90, 1994

A/Title: Structure of an electron transfer complex: methylamine dehydrogenase, amicyan:

A/Reference number: A57985; PMID:94188715; PMID:8140419

A/Contents: annotation; X-ray crystallography, 2.4 angstroms, residues 23-177

R/Chen, L.; Matthews, F.S.

submitted to the Brookhaven Protein Data Bank, October 1993

A/Reference number: A52094; PDB:2MTA

A/Contents: annotation; X-ray crystallography, 2.4 angstroms, residues 23-169

C/Genetics:

A/Genes: moxG

C/Complex: associates in a heterotrimer with methylamine dehydrogenase large and sma;

C/Function:

A/Description: electron acceptor for methanol dehydrogenase; can also accept an electr

A/Pathway: methanol oxidation; methylamine oxidation

C/Superfamily: cytochrome c-L; cytochrome c6 homology

C/Keywords: chromoprotein; electron transfer; heme; heterotrimer; iron; metalloprotei

F/1-22/Domain: signal sequence #status predicted <SIG>

F/23-177/Product: cytochrome c-L #status experimental <MAT>

F/59-142/Domain: cytochrome c6 homology <CY6>

F/79,82/Binding site: heme (Cys) (covalent) #status experimental

F/83,123/Binding site: heme iron (His, Met) (axial ligands) #status experimental

Query Match 87.9%; Score 29; DB 1; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DASWL 6  
 |||||  
 DB 152 DASWL 156

Search completed: February 18, 2004, 14:38:44  
 Job time : 7.5921 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 (Search time 16.6974 Seconds)

(without alignments)  
75.239 Million cell updates/sec

Title: US-09-643-260-10

Perfect score: 33

Sequence: 1 LDASWL 6

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
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9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
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12: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
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15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	6	10 US-09-847-940B-10	Sequence 10, Appl
2	33	100.0	6	11 US-09-847-946A-10	Sequence 10, Appl
3	33	100.0	105	10 US-09-738-626-6278	Sequence 6278, Ap
4	30	90.9	191	12 US-10-291-265-782	Sequence 782, App
5	30	90.9	221	15 US-10-169-048-2	Sequence 2, Appl
6	30	90.9	261	9 US-09-765-205-14	Sequence 14, Appl
7	30	90.9	261	12 US-10-360-849A-12	Sequence 12, Appl
8	30	90.9	261	12 US-10-360-849A-15	Sequence 15, Appl
9	30	90.9	261	12 US-10-360-849A-18	Sequence 18, Appl
10	30	90.9	277	12 US-10-291-265-310	Sequence 310, App
11	30	90.9	919	10 US-09-738-626-6970	Sequence 6970, Ap
12	30	90.9	935	9 US-09-784-208-3	Sequence 3, Appl
13	30	90.9	935	12 US-10-077-745-1	Sequence 1, Appl
14	30	90.9	935	12 US-10-338-915-1	Sequence 1, Appl
15	30	90.9	935	14 US-10-078-107-1	Sequence 1, Appl

16	30	90.9	935	14 US-10-077-751-1	Sequence 1, Appl
17	30	90.9	935	15 US-10-315-023-3	Sequence 3, Appl
18	30	90.9	935	15 US-10-315-023-8	Sequence 8, Appl
19	29	87.9	136	10 US-09-738-973-123	Sequence 123, App
20	29	87.9	136	10 US-09-854-133-123	Sequence 123, App
21	29	87.9	136	15 US-10-144-649A-123	Sequence 123, App
22	29	87.9	238	12 US-10-108-608A-3740	Sequence 3740, App
23	29	87.9	269	12 US-10-369-493-592	Sequence 592, App
24	29	87.9	277	12 US-10-369-493-5377	Sequence 5377, App
25	29	87.9	278	12 US-10-369-493-7867	Sequence 7867, App
26	29	87.9	279	12 US-10-369-493-11783	Sequence 11783, A
27	29	87.9	279	12 US-10-369-493-14664	Sequence 14664, A
28	29	87.9	279	12 US-10-369-493-15142	Sequence 15142, A
29	29	87.9	285	12 US-10-369-493-7936	Sequence 7936, App
30	29	87.9	286	12 US-10-369-493-821	Sequence 821, App
31	29	87.9	293	12 US-10-369-493-21834	Sequence 21834, A
32	29	87.9	305	9 US-09-981-353-90	Sequence 90, Appl
33	29	87.9	314	10 US-09-815-242-12482	Sequence 12482, A
34	29	87.9	322	9 US-09-738-626-6011	Sequence 6011, App
35	29	87.9	322	9 US-09-815-242-5327	Sequence 5327, App
36	29	87.9	397	14 US-10-029-180-40	Sequence 40, Appl
37	29	87.9	437	15 US-10-145-415-101	Sequence 101, Appl
38	29	87.9	465	15 US-10-156-761-10355	Sequence 10355, A
39	29	87.9	491	12 US-10-369-493-23656	Sequence 23656, A
40	29	87.9	501	12 US-10-094-749-1887	Sequence 1887, App
41	29	87.9	512	12 US-10-320-797-3205	Sequence 3205, App
42	29	87.9	571	12 US-10-369-493-3747	Sequence 3747, App
43	29	87.9	854	11 US-09-770-107-2	Sequence 2, Appl
44	29	87.9	865	12 US-10-347-470A-17	Sequence 17, Appl
45	29	87.9	1066	15 US-10-128-714-3190	Sequence 3190, App

#### ALIGNMENTS

RESULT 1  
US-09-847-940B-10  
Sequence 10, Application US/09847940B  
Patent No. US20020156000A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J.  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PRI-117CP  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-10

Query Match  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OR 1 LDASWL 6  
Db 1 LDASWL 6

RESULT 2  
US-09-847-946A-10  
Sequence 10, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J

```
APPLICANT: Ghosh, Sankar
APPLICANT: Finkle, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hamms, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PFI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 10
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: NBD peptide
US-09-847-946A-10
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Query Match          100.0%; Score 33; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDASWL 6
        |||||
Db       1 LDASWL 6
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RESULT 3
US-09-738-626-6278
; Sequence 6278, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: MAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIRO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASARO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280968
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6278
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6278
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Query Match          100.0%; Score 33; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDASWL 6
        |||||
Db       48 LDASWL 53
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RESULT 4
US-10-291-265-782
; Sequence 782, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: NO. US20030232054A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 782
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-782
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Query Match          90.9%; Score 30; DB 12; Length 191;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDASWL 6
        |||||
Db       161 LDASWL 166
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RESULT 5
US-10-169-048-2
; Sequence 2, Application US/10169048
; Publication No. US20030072769A1
; GENERAL INFORMATION:
; APPLICANT: Clarke, Edna Elizabeth
; APPLICANT: Zhou, Liqing
; APPLICANT: Shea, Jacqueline Elizabeth
; APPLICANT: Feldman, Robert Graham
; APPLICANT: Holden, David William
; TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And Their Use
; FILE REFERENCE: G1E-97
; CURRENT APPLICATION NUMBER: US/10/169,048
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: PCT/GB00/04997
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-169-048-2
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Query Match          90.9%; Score 30; DB 15; Length 221;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 LDASWL 6
        |||||
Db       36 LDASWL 41
```

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RESULT 6
US-09-765-205-14
; Sequence 14, Application US/09765205
; Patent No. US20020034800A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/20010.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 261
; TYPE: PRT
; ORGANISM: human
US-09-765-205-14

Query Match          90.9%; Score 30; DB 9; Length 261;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASWL 6
        |||||:
        161 LDASWV 166

Db

RESULT 7
US-10-360-849A-12
; Sequence 12, Application US/10360849A
; Publication No. US20030220249A1
; GENERAL INFORMATION:
; APPLICANT: Discovery Genomics, Inc.
; APPLICANT: Hackett, Perry
; APPLICANT: Nasevicius, Aldas
; APPLICANT: Essner, Jeffrey
; APPLICANT: Clark, Karl
; APPLICANT: Larson, Jon
; APPLICANT: Ekker, Stephen
; APPLICANT: Roberg-Perez, Sharon
; APPLICANT: Wadman, Shannon
; TITLE OF INVENTION: FACTORS FOR ANGIOGENESIS, VASCULOGENESIS, CARTILAGE FORMATION,
; FILE REFERENCE: 3021.05US02
; CURRENT APPLICATION NUMBER: US/10/360,849A
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/354,978
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 261
; TYPE: PRT
; ORGANISM: danio rerio
US-10-360-849A-12

Query Match          90.9%; Score 30; DB 12; Length 261;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASWL 6
        |||||:
        161 LDASWV 166

Db

RESULT 8
US-10-360-849A-15
; Sequence 15, Application US/10360849A
; Publication No. US20030220249A1
; GENERAL INFORMATION:
; APPLICANT: Discovery Genomics, Inc.
; APPLICANT: Hackett, Perry
; APPLICANT: Nasevicius, Aldas
; APPLICANT: Essner, Jeffrey
; APPLICANT: Clark, Karl
```

```

; APPLICANT: Larson, Jon
; APPLICANT: Ekker, Stephen
; APPLICANT: Roberg-Perez, Sharon
; APPLICANT: Wadman, Shannon
; TITLE OF INVENTION: FACTORS FOR ANGIOGENESIS, VASCULOGENESIS, CARTILAGE FORMATION,
; FILE REFERENCE: 3021.05US02
; CURRENT APPLICATION NUMBER: US/10/360,849A
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/354,978
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 261
; TYPE: PRT
; ORGANISM: mus musculus
US-10-360-849A-15

Query Match          90.9%; Score 30; DB 12; Length 261;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASWL 6
        |||||:
        161 LDASWV 166

Db

RESULT 9
US-10-360-849A-18
; Sequence 18, Application US/10360849A
; Publication No. US20030220249A1
; GENERAL INFORMATION:
; APPLICANT: Discovery Genomics, Inc.
; APPLICANT: Hackett, Perry
; APPLICANT: Nasevicius, Aldas
; APPLICANT: Essner, Jeffrey
; APPLICANT: Clark, Karl
; APPLICANT: Larson, Jon
; APPLICANT: Ekker, Stephen
; APPLICANT: Roberg-Perez, Sharon
; APPLICANT: Wadman, Shannon
; TITLE OF INVENTION: FACTORS FOR ANGIOGENESIS, VASCULOGENESIS, CARTILAGE FORMATION,
; FILE REFERENCE: 3021.05US02
; CURRENT APPLICATION NUMBER: US/10/360,849A
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/354,978
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 261
; TYPE: PRT
; ORGANISM: home sapiens
US-10-360-849A-18

Query Match          90.9%; Score 30; DB 12; Length 261;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASWL 6
        |||||:
        161 LDASWV 166

Db

RESULT 10
US-10-291-265-310
; Sequence 310, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseed, Inc.
; APPLICANT: Tang et al
```

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; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FaecSeq for Windows Version 3.0
; SEQ ID NO 310
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-310

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Query Match          90.9%; Score 30; DB 12; Length 277;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LDASWL 6
    |||:|
Db 161 LDASWL 166

```

```

RESULT 11
US-09-738-626-6970
; Sequence 6970, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASARO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6970
; LENGTH: 919
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6970

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Query Match          90.9%; Score 30; DB 10; Length 919;
Best Local Similarity 83.3%; Pred. No. 3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LDASWL 6
    |||:|
Db 105 LDASWL 110

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RESULT 12
US-09-784-208-3

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; Sequence 3, Application US/09784208
; Patent No. US20010019836A1
; GENERAL INFORMATION:
; APPLICANT: IZUI, HIROSHI
; APPLICANT: ONO, Eiji
; APPLICANT: MATSUI, Kazuhiko
; APPLICANT: MORIYA, Mika
; APPLICANT: ITO, Hisao
; APPLICANT: HARA, Yoshihiko
; TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR
; TITLE OF INVENTION: PRODUCING L-GLUTAMIC ACID
; FILE REFERENCE: 0010-0989-0
; CURRENT APPLICATION NUMBER: US/09/784,208
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/271,438
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: JP 10-69068
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: JP 10-297129
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Enterobacter agglomerans
US-09-784-208-3

```

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Query Match          90.9%; Score 30; DB 9; Length 935;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LDASWL 6
    |||:|
Db 10 LDASWL 15

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RESULT 13
US-10-077-745-1
; Sequence 1, Application US/10077745
; Publication No. US20030172698A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KAZUHIRO
; APPLICANT: KODA, TAKAYUKI
; TITLE OF INVENTION: ORGANIC NITROGEN-CONTAINING COMPOSITION AND FERTILIZER COMPRISIN
; FILE REFERENCE: 219843U50
; CURRENT APPLICATION NUMBER: US/10/077,745
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: JP 2001-044137
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Enterobacter agglomerans
US-10-077-745-1

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Query Match          90.9%; Score 30; DB 12; Length 935;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LDASWL 6
    |||:|
Db 10 LDASWL 15

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RESULT 14
US-10-338-915-1
; Sequence 1, Application US/10338915
; Publication No. US20030190713A1
; GENERAL INFORMATION:

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; APPLICANT: Ueda, Hiroshi
; APPLICANT: Koda, Takayuki
; APPLICANT: Sato, Masakazu
; TITLE OF INVENTION: METHOD FOR PRODUCING L-GLUTAMIC ACID
; FILE REFERENCE: 232696USCONT
; CURRENT APPLICATION NUMBER: US/10/338,915
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 10/077,999
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: JP 2001-044136
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Enterobacter agglomerans
US-10-338-915-1

```

```

Query Match          90.9%; Score 30; DB 12; Length 935;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LDASWL 6
        ||:||||
Db      10 LDSSWL 15

```

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RESULT 15
US-10-078-107-1
; Sequence 1, Application US/10078107
; Publication No. US20020182688A1
; GENERAL INFORMATION:
; APPLICANT: IZUI, HIROSHI
; APPLICANT: HARA, YOSHIIKO
; APPLICANT: SATO, MASAKAZU
; APPLICANT: AKIYOSHI, NAOKI
; TITLE OF INVENTION: METHOD FOR PRODUCING L-GLUTAMIC ACID
; FILE REFERENCE: 219846USO
; CURRENT APPLICATION NUMBER: US/10/078,107
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: JP 2001-044134
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Enterobacter agglomerans
US-10-078-107-1

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Query Match          90.9%; Score 30; DB 14; Length 935;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LDASWL 6
        ||:||||
Db      10 LDSSWL 15

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Search completed: February 18, 2004, 15:41:58  
Job time : 17.7529 secs



PF 02-MAY-2001; 2001WO-US40654.  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S;  
 DR WPI; 2002-179350/23.  
 XX  
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 XX  
 PS Claim 23; Page 44; 82pp; English.  
 XX  
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprising contacting a cell with an anti-inflammatory compound  
 CC (AB08725-AB08742) comprising at least one NEMO binding domain  
 CC (AB077313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of IkbppaB. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polyarthritis, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis, in  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
 CC binding domain of IKKbeta.  
 CC  
 XX  
 SQ Sequence 6 AA;  
 QY  
 Db 1 LDASWL 6  
 1 LDASWL 6  
 Query Match 100.0%; Score 33; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX  
 XX Antiinflammatory; antiaesthetic; cytostatic; antipsoriatic; nootropic;  
 XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 XX autoimmune disorder; multiple sclerosis; transplant rejection;  
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 OS  
 XX Synthetic.  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Finkelstein MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 XX  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 XX Example 6; Page 47; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627) or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IKKbeta. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis, autoimmune diseases such as lupus, polyarthritis, scleroderma,  
 CC granulomatosis, multiple sclerosis, transplant rejection, osteoporosis;  
 CC Alzheimer's disease, atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX  
 SQ Sequence 6 AA;  
 QY  
 Db 1 LDASWL 6  
 1 LDASWL 6  
 Query Match 100.0%; Score 33; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3  
 ABU08425  
 ID ABU08425 standard; peptide; 6 AA.

```

XX AC ABU08425;
XX XX 12-JUN-2003 (first entry)
XX XX
XX DE Human NEMO binding site (NBD) mutant peptide #8.
XX XX
XX KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
XX KW Ikappab kinase-beta; Ikappab kinase-alpha; IKKalpha; NF-kappab;
XX KW nuclear factor-kappaB induction; inflammatory disorder;
XX KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
XX KW atherosclerosis; viral infection; Ataxia telangiectasia;
XX KW transplantation detection; immunosuppressive; osteopathic;
XX KW cyostatic; nocotropic; neuroprotective; antiatherosclerotic; virucide;
XX KW vasotropic; antineumatic; antiahrilic; mutant; mutein.
XX XX
XX OS Homo sapiens.
XX OS Synthetic.
XX XX
XX PN US2002156000-A1.
XX XX
XX PD 24-OCT-2002.
XX XX
XX PP 02-MAY-2001; 2001US-0847940.
XX XX
XX PR 02-MAY-2000; 2000US-201261P.
XX PR 22-AUG-2000; 2000US-0643260.
XX XX
XX PA (MAYM/) MAY M J.
XX PA (GHOS/) GHOSH S.
XX XX
XX PI May MJ, Ghosh S;
XX XX
XX DR WPI; 2003-209142/20.
XX XX
XX PT Novel antiinflammatory peptide compounds comprising NEMO binding
XX PT domain, useful for modulating NF-kappaB induction in a cell and for
XX PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
XX PT psoriasis, vasculitis -
XX XX
XX PS Claim 22; Page 17; 47pp; English.
XX XX
XX CC The present invention relates to antiinflammatory compounds comprising
XX CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
XX CC found on Ikappab kinase-beta (IKKbeta) and Ikappab kinase-alpha
XX CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
XX CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
XX CC in a cell, where the compounds are capable of blocking the interaction
XX CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
XX CC antiinflammatory compound further comprises at least one membrane
XX CC translocation domain. The compounds are useful for treating
XX CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
XX CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
XX CC telangiectasia, and for transplantation detection. The compounds of
XX CC the invention block NF-kappaB induction by IKK but do not inhibit
XX CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
XX CC NBD mutant peptides.
XX XX
XX SQ Sequence 6 AA;

```

```

Query Match 100.0%; Score 33; DB 24; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 LDASWL 6
DB 1 LDASWL 6

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```

RESULT 4
AAG92524
ID AAG92524 standard; Protein; 105 AA.
XX

```

```

AC AAG92524;
XX XX 26-SEP-2001 (first entry)
XX XX
XX DE C glutamicum protein fragment SEQ ID NO: 6278.
XX XX
XX KW Corynebacterium; amino acid synthesis; vitamin; saccharide;
XX KW organic acid synthesis.
XX XX
XX OS Corynebacterium glutamicum.
XX XX
XX PN EPI108790-A2.
XX XX
XX PD 20-JUN-2001.
XX XX
XX PP 18-DEC-2000; 2000EP-0127688.
XX XX
XX PR 16-DEC-1999; 99JP-0377484.
XX PR 07-APR-2000; 2000JP-0159152.
XX PR 03-AUG-2000; 2000JP-0280988.
XX XX
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX XX
XX PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
XX PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX XX
XX DR WPI; 2001-376931/40.
XX DR N-PSDB; AAH67743.
XX XX
XX XX Novel polynucleotides derived from Corynebacterium bacteria, for identifying
XX PT mutation point of a gene, measuring expression of a gene, analysing
XX PT expression profile or pattern of a gene and identifying homologous gene
XX PT
XX PS Claim 17; SEQ ID NO: 6278; 246pp + sequence listing; English.
XX XX
XX CC The present invention provides a number of nucleotide and protein
XX CC sequences from the Corynebacterium glutamicum. These
XX CC are useful for identifying the mutation point of a gene derived from a
XX CC mutant of corynebacterium, measuring expression amount and
XX CC analysing the expression profile or expression pattern of a gene derived
XX CC from Corynebacterium bacterium, and identifying a homologue of a gene derived
XX CC from corynebacterium. Corynebacterium bacteria are useful for producing
XX CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
XX CC particularly L-lysine. The present sequence is a protein described
XX CC in the exemplification of the invention.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from the
XX CC European Patent Office.
XX XX
XX SQ Sequence 105 AA;

```

```

Query Match 100.0%; Score 33; DB 22; Length 105;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 LDASWL 6
DB 48 LDASWL 53

```

```

RESULT 5
ABB77295
ID ABB77295 standard; protein; 756 AA.
XX

```

```

XX AC ABB77295;
XX XX 14-JUN-2002 (first entry)
XX XX
XX DE Human IKKbeta mutant W739A.
XX XX
XX KW IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
XX KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
XX

```

KM autoimmune disease; transplant rejection; osteoporosis; cancer;  
 KM Alzheimer's disease; viral; infection; aschma; anaphylaxis; psoriasis;  
 KM rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 KM corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;  
 KM osteopathic; cytoskeletal; nocotropic; neuroprotective; anti-HIV; human;  
 KM antiarteriosclerotic; virucide; antiaslomatic; anti-allergic;  
 KM dermatological; antibacterial; antipsoriatic; antineumatic;  
 KM antirheumatic; osteopathic; antitumor; mutant; mutagen.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FH MISC-difference 739 /note= "Wildtype Trp substituted by Ala"  
 FT  
 PN MO200183547-A2.  
 PD 08-NOV-2001.  
 XX 02-MAY-2001; 2001MO-US40654.  
 PF  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX (UYVA ) UNIV YALE.  
 PA May MJ, Ghosh S;  
 PI WPI; 2002-179350/23.  
 DR  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 XX Example 11; Page -: 82pp; English.  
 PS  
 XX The invention relates to modulating NF-kappaB (NF-KB) induction in a cell  
 CC comprising contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-KB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of IkbppaB. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-KB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polyomyelitis, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections,  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta  
 CC mutant, useful in examples of the invention.  
 CC Note: The present sequence is not given in the specification but is

CC derived from Genbank Accession No. 014920 (ABB772294).  
 XX  
 SQ Sequence 756 AA;  
 Query Match 100.0%; Score 33; DB 23; Length 756;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 IDASWL 6  
 DB 737 IDASWL 742  
 RESULT 6  
 AAG32182  
 ID AAG32182 standard; Protein; 618 AA.  
 XX  
 AC AAG32182;  
 XX  
 DT 17-OCT-2000 (first entry)  
 XX  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 38774.  
 XX  
 KW Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN EP103405-A2.  
 PD 06-SEP-2000.  
 XX  
 PF 25-FEB-2000; 2000EP-0301439.  
 XX  
 PR 25-FEB-1999; 99US-0121825.  
 PR 05-MAR-1999; 99US-0123180.  
 PR 09-MAR-1999; 99US-0123548.  
 PR 23-MAR-1999; 99US-0125788.  
 PR 25-MAR-1999; 99US-0126264.  
 PR 29-MAR-1999; 99US-0126785.  
 PR 01-APR-1999; 99US-0127462.  
 PR 06-APR-1999; 99US-0128234.  
 PR 08-APR-1999; 99US-0128714.  
 PR 16-APR-1999; 99US-0128845.  
 PR 19-APR-1999; 99US-0130077.  
 PR 21-APR-1999; 99US-0130449.  
 PR 23-APR-1999; 99US-0130510.  
 PR 23-APR-1999; 99US-0130891.  
 PR 28-APR-1999; 99US-0131449.  
 PR 30-APR-1999; 99US-0132408.  
 PR 30-APR-1999; 99US-0132407.  
 PR 04-MAY-1999; 99US-0132484.  
 PR 05-MAY-1999; 99US-0132485.  
 PR 06-MAY-1999; 99US-0132486.  
 PR 06-MAY-1999; 99US-0132487.  
 PR 07-MAY-1999; 99US-0132863.  
 PR 11-MAY-1999; 99US-0134256.  
 PR 14-MAY-1999; 99US-0134218.  
 PR 14-MAY-1999; 99US-0134219.  
 PR 14-MAY-1999; 99US-0134221.  
 PR 14-MAY-1999; 99US-0134370.  
 PR 18-MAY-1999; 99US-0134768.  
 PR 19-MAY-1999; 99US-0134941.  
 PR 20-MAY-1999; 99US-0135124.  
 PR 21-MAY-1999; 99US-0135353.  
 PR 24-MAY-1999; 99US-0135629.  
 PR 25-MAY-1999; 99US-0136021.  
 PR 27-MAY-1999; 99US-0136392.  
 PR 28-MAY-1999; 99US-0136782.  
 PR 01-JUN-1999; 99US-0137222.  
 PR 03-JUN-1999; 99US-0137528.  
 PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139493.  
PR 18-JUN-1999; 99US-0139494.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139750.  
PR 21-JUN-1999; 99US-0139763.  
PR 22-JUN-1999; 99US-0139817.  
PR 23-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 24-JUN-1999; 99US-0140354.  
PR 28-JUN-1999; 99US-0140695.  
PR 29-JUN-1999; 99US-0140823.  
PR 30-JUN-1999; 99US-0140991.  
PR 01-JUL-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 02-JUL-1999; 99US-0142154.  
PR 06-JUL-1999; 99US-0142055.  
PR 08-JUL-1999; 99US-0142390.  
PR 09-JUL-1999; 99US-0142803.  
PR 12-JUL-1999; 99US-0142920.  
PR 13-JUL-1999; 99US-0142977.  
PR 14-JUL-1999; 99US-0143542.  
PR 15-JUL-1999; 99US-0143624.  
PR 16-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
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PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
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PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.

PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
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PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
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PR 26-AUG-1999; 99US-0150864.  
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PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151067.  
PR 30-AUG-1999; 99US-0151080.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
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PR 15-SEP-1999; 99US-0154019.  
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PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155119.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0156539.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
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PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
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PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
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PR 21-OCT-1999; 99US-0160815.  
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PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 93.9%; Score 31; DB 21; Length 618;  
Beet local Similarity 83.3%; Pred. No. 1.5e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;







PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 28-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
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PR 09-JUL-1999; 99US-0142920.  
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PR 15-JUL-1999; 99US-0144005.  
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PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
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PR 09-AUG-1999; 99US-0147493.  
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PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
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PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
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PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
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PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
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PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
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PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
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PR 18-OCT-1999; 99US-0159884.  
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PR 22-OCT-1999; 99US-0160989.  
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PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161922.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 93.9%; Score 31; DB 21; Length 763;  
Best Local Similarity 83.3%; Pred. No. 1.8e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
DB 613 LDASWI 618

RESULT 9  
ABG20551  
ID ABG20551 standard; Protein; 117 AA.

XX ABG20551;  
AC  
XX  
XX 18-FEB-2002 (first entry)  
DT  
XX

DE		Novel human diagnostic protein #20542.
XX		
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;	
KW	food supplement; medical imaging; diagnostic; genetic disorder.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200175067-A2.	
XX		
PD	11-OCT-2001.	
XX		
PF	30-MAR-2001; 2001WO-US08631.	
XX		
PR	31-MAR-2000; 2000US-0540217.	
RR	23-AUG-2000; 2000US-0649167.	
XX		
PA	(HYSE-) HYSEQ INC.	
XX		
PI	Drimac RT, Liu C, Tang YT,	
XX		
DR	WPI; 2001-639362/73.	
XX	N-PsDB; AAS84738.	
XX		
PT	New isolated polynucleotide and encoded polypeptides, useful in	
PT	diagnostics, forensics, gene mapping, identification of mutations	
PT	responsible for genetic disorders or other traits and to assess	
PT	biodiversity -	
PS		
PS	Claim 20; SEQ ID No 50910; 103pp; English.	
XX		
CC	The invention relates to isolated polynucleotide (I) and	
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,	
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome	
CC	and genome mapping, and in recombinant production of (II). The	
CC	polynucleotides are also used in diagnostics as expressed sequence tags	
CC	for identifying expressed genes. (I) is useful in gene therapy techniques	
CC	to restore normal activity of (II) or to treat disease states involving	
CC	(II). (II) is useful for generating antibodies against it, detecting or	
CC	quantitating a polypeptide in tissue, as molecular weight markers and as	
CC	a food supplement. (II) and its binding partners are useful in medical	
CC	imaging of sites expressing (II). (I) and (II) are useful for treating	
CC	disorders involving aberrant protein expression or biological activity.	
CC	The polypeptide and polynucleotide sequences have applications in	
CC	diagnostics, forensics, gene mapping, identification of mutations	
CC	responsible for genetic disorders or other traits to assess biodiversity	
CC	and to produce other types of data and products dependent on DNA and	
CC	amino acid sequences. ABG00010-ABG3037 represent novel human	
CC	diagnostic amino acid sequences of the invention.	
CC	Note: The sequence data for this patent did not appear in the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences.	
XX		
SQ	Sequence 117 AA:	
OY	Query Match 90.9%; Score 30; DB 22; Length 117;	
	Best Local Similarity 83.3%; Pred. No. 3.8e+02;	
Db	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0.	
	1 LDASWL 6	
	:	
	38 LIDANWL 43	
RESULT 10		
ID	AAB42606 standard; Protein; 119 AA.	
XX	AAB42606	
AC	AAB42606;	
XX		
DT	08-FEB-2001 (first entry)	
XX		
DE	Human ORFX ORF2370 polypeptide sequence SEQ ID NO:4740.	
XX		

KV		Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW	vulnerary; antiposoriatic; antiparkinsonian; nootropic; neuroprotective;	
KM	anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiac;	
KX	immunostimulant; thrombolytic coagulant; vasotrophic; antididiabetic;	
KY	hypotenusive; dermatological; immunosuppressive; antifibrematous;	
KZ	antiviral; antibacterial; antifungal; antirheumatic; antichyroid;	
LA	antihaemic; gene therapy; cancer; proliferative disorder; hypertension;	
LB	neurodegenerative disorder; osteoarthritis; graft vs host disease;	
LC	cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;	
LD	cholesterol ester storage; systemic lupus erythematosus; infection;	
LE	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;	
LF	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;	
LK	bone damage; cartilage damage; antiinflammatory disease; coagulation;	
LM	thrombolysis; contraceptive.	
LN		
LO	Homo sapiens.	
LP		
LQ	WO200058473-A2.	
LR		
LS	05-OCT-2000.	
LT		
LU	31-MAR-2000; 200OWO-US08621.	
LV		
LW	31-MAR-1999; 99US-0127607.	
LX	02-APR-1999; 99US-0127636.	
LY	05-APR-1999; 99US-0127728.	
LZ	30-MAR-2000; 2000US-0540763.	
MA	(CURA-) CURAGEN CORP.	
MB		
MC	Shinkets RA, Leach M;	
MD	WP1; 2000-602362/57.	
ME	DR N-PADB; AAC76815.	
MF		
MG	XX Novel nucleic acids and peptides derived from open reading frame X,	
MH	PT useful for treating e.g. cancers, proliferative disorders,	
MI	PD neurodegenerative disorders and cardiovascular disease -	
MJ	PS Claim 11; Page 3920; 5507PP; English.	
ML	XX	
MM	XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,	
MN	CC which represent the human ORFX open reading frames 1 to 3161. The ORFX	
MO	CC sequences have activities such as: cytotoxic; hepatocytropic; vulnerary;	
MP	CC antipsoriasis; antiparkinsonian; nocrotic; neutropoietic;	
MQ	CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;	
MR	CC immunostimulant; cardiac; thrombolytic coagulant; vasotrophic;	
MS	CC antidiabetic; hypotensive; dermatologic; immunosuppressive;	
MT	CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;	
MU	CC antichyroid; and antihaemic. The sequences can be used for determining	
MV	CC the presence of or predisposition to, or preventing or treating	
MW	CC pathological conditions associated with an ORFX-associated disorder. The	
MX	CC nucleic acids can be used to express ORFX proteins in gene therapy	
MY	CC vectors. The proteins and nucleic acids may be used to treat cancers,	
MZ	CC proliferative disorders, neurodegenerative disorders, osteoarthritis,	
NA	CC graft vs host disease, cardiovascular disease, diabetes mellitus,	
NB	CC hyperextension, hypothyroidism, cholesterol ester storage, systemic lupus	
NC	CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,	
ND	CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,	
NE	CC allergic, aplastic anaemia, burns, wounds, bone and cartilage damage,	
NF	CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance	
NG	CC coagulation; to inhibit thrombolysis; and as a contraceptive.	
NH	CC	
NI	Sequence 119 AA;	
NL		
NN	Query Match 90.9%; Score 30; DB 21; Length 119;	
NO	Best Local Similarity 83.3%; Pred. No. 3.9e+02;	
NP	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
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NS		
NT	29 LDAAAML 34	
NU		
NV		
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NX		
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OC		
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OJ		
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OX		
OY		
OA		
OB		

RESULT 11  
AAE03936  
ID AAE03936 standard; Protein; 156 AA.  
XX  
XX AAE03936;  
AC  
XX  
DT 09-AUG-2001 (first entry)  
XX  
XX Human gene 39 encoded secreted protein HBMD08, SEQ ID NO:39.  
XX  
XX Human; secreted protein; proliferative disorder; cancer; tumour;  
XX foetal abnormality; developmental abnormality; hematopoietic disorder;  
XX immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
XX inflammation; allergy; neurological disorder; Alzheimer's disease;  
XX Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
XX skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
XX cardiovascular disorder; angioimmunoblastic lymphadenopathy;  
XX gastrointestinal disorder; pregnancy-related disorder;  
XX endocrine disorder; infection; wound healing; vulnery;  
XX cell culture; chemotaxis; food additive; gene therapy;  
XX binding partner identification.  
XX  
XX Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..28  
XX /label= signal\_peptide  
XX FT 29..156  
XX FT Protein /note= "Mature secreted protein"  
XX  
XX  
XX NO200077022-A1.  
XX  
XX 21-DEC-2000.  
XX  
XX 01-JUN-2000; 2000WO-US15136.  
XX  
XX 11-JUN-1999; 99US-0138629.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX  
XX Rosen CA, Ruben SM, Komatsoulis GA;  
XX  
XX WPI; 2001-367020/38.  
XX  
XX N-PSDB; AAD08383.  
XX  
XX  
XX Nucleic acids encoding 50 human secreted polypeptides, useful for  
XX preventing, diagnosing and/or treating diseases, e.g. Parkinson's  
XX disease, botulism, cancers and Scimitar syndrome -  
XX  
XX  
XX Claim 11; Page 547; 614pp; English.  
XX  
XX  
XX AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted  
XX protein genes and AAE03898-AAE03947 represent the proteins they encode.  
XX AAE03948-AAE03996 represent human secreted protein fragments or variants.  
XX  
XX The genes and their secreted proteins are useful for preventing,  
XX treating or ameliorating medical conditions, e.g., by protein or gene  
XX therapy. Pathological conditions can be diagnosed by determining the  
XX amount of the new protein in a sample or by determining the presence of  
XX mutations in the new genes. Specific uses are described for each of the  
XX 50 genes, based on the tissues in which they are most highly expressed,  
XX and include developing products for the diagnosis or treatment of  
XX proliferative disorders, cancer, tumours, foetal and developmental  
XX abnormalities, hematopoietic disorders, diseases of the immune system,  
XX AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,  
XX allergies, neurological disorders (e.g., Alzheimer's disease,  
XX Parkinson's disease), cognitive disorders, schizophrenia, asthma,  
XX skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,  
XX cardiovascular disorders, angiogenic disorders, kidney disorders,  
XX gastrointestinal disorders, pregnancy-related disorders, endocrine  
XX disorders, and infections. The proteins can also be used to aid wound  
XX healing and epithelial cell proliferation, to prevent skin aging due to  
XX sunburn, to maintain organs before transplantation, for supporting cell

CC culture of primary tissues, to regenerate tissues, to identify their  
CC cognate ligands or binding partners, and in chemotaxis, and can be used  
CC as a food additive or preservative to modify storage properties.  
CC Antibodies specific for a protein of the invention can be used in  
CC alleviating symptoms associated with the disorders mentioned above, and  
CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked  
CC immunosorbent assay (ELISA). The present sequence represents a human  
CC secreted protein of the invention.  
XX  
XX  
SQ Sequence 156 AA;  
XX  
XX  
Query Match 90.9%; Score 30; DB 22; Length 156;  
Best Local Similarity 83.3%; Pred. No. 5.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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XX  
QY 1 LDASWL 6  
XXXXXX  
Db 56 LDASWV 61  
XX  
XX  
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AAE03978  
ID AAE03978 standard; Protein; 189 AA.  
XX  
XX AAE03978;  
AC  
XX  
XX  
XX 09-AUG-2001 (first entry)  
XX  
XX  
XX Human gene 39 encoded secreted protein fragment, SEQ ID NO:172.  
XX  
XX  
XX Human; secreted protein; proliferative disorder; cancer; tumour;  
XX foetal abnormality; developmental abnormality; hematopoietic disorder;  
XX immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
XX inflammation; allergy; neurological disorder; Alzheimer's disease;  
XX Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
XX skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
XX cardiovascular disorder; angioimmunoblastic lymphadenopathy;  
XX gastrointestinal disorder; pregnancy-related disorder;  
XX endocrine disorder; infection; wound healing; vulnery;  
XX cell culture; chemotaxis; food additive; gene therapy;  
XX binding partner identification.  
XX  
XX  
XX Homo sapiens.  
XX  
XX  
XX NO200077022-A1.  
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XX 21-DEC-2000.  
XX  
XX 01-JUN-2000; 2000WO-US15136.  
XX  
XX 11-JUN-1999; 99US-0138629.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
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XX Rosen CA, Ruben SM, Komatsoulis GA;  
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XX WPI; 2001-367020/38.  
XX  
XX  
XX Nucleic acids encoding 50 human secreted polypeptides, useful for  
XX preventing, diagnosing and/or treating diseases, e.g. Parkinson's  
XX disease, botulism, cancers and Scimitar syndrome -  
XX  
XX  
XX Disclosure; Page 593; 614pp; English.  
XX  
XX  
XX AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted  
XX protein genes and AAE03898-AAE03947 represent the proteins they encode.  
XX AAE03948-AAE03996 represent human secreted protein fragments or variants.  
XX  
XX The genes and their secreted proteins are useful for preventing,  
XX treating or ameliorating medical conditions, e.g., by protein or gene  
XX therapy. Pathological conditions can be diagnosed by determining the  
XX amount of the new protein in a sample or by determining the presence of  
XX mutations in the new genes. Specific uses are described for each of the  
XX 50 genes, based on the tissues in which they are most highly expressed,

CC and include developing products for the diagnosis or treatment of  
 CC proliferative disorders, cancer, tumours, foetal and developmental  
 CC abnormalities, haematopoietic disorders, diseases of the immune system,  
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,  
 CC allergies, neurological disorders (e.g., Alzheimer's disease,  
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,  
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,  
 CC cardiovascular disorders, angiotensin disorders, kidney disorders,  
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine  
 CC disorders, and infections. The proteins can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin aging due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues, to identify their  
 CC cognate ligands or binding partners, and in chemotaxis, and can be used  
 CC as a food additive or preservative to modify storage properties.  
 CC Antibodies specific for a protein of the invention can be used in  
 CC alleviating symptoms associated with the disorders mentioned above, and  
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked  
 CC immunosorbent assay (ELISA). The present sequence represents a human  
 CC secreted protein fragment referred to in the disclosure of the invention.

XX Sequence 189 AA;

Query Match 90.9%; Score 30; DB 22; Length 189;  
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
 |||||  
 Db 164 LDASWV 169

#### RESULT 13

AAU14439  
 ID AAU14439 standard; Protein; 191 AA.

AC AAU14439;

DT 24-OCT-2001 (first entry)

DE Human novel protein #310.

XX Human; novel protein; Antinaemic; osteopathic; antiinflammatory;  
 KW immunomodulatory; cytoskeletal; neuroprotective; vulnery; nocrotic;  
 KW anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;  
 KW antibacterial; antiallergic; dermatological; haemostatic; antiaesthetic;  
 KW chemoalytic; immunogen; antibody; gene therapy; neurological disorder;  
 KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;  
 KW tissue regeneration; immune disorder.

XX Homo sapiens.

OS WO200155437-A2.

PN 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02623.

PR 25-JAN-2000; 2000US-0491404.

PA (HSE-) HSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-451939/48.

DR N-PSDB; AAS22744.

XX Isolated polypeptides useful for treating anti-inflammatory diseases,  
 PT nervous system disorders, and for regenerating bone and cartilage -

PS Example 4; Page 816; 894pp; English.

XX The invention relates to polynucleotides encoding novel human

CC proteins or their active domains. The polypeptides, polynucleotides and  
 CC antibodies raised against the polypeptides are used in a method of  
 CC treatment of a mammal and prevention of disorders caused by the aberrant  
 CC protein expression or activity. The polypeptides can be used as  
 CC molecular weight markers, food supplements, and in antibody production.  
 CC The polypeptides are used to identify compounds which bind to the  
 CC polypeptides. Polynucleotides of the invention are used as probes and  
 CC primers, for sequencing, for chromosome or gene mapping, in the  
 CC production of recombinant proteins, and in generating anti-gene DNA or  
 CC RNA and in gene therapy. Polypeptides of the invention can be used to  
 CC target drugs to a tumour, in assays to determine biological activity, to  
 CC raise antibodies/elicits an immune response, to determine quantitative  
 CC protein levels, as tissue markers, and to isolate receptors or ligands.  
 CC Polypeptides of the invention may also be useful in treating platelet  
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting  
 CC the proliferation, differentiation and survival of stem cells, as a  
 CC contraceptive, treating osteoporosis and osteoarthritis, anemia,  
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
 CC fungal infection or from autoimmunity, cancer, allergy, asthma,  
 CC graft-versus-host disease, eczema, haemophilia, thrombosis,  
 CC anti-inflammatory diseases, nervous system disorders, and infection.  
 CC The present sequence represents a protein of the invention.

XX Sequence 191 AA;

Query Match 90.9%; Score 30; DB 22; Length 191;  
 Best Local Similarity 83.3%; Pred. No. 6.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
 |||||  
 Db 161 LDASWV 166

#### RESULT 14

AAU03119  
 ID AAU03119 standard; Protein; 221 AA.

AC AAU03119;

DT 23-OCT-2001 (first entry)

DE Streptococcus pyogenes virulence protein #1.

XX Virulence; attenuated microorganism; Streptococcal infection;  
 KW Gram-positive bacteria; antimicrobial; impetigo; pneumonia.

XX Streptococcus pyogenes.

OS WO200148208-A2.

PN 05-JUL-2001.

XX 22-DEC-2000; 2000WO-GB04997.

PR 23-DEC-1999; 99GB-0030462.

PR 23-DEC-1999; 99GB-0030463.

PR 23-DEC-1999; 99GB-0030464.

PR 23-DEC-1999; 99GB-0030465.

PR 23-DEC-1999; 99GB-0030466.

PR 23-DEC-1999; 99GB-0030467.

PR 23-DEC-1999; 99GB-0030468.

PR 23-DEC-1999; 99GB-0030469.

PR 23-DEC-1999; 99GB-0030470.

PR 23-DEC-1999; 99GB-0030471.

PR 23-DEC-1999; 99GB-0030472.

PR 23-DEC-1999; 99GB-0030473.

PR 23-DEC-1999; 99GB-0030474.

PR 17-FEB-2000; 2000GB-0003725.

PR 17-FEB-2000; 2000GB-0003726.

PR 17-FEB-2000; 2000GB-0003727.

PR 17-FEB-2000; 2000GB-0003728.

PR 17-FEB-2000; 2000GB-0003729.

PR 17-FEB-2000; 2000GB-0003730.

PR 17-FEB-2000; 2000GB-0003731.  
 PR 17-FEB-2000; 2000GB-0003732.  
 PR 17-FEB-2000; 2000GB-0003733.  
 PR 02-MAY-2000; 2000GB-0010585.  
 PR 02-MAY-2000; 2000GB-0010587.  
 XX  
 PA (MICR-) MICROSCIENCE LTD.  
 PI  
 PI Clarke BE, Zhou L, Shea JE, Feldman RG, Holden DW;  
 DR WPI; 2001-41825/44.  
 DR N-PSDB; AAS06351.  
 XX  
 PT Novel peptide obtained from Streptococcus pyogenes useful for treating  
 PT or preventing a condition associated with infection by Streptococcal or  
 PT Gram-positive bacteria, preferably pneumonia -  
 XX  
 PS Claim 4; Page 26-27; 91pp; English.  
 CC  
 CC AAU03119-AAU03149 represent novel Streptococcus pyogenes virulence  
 CC proteins #1-31. The S. pyogenes virulence genes can be used to  
 CC produce attenuated microorganisms comprising a mutation that disrupt  
 CC the expression of the virulence protein. The virulence genes, proteins  
 CC or an attenuated microorganism are useful for therapeutic or diagnostic  
 CC purposes. DNA encoding the virulence proteins, the proteins themselves,  
 CC an attenuated microorganism or a vaccine comprising the virulence  
 CC protein are useful for the manufacture of a medicament for use in  
 CC the treatment or prevention of a condition associated with infection  
 CC by Streptococcal or Gram-positive bacteria, for veterinary treatment,  
 CC and in a screening assay for the identification of an antimicrobial  
 CC drug. Disorders which can be treated using S. pyogenes virulence  
 CC polynucleotide and polypeptide sequences include non-invasive infections  
 CC and invasive infections e.g. impetigo, pharyngitis, necrotising  
 CC fasciitis, bacteraemia, streptococcal toxic shock syndrome (STSS),  
 CC pneumonia and rheumatic fever. The virulence proteins are also useful  
 CC in the preparation of antibodies.  
 CC  
 SQ Sequence 221 AA;  
 XX  
 Query Match 90.9%; Score 30; DB 22; Length 221;  
 Best Local Similarity 83.3%; Pred. No. 7.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDASWL 6  
 Db 36 LDAAWL 41  
 RESULT 15  
 ABP27441  
 ID ABP27441 standard; Protein; 221 AA.  
 XX  
 AC ABP27441;  
 XX  
 DT 02-JUL-2002 (first entry)  
 XX  
 DE Streptococcus polypeptide SEQ ID NO 4056.  
 XX  
 KM Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
 KM group A streptococcus; Streptococcus pyogenes; antibacterial;  
 KM antiinflammatory; infection; vaccine; meningitis; gene therapy.  
 XX  
 OS Streptococcus pyogenes.  
 XX  
 PN MO200234771-A2.  
 XX  
 PD 02-MAY-2002.  
 XX  
 PP 29-OCT-2001; 2001WO-GB04789.  
 XX  
 PR 27-OCT-2000; 2000GB-0026333.  
 PR 24-NOV-2000; 2000GB-0028727.  
 PR 07-MAR-2001; 2001GB-0005640;

XX  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 XX  
 PI Telford J, Maignani V, Margalit Ros YI, Grandi G, Fraser C;  
 PI Tettein H;  
 XX  
 DR WPI; 2002-352536/38.  
 DR N-PSDB; ABN68072.  
 XX  
 PT New Streptococcus protein for the treatment or prevention of infection  
 PT or disease caused by Streptococcus bacteria, such as meningitis, and  
 PT for detecting a compound that binds to the protein -  
 XX  
 PS Claim 1; Page 3561; 4525pp; English.  
 CC  
 CC The invention relates to a protein (ABP25413-ABP30895) from group B  
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
 CC the specification. The proteins have antibacterial and antiinflammatory  
 CC activity. (I), nucleic acids encoding (I), ABN6604-ABN71526 and  
 CC antibodies that bind (I) are used in the manufacture of medicaments for  
 CC the treatment or prevention of infection or disease caused by  
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
 CC biological sample. (I) is used to determine whether a compound binds to  
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
 CC used as a vaccine or diagnostic composition. The disease caused by  
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
 CC acid encoding (I) may be used to recombinantly produce (I) and may be  
 CC used in gene therapy. Antibodies to (I) are used for affinity  
 CC chromatography, immunoassays, and distinguishing/identifying  
 CC Streptococcus proteins.  
 CC  
 SQ Sequence 221 AA;  
 XX  
 Query Match 90.9%; Score 30; DB 23; Length 221;  
 Best Local Similarity 83.3%; Pred. No. 7.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDASWL 6  
 Db 36 LDAAWL 41  
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 Job time : 23.7763 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds  
(without alignments)  
75.239 Million cell updates/sec

Title: US-09-643-260-9

Perfect score: 40

Sequence: 1 LNMWML 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
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11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	10 US-09-847-940B-9	Sequence 9, Appl1
2	40	100.0	6	11 US-09-847-946A-9	Sequence 9, Appl1
3	36	90.0	117	11 US-09-809-391-360	Sequence 360, App
4	36	90.0	117	12 US-09-882-171-360	Sequence 360, App
5	36	90.0	117	12 US-10-108-260A-2983	Sequence 2983, App
6	36	90.0	464	9 US-09-815-242-10647	Sequence 10647, A
7	36	90.0	9	US-09-815-242-4997	Sequence 4997, App
8	36	90.0	864	12 US-10-436-715-82	Sequence 82, Appl1
9	36	90.0	864	12 US-10-436-715-82	Sequence 82, Appl1
10	35	87.5	6	10 US-09-847-940B-2	Sequence 2, Appl1
11	35	87.5	6	11 US-09-847-946A-2	Sequence 2, Appl1
12	35	87.5	6	11 US-09-847-946A-3	Sequence 3, Appl1
13	35	87.5	7	11 US-09-847-946A-37	Sequence 37, Appl1
14	35	87.5	8	11 US-09-847-946A-30	Sequence 30, Appl1
15	35	87.5	8	11 US-09-847-946A-38	Sequence 38, Appl1

16	35	87.5	9	11 US-09-847-946A-29	Sequence 29, Appl1
17	35	87.5	9	11 US-09-847-946A-32	Sequence 32, Appl1
18	35	87.5	9	11 US-09-847-946A-35	Sequence 35, Appl1
19	35	87.5	9	11 US-09-847-946A-36	Sequence 36, Appl1
20	35	87.5	10	11 US-09-847-946A-31	Sequence 31, Appl1
21	35	87.5	10	11 US-09-847-946A-34	Sequence 34, Appl1
22	35	87.5	11	11 US-09-847-946A-28	Sequence 28, Appl1
23	35	87.5	11	11 US-09-847-946A-132	Sequence 132, Appl1
24	35	87.5	11	11 US-09-847-946A-140	Sequence 140, App
25	35	87.5	13	11 US-09-847-946A-143	Sequence 143, App
26	35	87.5	13	11 US-09-847-946A-144	Sequence 144, App
27	35	87.5	13	11 US-09-847-946A-145	Sequence 145, App
28	35	87.5	13	11 US-09-847-946A-148	Sequence 148, App
29	35	87.5	17	11 US-09-847-946A-141	Sequence 141, App
30	35	87.5	17	11 US-09-847-946A-142	Sequence 142, App
31	35	87.5	17	11 US-09-847-946A-146	Sequence 146, App
32	35	87.5	17	11 US-09-847-946A-147	Sequence 147, App
33	35	87.5	18	11 US-09-847-946A-131	Sequence 131, App
34	35	87.5	18	11 US-09-847-946A-135	Sequence 135, App
35	35	87.5	18	11 US-09-847-946A-136	Sequence 136, App
36	35	87.5	22	11 US-09-847-946A-133	Sequence 133, App
37	35	87.5	22	11 US-09-847-946A-134	Sequence 134, App
38	35	87.5	22	11 US-09-847-946A-137	Sequence 137, App
39	35	87.5	22	11 US-09-847-946A-139	Sequence 139, App
40	35	87.5	28	10 US-09-847-940B-18	Sequence 18, Appl1
41	35	87.5	28	10 US-09-847-940B-18	Sequence 18, Appl1
42	35	87.5	222	10 US-09-771-161A-141	Sequence 141, App
43	35	87.5	745	9 US-09-796-872-2	Sequence 2, Appl1
44	35	87.5	745	10 US-09-844-908-10	Sequence 10, Appl1
45	35	87.5	745	10 US-09-844-908-10	Sequence 10, Appl1

## ALIGNMENTS

RESULT 1  
US-09-847-940B-9  
Sequence 9, Application US/09847940B  
Patent No. US2002015600A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J.  
TITLE OR INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-117CP  
CURRENT APPLICATION NUMBER: US/09/847, 940B  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-9

Query Match 100.0%; Score 40; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LNMWML 6  
Db 1 LNMWML 6

RESULT 2  
US-09-847-946A-9  
Sequence 9, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar  
APPLICANT: Fındeıs, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hamid, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PRI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NBD peptide  
US-09-647-946A-9

Query Match 100.0%; Score 40; DB 11; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7e+05; 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;

QY 1 LNMSWL 6  
Db 1 LNMSWL 6

RESULT 3  
US-09-809-391-360  
Sequence 360, Application US/09809391  
Publication No. US20030049618A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P2  
CURRENT APPLICATION NUMBER: US/09/809,391  
CURRENT FILING DATE: 2001-03-16  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 761  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 360  
LENGTH: 117  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-809-391-360

Query Match 90.0%; Score 36; DB 11; Length 117;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSW 5  
Db 30 LNMSW 34

RESULT 4  
US-09-882-171-360  
Sequence 360, Application US/09882171  
Publication No. US20030175858A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P2  
CURRENT APPLICATION NUMBER: US/09/882,171  
CURRENT FILING DATE: 2001-06-18  
PRIOR APPLICATION NUMBER: 09/809,391  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 09/149,476  
PRIOR FILING DATE: 1998-09-08

PRIOR APPLICATION NUMBER: PCT/US98/04493  
PRIOR FILING DATE: 1998-03-06  
PRIOR APPLICATION NUMBER: 60/040,162  
PRIOR FILING DATE: 1997-03-07  
PRIOR APPLICATION NUMBER: 60/040,333  
PRIOR FILING DATE: 1997-03-07  
PRIOR APPLICATION NUMBER: 60/038,621  
PRIOR FILING DATE: 1997-03-07  
PRIOR APPLICATION NUMBER: 60/040,626  
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PRIOR FILING DATE: 1997-03-07  
PRIOR APPLICATION NUMBER: 60/040,336  
PRIOR FILING DATE: 1997-03-07  
PRIOR APPLICATION NUMBER: 60/040,163  
PRIOR FILING DATE: 1997-03-07  
PRIOR APPLICATION NUMBER: 60/047,600  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: 60/047,615  
PRIOR FILING DATE: 1997-05-23  
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PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: 60/047,584  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: 60/047,500  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: 60/047,587  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: 60/047,492  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: 60/047,598  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: 60/047,613  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: 60/047,582  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: 60/047,596  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: 60/047,612  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: 60/047,632  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: 60/047,601  
PRIOR FILING DATE: 1997-05-23  
PRIOR APPLICATION NUMBER: 60/043,580  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: 60/043,568  
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PRIOR APPLICATION NUMBER: 60/043,314  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: 60/043,569  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: 60/043,311  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: 60/043,671  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: 60/043,674

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;; PRIOR APPLICATION NUMBER: 60/056,893  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,630  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,878  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,662  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,872  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,882  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,637  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,903  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,888  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,879  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,880  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,894  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,911  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,636  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,874  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,910  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,864  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,631  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,845  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,892  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/057,761  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/047,595  
;; PRIOR FILING DATE: 1997-05-23  
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;; PRIOR APPLICATION NUMBER: 60/047,588  
;; PRIOR FILING DATE: 1997-05-23  
;; PRIOR APPLICATION NUMBER: 60/047,585  
;; PRIOR FILING DATE: 1997-05-23  
;; PRIOR APPLICATION NUMBER: 60/047,586  
;; PRIOR FILING DATE: 1997-05-23  
;; PRIOR APPLICATION NUMBER: 60/047,590  
;; PRIOR FILING DATE: 1997-05-23

;; PRIOR APPLICATION NUMBER: 60/047,594  
;; PRIOR FILING DATE: 1997-05-23  
;; PRIOR APPLICATION NUMBER: 60/047,589  
;; PRIOR FILING DATE: 1997-05-23  
;; PRIOR APPLICATION NUMBER: 60/047,593  
;; PRIOR FILING DATE: 1997-05-23  
;; PRIOR APPLICATION NUMBER: 60/047,614  
;; PRIOR FILING DATE: 1997-05-23  
;; PRIOR APPLICATION NUMBER: 60/043,578  
;; PRIOR FILING DATE: 1997-04-11  
;; PRIOR APPLICATION NUMBER: 60/043,576  
;; PRIOR FILING DATE: 1997-04-11  
;; PRIOR APPLICATION NUMBER: 60/047,501  
;; PRIOR FILING DATE: 1997-05-23  
;; PRIOR APPLICATION NUMBER: 60/043,670  
;; PRIOR FILING DATE: 1997-04-11  
;; PRIOR APPLICATION NUMBER: 60/056,632  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,664  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,876  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,881  
;; PRIOR FILING DATE: 1997-08-22  
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;; PRIOR APPLICATION NUMBER: 60/056,862  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,887  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/048,964  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,908  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/056,964  
;; PRIOR FILING DATE: 1997-06-06  
;; PRIOR APPLICATION NUMBER: 60/057,650  
;; PRIOR FILING DATE: 1997-09-05  
;; PRIOR APPLICATION NUMBER: 60/056,884  
;; PRIOR FILING DATE: 1997-08-22  
;; PRIOR APPLICATION NUMBER: 60/057,669  
;; PRIOR FILING DATE: 1997-09-05

Query Match 90.0%; Score 36; DB 12; Length 117;  
Best Local Similarity 100.0%; Pred. No. 4,56+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSW 5  
Db 30 LNWSW 34

RESULT 5  
US-10-108-260A-2983  
; Sequence 2983, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20040005560A1 full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2983  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-108-260A-2983

Query Match 90.0%; Score 36; DB 12; Length 117;  
Best Local Similarity 100.0%; Pred. No. 4,56+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 2 NWSWL 6  
Db 20 NWSWL 24

RESULT 6  
US-09-815-242-10647  
Sequence 10647, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Hagelbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyckind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE OF INVENTION: Prokaryotes  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 10647  
LENGTH: 464  
TYPE: PRT  
ORGANISM: Enterococcus faecalis  
US-09-815-242-10647

Query Match  
Best Local Similarity 90.0%; Score 36; DB 9; Length 464;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWSWL 6  
Db 422 NWSWL 426

RESULT 7  
US-09-815-242-4997  
Sequence 4997, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Hagelbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyckind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE OF INVENTION: Prokaryotes  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 4997  
LENGTH: 467  
TYPE: PRT  
ORGANISM: Enterococcus faecalis  
US-09-815-242-4997

Query Match  
Best Local Similarity 90.0%; Score 36; DB 9; Length 467;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWSWL 6  
Db 425 NWSWL 429

RESULT 8  
US-10-436-715-29  
Sequence 29, Application US/10436715  
Publication No. US20040018976A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,  
FILE REFERENCE: D0262 NP  
CURRENT APPLICATION NUMBER: US/10/436,715  
CURRENT FILING DATE: 2003-05-13  
PRIOR APPLICATION NUMBER: U.S. 60/380,336  
PRIOR FILING DATE: 2002-05-14  
NUMBER OF SEQ ID NOS: 471  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 29  
LENGTH: 864  
TYPE: PRT  
ORGANISM: Fugu rubripes  
US-10-436-715-29

Query Match  
Best Local Similarity 90.0%; Score 36; DB 12; Length 864;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNWOWL 6  
Db 481 LNWOWL 486

RESULT 9  
US-10-436-715-82  
Sequence 82, Application US/10436715  
Publication No. US20040018976A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,  
FILE OF INVENTION: AND SPLICE VARIANTS THEREOF  
FILE REFERENCE: D0262 NP  
CURRENT APPLICATION NUMBER: US/10/436,715  
CURRENT FILING DATE: 2003-05-13  
PRIOR APPLICATION NUMBER: U.S. 60/380,336

;; PRIOR FILING DATE: 2002-05-14  
;; NUMBER OF SEQ ID NOS: 471  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 82  
;; LENGTH: 864  
;; TYPE: PRT  
;; ORGANISM: Fugu rubripes  
US-10-436-715-82

Query Match 90.0%; Score 36; DB 12; Length 864;  
Best Local Similarity 83.3%; Pred. No. 2.1e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNWSWL 6  
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Db 481 LNWQWL 486

RESULT 10  
US-09-847-940B-2  
; Sequence 2, Application US/09847940B  
; Patent No. US2002015600A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J.  
; APPLICANT: Ghosh, Sankar  
; FILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-117CP  
; CURRENT APPLICATION NUMBER: US/09/847,940B  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants  
US-09-847-940B-2

Query Match 87.5%; Score 35; DB 10; Length 6;  
Best Local Similarity 83.3%; Pred. No. 7e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6  
|:||||  
Db 1 LDMWSL 6

RESULT 11  
US-09-847-946A-2  
; Sequence 2, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: PRT

;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide  
US-09-847-946A-2

Query Match 87.5%; Score 35; DB 11; Length 6;  
Best Local Similarity 83.3%; Pred. No. 7e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6  
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Db 1 LDMWSL 6

RESULT 12  
US-09-847-946A-33  
; Sequence 33, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 33  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NBD binding  
US-09-847-946A-33

Query Match 87.5%; Score 35; DB 11; Length 6;  
Best Local Similarity 83.3%; Pred. No. 7e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6  
|:||||  
Db 1 LDMWSL 6

RESULT 13  
US-09-847-946A-37  
; Sequence 37, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 37

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; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-37
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Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LNWSQL 6
        |||||
Db      1 LDWSQL 6
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## RESULT 14

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US-09-847-946A-30
; Sequence 30, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Pindels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-30
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```
Query Match      87.5%; Score 35; DB 11; Length 8;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LNWSQL 6
        |||||
Db      3 LDWSQL 8
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## RESULT 15

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US-09-847-946A-38
; Sequence 38, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Pindels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
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; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-38
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Query Match      87.5%; Score 35; DB 11; Length 8;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LNWSQL 6
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Db      1 LDWSQL 6
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Job time : 17.7529 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds  
(without alignment)  
41.814 Million cell updates/sec

Title: US-09-643-260-9

Perfect score: 40  
Sequence: 1 LMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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25: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	23	ABB08731
2	40	100.0	6	23	AA048514
3	40	100.0	6	24	ABU08424
4	40	100.0	6	22	ABB62034
5	40	100.0	6	23	ABB77304
6	38	95.0	135	20	AAV76530
7	37	92.5	130	22	AA085139
8	37	92.5	464	21	AA053151
9	36	90.0	117	23	ABG95220

10	36	90.0	464	22	AAU35054	Enterococcus faeca
11	36	90.0	467	22	AAU33501	Enterococcus faeca
12	36	90.0	767	23	ABP65725	Bifidobacterium 10
13	35	87.5	6	23	ABB08725	IKKbeta NEMO bindi
14	35	87.5	6	23	AA048530	Anti-inflammatory
15	35	87.5	6	23	AA048555	NBD mutant peptide
16	35	87.5	6	24	ABU08418	Human NEMO binding
17	35	87.5	7	23	AA048534	Anti-inflammatory
18	35	87.5	8	23	AA048527	Anti-inflammatory
19	35	87.5	8	23	AA048535	Anti-inflammatory
20	35	87.5	9	20	AA048512	IKK-alpha polypept
21	35	87.5	9	23	AA048526	Anti-inflammatory
22	35	87.5	9	23	AA048529	Anti-inflammatory
23	35	87.5	9	23	AA048532	Anti-inflammatory
24	35	87.5	9	23	AA048533	Anti-inflammatory
25	35	87.5	10	23	ABB77313	IKKbeta NEMO bindi
26	35	87.5	10	23	AA048528	Anti-inflammatory
27	35	87.5	10	23	AA048531	Anti-inflammatory
28	35	87.5	11	23	ABB77311	Human NBD peptide
29	35	87.5	11	23	AA048506	Human NBD peptide
30	35	87.5	11	23	AA048525	Anti-inflammatory
31	35	87.5	11	23	AA048525	NBD peptide. Sync
32	35	87.5	13	23	AA048653	Anti-inflammatory
33	35	87.5	13	23	AA048640	Anti-inflammatory
34	35	87.5	13	23	AA048641	Anti-inflammatory
35	35	87.5	13	23	AA048642	Anti-inflammatory
36	35	87.5	17	23	AA048645	Anti-inflammatory
37	35	87.5	17	23	AA048638	Anti-inflammatory
38	35	87.5	17	23	AA048639	Anti-inflammatory
39	35	87.5	17	23	AA048643	Anti-inflammatory
40	35	87.5	18	23	AA048644	Anti-inflammatory
41	35	87.5	18	23	AA048628	Anti-inflammatory
42	35	87.5	18	23	AA048629	Anti-inflammatory
43	35	87.5	18	23	AA048632	Anti-inflammatory
44	35	87.5	22	23	AA048633	Anti-inflammatory
45	35	87.5	22	23	AA048630	Anti-inflammatory

#### ALIGNMENTS

RESULT 1	ABB08731	standard; peptide; 6 AA.
ID	ABB08731	
XX	ABB08731	
AC	ABB08731	
XX	ABB08731	
DT	14-JUN-2002	(first entry)
XX	14-JUN-2002	
DE	Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 9.	
XX	IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;	
XX	kinase activation; leukocyte; inflammation; E-selectin; osteoclast;	
KW	autoimmune disease; transplant rejection; osteoporosis; cancer;	
KW	Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;	
KW	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;	
KW	corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;	
KW	osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;	
KW	antiartherosclerotic; vitruclide; antiasthmatic; antiallergic;	
KW	dermatological; antibacterial; antipruritic; antirheumatic;	
KW	antiarthritic; osteopathic; antitumor; mutant; mucin.	
OS	Human sepiens.	
OS	Synthetic.	
XX	Key	Location/Qualifiers
XX	Misc-difference	/note= "wildtype Asp substituted by Asn"
FT	WO200183547-A2.	
XX	08-NOV-2001.	
XX		

PF 02-MAY-2001; 2001WO-US40654.  
XX  
XX 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
XX  
XX (UYVA ) UNIV YALB.  
PA  
PI May MJ, Ghosh S;  
XX  
XX WPI; 2002-179350/23.  
DR  
XX  
PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
PT cell with an anti-inflammatory compound comprising at least one NEMO  
PT binding domain -  
XX  
XX  
PS Claim 23; Page 44; 82pp; English.  
XX  
XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
CC comprises contacting a cell with an anti-inflammatory compound  
CC (AB08723-AB08742) comprising at least one NEMO binding domain  
CC (AB07713). The compound has acts through selective inhibition of  
CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
CC interaction results in inhibition of IKKbeta kinase activation and  
CC subsequent decreased phosphorylation of Ikbppa. The compound may also  
CC act (directly or indirectly) by blocking the recruitment of leukocytes  
CC into sites of acute and chronic inflammation, by down-regulating the  
CC expression of E-selectin on leukocytes or by blocking osteoclast  
CC differentiation. The compound is useful in treating NF-kB mediated  
CC conditions, where the condition is an inflammatory disorder, an  
CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
CC telangiectasia. The inflammatory disorder is asthma, allergies,  
CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammation  
CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
CC burstitis. The inflammatory disorder may also be dermatitis, eczema,  
CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,  
CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
CC diseases include HIV and influenza. The compound may also be useful for  
CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
CC sunburn or aging. The compound may be used to replace corticosteroids in  
CC any application in which corticosteroids are used, including  
CC immunosuppression in transplants and cancer therapy. Also for identifying  
CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
CC The compound may be administered alone or in combination with other known  
CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
CC binding domain of IKKbeta.  
XX  
SQ Sequence 6 AA;  
Query Match 100.0%; Score 40; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 LNMSWL 6  
|||  
Db 1 LNMSWL 6  
RESULT 2  
ID AAM48514 standard; Peptide: 6 AA.  
XX  
XX AAM48514;  
AC  
XX 20-MAR-2002 (First entry)  
DT  
XX NBD mutant peptide SEQ ID NO 9.  
DE

XX  
XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;  
XX antirheumatic; antiarthritic; osteopachic; antiparasitic; virucide;  
XX immunosuppressive; dermatological; neuroprotective; antihemorrhagic;  
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
XX cytokine; NFkappaB; Ikbppa kinase beta; IKKbeta; cancer; psoriasis;  
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX autoimmune disorder; multiple sclerosis; transplant rejection;  
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
OS  
XX Synthetic.  
XX  
XX WO200183554-A2.  
XX  
XX 08-NOV-2001.  
XX  
XX  
XX 02-MAY-2001; 2001WO-US14346.  
XX  
XX  
XX 02-MAY-2000; 2000US-201261P.  
XX 22-AUG-2000; 2000US-0643260.  
XX  
XX (PRAE-) PRAECTS PHARM INC.  
XX (UYVA ) UNIV YALB.  
XX  
XX May MJ, Ghosh S, Flindels MA, Phillips K;  
XX  
XX WPI; 2002-121889/16.  
XX  
XX  
XX Novel antiinflammatory compound comprising membrane translocation  
XX domain fused to NEMO binding sequence, useful for blocking nuclear  
XX factor kappaB activation, and for treating asthma, lung inflammation,  
XX psoriasis -  
XX  
XX Example 6; Page 47; 88pp; English.  
XX  
XX The invention relates to an antiinflammatory compound (especially  
XX AAM48628-AAM48645), comprising a membrane translocation domain  
XX (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
XX amino acid residues, fused to a NEMO binding sequence  
XX (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
XX cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopachic,  
XX antiparasitic, immunosuppressive, dermatological, neuroprotective,  
XX nootropic, antihemorrhagic, virucide and antiallergic activity. The  
XX compounds act as selective inhibitors of cytokine-mediated NFkappaB  
XX activation by blocking interaction of Ikbppa kinase beta (IKKbeta) at  
XX the NEMO binding domain that results in inhibition of IKKbeta kinase  
XX activation and subsequent decreased phosphorylation of Ikbppa. The  
XX compounds are useful for treating inflammatory disorders, e.g. asthma,  
XX lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
XX osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
XX burstitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
XX granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
XX Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
XX telangiectasia. The compounds are also useful for treating  
XX pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
XX drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
XX arthritis.  
XX  
SQ Sequence 6 AA;  
Query Match 100.0%; Score 40; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 LNMSWL 6  
|||  
Db 1 LNMSWL 6  
RESULT 3  
ID ABU08424 standard; peptide; 6 AA.  
ABU08424

```

XX AC ABU08424;
XX DT 12-JUN-2003 (first entry)
XX DE Human NEMO binding site (NBD) mutant peptide #7.
XX DE
XX KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
XX KW IKKappa kinase-beta; IKKappa kinase-alpha; IKKalpha; NF-kappaB;
XX KW nuclear factor-kappaB induction; inflammatory disorder;
XX KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
XX KW atherosclerosis; viral infection; Ataxia telangiectasia;
XX KW transplantation detection; immunosuppressive; osteopathic;
XX KW cytosolic; neurotrophic; neuroprotective; antiatherosclerotic; virucide;
XX KW vasotropic; antineumatic; antiarthritic; mutant; mutein.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN US2002156000-A1.
XX PD 24-OCT-2002.
XX PF 02-MAY-2001; 2001US-0847940.
XX PR 02-MAY-2000; 2000US-201261P.
XX PR 22-AUG-2000; 2000US-0643260.
XX PA (MAYM/) MAY M J.
XX PA (GHOS/) GHOSH S.
XX PI May MJ, Ghosh S;
XX DR WPI; 2003-209142/20.
XX PT Novel antiinflammatory peptide compounds comprising NEMO binding
XX PT domain, useful for modulating NF-kappaB induction in a cell and for
XX PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
XX PT psoriasis, vasculitis -
XX PS Claim 22; Page 17; 47pp; English.
XX CC The present invention relates to antiinflammatory compounds comprising
XX CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
XX CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
XX CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
XX CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
XX CC in a cell, where the compounds are capable of blocking the interaction
XX CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
XX CC antiinflammatory compound further comprises at least one membrane
XX CC translocation domain. The compounds are useful for treating
XX CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
XX CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
XX CC telangiectasia, and for transplantation detection. The compounds of
XX CC the invention block NF-kappaB induction by IKK but do not inhibit
XX CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
XX CC NBD mutant peptides.
XX SQ Sequence 6 AA;
XX
XX Query Match 100.0%; Score 40; DB 24; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LNMSWL 6
XX | | | | |
XX DB 1 LNMSWL 6
XX
XX RESULT 4
XX ABB62034
XX ID ABB62034 standard; Protein; 295 AA.
XX

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AC AC ABB62034;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 12894.
XX DE
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX PA (PERK ) PB CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI; 2001-656860/75.
XX DR N-PSDB; ABL06137.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions -
XX PS Disclosure; SEQ ID NO 12894; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
XX CC sequences (AB57737-AB872072).
XX CC (AB57737-AB872072).
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 295 AA;
XX
XX Query Match 100.0%; Score 40; DB 22; Length 295;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+02;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LNMSWL 6
XX | | | | |
XX DB 286 LNMSWL 291
XX
XX RESULT 5
XX ABB77304
XX ID ABB77304 standard; protein; 756 AA.
XX AC ABB77304;
XX DT 14-JUN-2002 (first entry)
XX DE Human IKKbeta mutant D738N.
XX DE
XX KW IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
XX KW kinase activation; leukocyte; inflammation; B-selectin; osteoclast;
XX KW autoimmune disease; transplant rejection; osteoporosis; cancer;
XX KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;
XX KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
XX KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
XX KW osteopathic; cytostatic; neurotrophic; neuroprotective; anti-HIV; human;
XX

```

OS	Homo sapiens.	
OS	Synthetic.	
XX	Key	Location/Qualifiers
FT	Mac-difference 738	
FT	/note= "Wildtype Asp substituted by Asn"	
XX	MO200183547-A2.	
XX		
XX	08-NOV-2001.	
PD		
XX		
XX	02-MAY-2001; 2001MO-US40654.	
XX		
FR	02-MAY-2000; 2000US-201261P.	
XX	22-AUG-2000; 2000US-0643260.	
XX		
PA	(UTYA ) UNIV YALE.	
XX		
PI	May MJ, Ghosh S;	
XX		
PS	WPI; 2002-179350/23.	
XX		
XX	Modulating NF-kappaB induction in a cell, useful for treating e.g.	
PT	inflammatory disorders, osteoporosis and cancer, comprises contacting a	
PT	cell with an anti-inflammatory compound comprising at least one NEMO	
PT	binding domain	
XX		
XX	Example 11; Page -; 82pp; English.	
XX		
XX	The invention relates to modulating NF-kappaB (NF-KB) induction in a cell	
CC	comprises contacting a cell with an anti-inflammatory compound	
CC	(ABB08725-ABB08742) comprising at least one NEMO binding domain	
CC	(ABB077313). The compound has acts through selective inhibition of	
CC	cytokine-mediated NF-KB activation by blocking the interaction of NEMO	
CC	with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO	
CC	interaction results in inhibition of IKKbeta kinase activation and	
CC	subsequent decreased phosphorylation of IkappaB. The compound may also	
CC	act (directly or indirectly) by blocking the recruitment of leukocytes	
CC	into sites of acute and chronic inflammation, by down-regulating the	
CC	expression of E-selectin on leukocytes or by blocking osteoclast	
CC	differentiation. The compound is useful in treating NF-KB mediated	
CC	conditions, where the condition is an inflammatory disorder, an	
CC	autoimmune disease, transplant rejection, osteoporosis, cancer,	
CC	Alzheimer's disease, atherosclerosis, a viral infection or ataxia	
CC	relanglectasia. The inflammatory disorder is asthma, allergies,	
CC	urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,	
CC	rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory	
CC	bowel disease, chronic obstructive pulmonary disease, vasculitis and	
CC	burns. The inflammatory disorder may also be dermatitis, eczema,	
CC	psoriasis, osteoarthritis, psoriatic arthritis, lupus and	
CC	spendylarthritis. Also for Crohn's disease, ulcerative colitis,	
CC	polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,	
CC	cryoglobulinemia or multiple sclerosis. For chronic viral infections	
CC	caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral	
CC	diseases include HIV and Influenza. The compound may also be useful for	
CC	treating anaphylaxis, drug and food sensitivity, contact dermatitis,	
CC	sunburn or aging. The compound may be used to replace corticosteroids in	
CC	any application in which corticosteroids are used, including	
CC	immunosuppression in transplants and cancer therapy. Also for identifying	
CC	anti-inflammatory compounds and for diagnosis of an inflammatory disorder.	
CC	The compound may be administered alone or in combination with other known	
CC	anti-inflammatory agents. The present sequence is that of an IKKbeta	
CC	mutant, useful in examples of the invention.	
CC	Note: The present sequence is not given in the specification but is	
CC	derived from GenBank Accession No. 014920 (ABB77294).	
XX		
XX	Sequence 756 AA;	

Query Match 100.0%; Score 40; DB 23; Length 756;

		Best Local Similarity	100.0%;	Pred. No.	3.8e+02;
		Matches	6;	Conservative	0;
				Mismatches	0;
				Indels	0;
				Gaps	0;
OY	1	LINMSWL	6		
Db	737	LINMSWL	742		

Accession	Protein Name	Gene Name	Species	Feature
AA76530	standard; Protein; 135 AA.			
AA76530				
AA76530				
10-APR-2000	(first entry)			
Human ovarian tumor	EST fragment encoded protein 26.			
Expressed sequence tag; EST; human; ovarian tumor; anticancer;				
gene therapy; treatment.				
Homo sapiens.				
DE19817557-A1.				
21-OCT-1999.				
09-APR-1998;	98DE-1017557.			
09-APR-1998;	98DE-1017557.			

PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E,  
XX  
XX  
DR WPI, 1999-591920/51.  
DR N-PSDB; AAZ77461.  
XX  
XX New nucleic acid sequences expressed in ovarian, and some other, cancer  
PT tissues, and derived polypeptides, for treatment of ovarian cancer and  
PT identification of therapeutic agents -  
XX  
XX Claim 25, Page 254, 310pp, German.

CC This invention describes novel nucleic acid (cDNA) sequences (A) which  
CC have anticancer activity and are highly expressed in ovarian tumor  
CC tissue (and some also in testis and breast cancer tissue). The products  
CC of the invention can be used for gene therapy. (A) are used (1) for  
CC recombinant expression of polypeptides (B) and (11) to isolate complete  
CC genes. (B) are used (1) to identify agents suitable for treatment of  
CC ovarian cancer; (11) directly for treating this form of cancer  
CC (including expression from gene therapy vectors) and (11) for generation  
CC of specific antibodies. (A) are identified by assembling ESTs (expressed  
CC sequence tags) from a particular tissue type before comparison of  
CC expression patterns. This allows a significantly longer fragment of the  
CC gene to be revealed, so should reduce the number of failures associated  
CC with the fact that ESTs from different libraries may represent different  
CC parts of the same unknown gene, distorting the estimated frequency of  
CC occurrence in a particular tissue. AY875505-Y76638 represent protein  
CC fragments encoded by the human ovarian tumor cDNA library derived EST  
CC fragments represented in A0277450-277572.

Query Match	95.0%	Score 38	DB 20	Length 135
Best Local Similarity	83.3%	Prod. No.	1.3e+03	
Matches	5	Conservative	0	Indels 0
				Gaps 0
QY	1	LNMSWL	6	
DB	69	LNMSWI	74	

RESULT 7  
AA085139  
ID AA085139 standard; Protein; 130 AA.  
XX  
AC AA085139;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
DE Human immune/haematopoietic antigen SEQ ID NO:12732.  
XX  
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis.  
XX  
OS Homo sapiens.  
XX  
PN WO200157182-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01354.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225477.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226179.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226688.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231142.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.

PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241788.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241825.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.



PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 06-DEC-2000; 2000US-0256719.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX  
 PT WPI; 2001-483426/52.  
 DR N-PSDB; AAK57920.  
 XX  
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
 PT useful for preventing, diagnosing and/or treating cancers and  
 PT metacastasis -  
 XX  
 PS Claim 11, SEQ ID NO 12732; 3071bp + Sequence Listing; English.  
 XX  
 CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)  
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic  
 CC activity, and can be used in gene therapy and vaccine production. (I)  
 CC proteins and polynucleotides may be used in the prevention, diagnosis and  
 CC treatment of diseases associated with inappropriate (I) expression. For  
 CC example, they may be used to treat disorders associated with decreased  
 CC expression by rectifying mutations or deletions in a patient's genome  
 CC that affect the activity of (I) by expressing inactive proteins or to  
 CC supplement the patient's own production of (I). Additionally, (I)  
 CC polynucleotides may be used to produce the secreted (I), by inserting the  
 CC nucleic acids into a host cell and culturing the cell to express the  
 CC protein. (I) proteins and polynucleotides may be used to prevent  
 CC diagnosis and treat immune/haematopoietic-related diseases, especially  
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
 CC to AAK87694 represent human immune/haematopoietic antigen genomic  
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169  
 CC represent sequences used in the exemplification of the present invention.  
 XX  
 SO Sequence 130 AA;  
 XX  
 Query Match 92.5%; Score 37; DB 22; Length 130;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LAMSWL 6  
 DB 55 LNMWTL 60  
 XX  
 DE Macaca mulatta rhadinovirus 17577 RRV ORF32 protein SEQ ID NO:59.  
 XX  
 XX Macaca mulatta rhadinovirus 17577; RRV; rhesus macaque rhadinovirus;  
 KM genome; Kaposi's sarcoma-associated herpesvirus; KSHV; interleukin 6;  
 KM IL-6; macrophage inflammatory protein; MIP; diagnosis; vaccine;  
 KM cytotoxic; anti-HIV; gene therapy; infection; Kaposi's sarcoma;  
 KM lymphoproliferative disorder; B-cell hyperplasia; lymphadenopathy;  
 KM epinephelus; hypergammaglobulinemia; autoimmune haemolytic anaemia.  
 XX  
 OS Macaca mulatta rhadinovirus 17577.

PN WO200028040-A2.  
 XX  
 PD 18-MAY-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US26260.  
 XX  
 PR 06-NOV-1998; 98US-0107507.  
 PR 20-NOV-1998; 98US-0109409.  
 XX  
 PA (UYOR-) UNIV OREGON HEALTH SCI.  
 XX  
 PI Wong SM, Axthelm MK, Searles RP;  
 XX  
 DR WPI; 2000-376552/32.  
 XX  
 PT New rhesus rhadino virus for producing non-human primate model useful  
 PT for testing potential treatments and efficacy of the candidate vaccine  
 PT for conditions associated with RRV infection -  
 XX  
 PS Claim 5; Page 128-129; 141bp; English.  
 XX  
 CC The present invention describes a novel rhesus macaque rhadinovirus  
 CC called macaca mulatta rhadinovirus 17577 (RRV). AAC64754 represents the  
 CC RRV genome sequence, and AAB53123 to AAB53204 represent the proteins  
 CC encoded by the genome sequence. The present invention also specifically  
 CC claims the individual open reading frame (ORF) nucleotide sequences from  
 CC the genome which encode the individual proteins, but these sequences are  
 CC not given. A non-human animal infected with RRV can be used for testing  
 CC the efficacy of drug in the treatment of condition associated with  
 CC infection with RRV such as Kaposi's sarcoma, lymphoproliferative  
 CC disorders, B-cell hyperplasia, lymphadenopathy, epinephelus,  
 CC hypergammaglobulinemia or autoimmune haemolytic anaemia, by  
 CC administering the drug to an immuno-compromised non-human primate  
 CC preferably Rhesus macaque monkey obtained by as a result of infection  
 CC by Simian Immunodeficiency Virus (SIV). RRV is useful for producing  
 CC non-human primate model for testing potential treatments for conditions  
 CC associated with RRV infection. It is also useful for testing the  
 CC efficacy of the candidate vaccine against RRV infection or conditions  
 CC associated with its infection by administering the vaccine to the  
 CC subject capable of infection with RRV, inoculating the subject with RRV  
 CC and observing the effect of vaccine. AAC64755 to AAC64765 and AAB53205  
 CC to AAB53213 represent sequence used in the exemplification of the  
 CC present invention.  
 XX  
 SO Sequence 464 AA;  
 XX  
 Query Match 92.5%; Score 37; DB 21; Length 464;  
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LAMSWL 6  
 DB 397 VNMSWL 402  
 XX  
 DE Human novel secreted protein #41.  
 XX  
 XX Human; secreted protein; autoimmune disease; chemotaxis;  
 KM rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;  
 KM liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;  
 KM cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;  
 KM nervous system disorders; Alzheimer's disease; infection;  
 KM ocular disorder; corneal infection; wound healing; tissue regeneration;  
 KM epithelial cell proliferation; organ transplantation; food additive;  
 KM preservative; nutritional.

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XX OS Homo sapiens.
XX XX US6420526-B1.
XX PD 16-JUL-2002.
XX PF 08-SEP-1998; 98US-0149476.
XX PR 07-MAR-1997; 97US-038621P.
XX PR 07-MAR-1997; 97US-040161P.
XX PR 07-MAR-1997; 97US-040162P.
XX PR 07-MAR-1997; 97US-040163P.
XX PR 07-MAR-1997; 97US-040333P.
XX PR 07-MAR-1997; 97US-040334P.
XX PR 07-MAR-1997; 97US-040336P.
XX PR 11-APR-1997; 97US-043311P.
XX PR 11-APR-1997; 97US-043312P.
XX PR 11-APR-1997; 97US-043313P.
XX PR 11-APR-1997; 97US-043314P.
XX PR 11-APR-1997; 97US-043315P.
XX PR 11-APR-1997; 97US-043568P.
XX PR 11-APR-1997; 97US-043569P.
XX PR 11-APR-1997; 97US-043576P.
XX PR 11-APR-1997; 97US-043578P.
XX PR 11-APR-1997; 97US-043580P.
XX PR 11-APR-1997; 97US-043669P.
XX PR 11-APR-1997; 97US-043670P.
XX PR 11-APR-1997; 97US-043672P.
XX PR 11-APR-1997; 97US-043674P.
XX PR 23-MAY-1997; 97US-047492P.
XX PR 23-MAY-1997; 97US-047500P.
XX PR 23-MAY-1997; 97US-047502P.
XX PR 23-MAY-1997; 97US-047503P.
XX PR 23-MAY-1997; 97US-047581P.
XX PR 23-MAY-1997; 97US-047582P.
XX PR 23-MAY-1997; 97US-047583P.
XX PR 23-MAY-1997; 97US-047584P.
XX PR 23-MAY-1997; 97US-047585P.
XX PR 23-MAY-1997; 97US-047586P.
XX PR 23-MAY-1997; 97US-047587P.
XX PR 23-MAY-1997; 97US-047588P.
XX PR 23-MAY-1997; 97US-047589P.
XX PR 23-MAY-1997; 97US-047590P.
XX PR 23-MAY-1997; 97US-047592P.
XX PR 23-MAY-1997; 97US-047593P.
XX PR 23-MAY-1997; 97US-047594P.
XX PR 23-MAY-1997; 97US-047595P.
XX PR 23-MAY-1997; 97US-047596P.
XX PR 23-MAY-1997; 97US-047597P.
XX PR 23-MAY-1997; 97US-047598P.
XX PR 23-MAY-1997; 97US-047599P.
XX PR 23-MAY-1997; 97US-047600P.
XX PR 23-MAY-1997; 97US-047601P.
XX PR 23-MAY-1997; 97US-047612P.
XX PR 23-MAY-1997; 97US-047613P.
XX PR 23-MAY-1997; 97US-047614P.
XX PR 23-MAY-1997; 97US-047615P.
XX PR 23-MAY-1997; 97US-047617P.
XX PR 23-MAY-1997; 97US-047618P.
XX PR 23-MAY-1997; 97US-047632P.
XX PR 23-MAY-1997; 97US-047633P.
XX PR 06-JUN-1997; 97US-048964P.
XX PR 06-JUN-1997; 97US-048974P.
XX PR 13-JUN-1997; 97US-049610P.
XX PR 08-JUL-1997; 97US-051926P.
XX PR 16-JUL-1997; 97US-052874P.
XX PR 18-AUG-1997; 97US-055724P.
XX PR 22-AUG-1997; 97US-056630P.
XX PR 22-AUG-1997; 97US-056631P.

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PR 22-AUG-1997; 97US-056632P.
PR 22-AUG-1997; 97US-056636P.
PR 22-AUG-1997; 97US-056637P.
PR 22-AUG-1997; 97US-056662P.
PR 22-AUG-1997; 97US-056664P.
PR 22-AUG-1997; 97US-056845P.
PR 22-AUG-1997; 97US-056862P.
PR 22-AUG-1997; 97US-056864P.
PR 22-AUG-1997; 97US-056872P.
PR 22-AUG-1997; 97US-056874P.
PR 22-AUG-1997; 97US-056875P.
PR 22-AUG-1997; 97US-056876P.
PR 22-AUG-1997; 97US-056877P.
PR 22-AUG-1997; 97US-056878P.
PR 22-AUG-1997; 97US-056879P.
PR 22-AUG-1997; 97US-056880P.
PR 22-AUG-1997; 97US-056881P.
PR 22-AUG-1997; 97US-056882P.
PR 22-AUG-1997; 97US-056884P.
PR 22-AUG-1997; 97US-056886P.
PR 22-AUG-1997; 97US-056887P.
PR 22-AUG-1997; 97US-056888P.
PR 22-AUG-1997; 97US-056889P.
PR 22-AUG-1997; 97US-056892P.
PR 22-AUG-1997; 97US-056893P.
PR 22-AUG-1997; 97US-056894P.
PR 22-AUG-1997; 97US-056903P.
PR 22-AUG-1997; 97US-056908P.
PR 22-AUG-1997; 97US-056909P.
PR 22-AUG-1997; 97US-056910P.
PR 22-AUG-1997; 97US-056911P.
PR 22-AUG-1997; 97US-057761P.
PR 05-SEP-1997; 97US-057650P.
PR 05-SEP-1997; 97US-057659P.
PR 12-SEP-1997; 97US-057855P.
PR 02-OCT-1997; 97US-061060P.
PR 06-MAR-1998; 98WO-US04493.
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX XX
XX XX Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bednarek DR;
XX PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Perrine AM;
XX PI Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
XX PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX DR WPI, 2002-634796/68.
XX DR N-PEDB; ABS73538.
XX PT New isolated human secreted protein for diagnosing, preventing,
XX PT treating or ameliorating medical conditions and used as a food additive
XX PT or preservative -
XX XX
XX PS Example 1; SEQ ID NO 360; 129pp; English.
XX XX
XX CC The invention relates to an isolated protein that is one of 186 human
XX CC secreted proteins, given in the specification, encoded by one of
XX CC 309 cDNA sequences also given in the specification. The protein is used
XX CC in a pharmaceutical composition used to prevent, treat or ameliorate a
XX CC medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
XX CC dogs, chickens or sheep. Disorders which are diagnosed or treated include
XX CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
XX CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
XX CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
XX CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
XX CC infections caused by bacteria, viruses and fungi and ocular disorders
XX CC e.g. corneal infection. The polypeptides can also be used to aid wound
XX CC healing and epithelial cell proliferation, to prevent skin aging due to
XX CC sunburn, to maintain organs before transplantation, for supporting cell
XX CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
XX CC polypeptides can also be used as a food additive or preservative to
XX CC increase or decrease storage capabilities, fat content, lipid, protein,
XX CC carbohydrate, vitamins, minerals, cofactors and other nutritional
XX CC components. The present sequence represents one of the novel human

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CC secreted proteins of the invention.  
 CC Note: This sequence did not form part of the printed specification,  
 CC but was obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?docid=6420526b1.

XX Sequence 117 AA;

Query Match 90.0%; Score 36; DB 23; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNWSW 5  
 |||||  
 DB 30 LNWSW 34

RESULT 10  
 AAU35054  
 ID AAU35054 standard; Protein; 464 AA.

XX AAU35054;

DT 13-FEB-2002 (first entry)

DE Enterococcus faecalis cellular proliferation protein #341.

KM Antisense; prokaryotic cellular proliferation protein;

KM antibiotic; antibacterial; drug design.

OS Enterococcus faecalis.

PN WO200170955-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US09180.

PR 21-MAR-2001; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

PA (ELIT-) ELITRA PHARM INC.

PI Haselbeck R, Ohlsen KL, Zykkind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

DR WPI; 2001-611495/70.

DR N-PSDB; AAS52913.

XX New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids -

XX Example 3; Seq ID No 10647; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to  
 CC prokaryotic cellular proliferation, their use in identifying the  
 CC genes, their use in the discovery of novel antibiotics, the essential  
 CC genes themselves and the encoded proteins. The prokaryotes used are  
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*  
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The  
 CC invention is also useful for the identification of potential new targets  
 CC for antibiotic development. The antisense nucleic acids can also be used  
 CC to identify proteins used in proliferation, to express these proteins,  
 CC and to obtain antibodies capable of binding to the expressed proteins.  
 CC The proteins can be used to screen compounds in rational drug discovery  
 CC programmes. The antisense nucleic acid sequence is also useful to screen  
 CC for homologous nucleic acids which are required for cell proliferation in  
 CC a wide variety of organisms. The present sequence represents an  
 CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pat\_sequences.

XX Sequence 464 AA;

Query Match 90.0%; Score 36; DB 22; Length 464;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NWSWL 6  
 |||||  
 DB 422 NWSWL 426

RESULT 11  
 AAU33501  
 ID AAU33501 standard; Protein; 467 AA.

XX AAU33501;

DT 14-FEB-2002 (first entry)

DE Enterococcus faecalis cellular proliferation protein #137.

KM Antisense; prokaryotic cellular proliferation protein;

KM antibiotic; antibacterial; drug design.

OS Enterococcus faecalis.

PN WO200170955-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US09180.

PR 21-MAR-2001; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

PA (ELIT-) ELITRA PHARM INC.

PI Haselbeck R, Ohlsen KL, Zykkind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

DR WPI; 2001-611495/70.

DR N-PSDB; AAS51360.

XX New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids -

XX Example 3; Seq ID No 4997; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to  
 CC prokaryotic cellular proliferation, their use in identifying the  
 CC genes, their use in the discovery of novel antibiotics, the essential  
 CC genes themselves and the encoded proteins. The prokaryotes used are  
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*  
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The  
 CC invention is also useful for the identification of potential new targets  
 CC for antibiotic development. The antisense nucleic acids can also be used  
 CC to identify proteins used in proliferation, to express these proteins,  
 CC and to obtain antibodies capable of binding to the expressed proteins.  
 CC The proteins can be used to screen compounds in rational drug discovery  
 CC programmes. The antisense nucleic acid sequence is also useful to screen  
 CC for homologous nucleic acids which are required for cell proliferation in  
 CC a wide variety of organisms. The present sequence represents an  
 CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 467 AA;

Query Match 90.0%; Score 36; DB 22; Length 467;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NMSWL 6

DB 425 NMSWL 429

#### RESULT 12

ABP65725 ID ABP65725 standard; Protein; 767 AA.

XX AC ABP65725;

XX DT 19-NOV-2002 (first entry)

XX DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:469.

XX KW Bifidobacterium longum NCC2705; Bifidobacterium; bacterial;  
 KW antiarthritic; antibacterial; inhibitor of Salmonella; detection;  
 KW identification; lactic acid bacterium; diarrhoea; pathogenic bacteria;  
 KW rotavirus; food composition; pharmaceutical composition.

XX OS Bifidobacterium longum.

XX PN EP1227152-A1.

XX PD 31-JUL-2002.

XX PF 30-JAN-2001; 2001EP-0102050.

XX PR 30-JAN-2001; 2001EP-0102050.

XX PA (NEST ) SOC PROD NESTLE SA.

XX DR WPI; 2002-668397/72.

XX PT Novel polynucleotide comprising Bifidobacterium genome sequence useful  
 XX as a probe or primer for detecting and/or identifying Bifidobacterium  
 XX longum in a biological sample -

XX PS Claim 3; SEQ ID 469; 80pp; English.

XX CC The present invention describes a polynucleotide (I) comprising a  
 CC sequence of a Bifidobacterium genome selected from the nucleotide  
 CC sequences given in AB081842 and AB081843, or a sequence exhibiting at  
 CC least 90% identity or which hybridises with the sequences given in  
 CC AB081842 and AB081843. Also described is a polynucleotide (II) encoding  
 CC a fusion protein, comprising a sequence selected from 1097 sequences  
 CC given in ABP65258 to ABP6354 ligated in frame to a polynucleotide  
 CC encoding a heterologous polypeptide. (I) has antiarthritic and  
 CC antibacterial activities, and can be used as an inhibitor of Salmonella.  
 CC (I) (which is a probe) is useful for the detection and/or identification  
 CC of Bifidobacterium longum in a biological sample. A carrier containing  
 CC the lactic acid bacterium Bifidobacterium longum NCC2705 (NCM 1-2618)  
 CC can be used for preventing and/or treating diarrhoea brought about by  
 CC pathogenic bacteria and/or rotavirus. The carrier is a food composition  
 CC selected from milk, yogurt, curd, cheese, fermented milks, milk based  
 CC fermented products, ice-creams, fermented cereal based products, milk  
 CC based powders, infant formula, pet food or a pharmaceutical composition  
 CC selected from tablets, liquid bacterial suspensions, dried oral  
 CC supplement, wet oral supplement, dry tube feeding or wet tube feeding.  
 CC (I) is useful in DNA arrays or chips to carry out analysis of the  
 CC expression of the Bifidobacterium gene. AB081844 to AB081850 represent  
 CC Bifidobacterium related nucleotide sequences given in the Sequence

CC Listing from the present invention but not mentioned further within the  
 CC specification.  
 CC N.B. The sequence data for this patent is not represented in the printed  
 CC specification but is based on sequence information supplied by the  
 CC European Patent Office.

XX SQ Sequence 767 AA;

Query Match 90.0%; Score 36; DB 23; Length 767;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMSW 5

DB 569 LNMSW 573

#### RESULT 13

ABB08725 ID ABB08725 standard; peptide; 6 AA.

XX AC ABB08725;

XX DT 14-JUN-2002 (first entry)

XX DE IKKbeta NEMO binding domain peptide SEQ ID NO 2.

XX KW IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
 KW kinase activation; leukocytes; inflammation; E-selectin; osteoclast;  
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;  
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;  
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;  
 KW osteopathic; cytotoxic; nootropic; neuroprotective; anti-HIV; human;  
 KW antiarteriosclerotic; virucide; antiasclerotic; antiallergic;  
 KW dermatological; antibacterial; antiparasitic; antineumatic;  
 KW antiarthritic; osteopathic; antitumor.

XX OS Homo sapiens.

XX PN WO200183547-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US40654.

XX PR 02-MAY-2000; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

XX PA (UYVA ) UNIV YALE.

XX PI May MJ, Ghosh S;

XX DR WPI; 2002-179350/23.

XX PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 XX PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 XX PT cell with an anti-inflammatory compound comprising at least one NEMO  
 XX binding domain -

XX PS Claim 23; Page 44; 82pp; English.

XX CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprises contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB077313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of IKKalpha. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast

CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polyarthralgia, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of the NEMO  
 CC binding domain of IKKbeta.

XX Sequence 6 AA;

Query Match 87.5%; Score 35; DB 23; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6  
 Db 1 LDMSWL 6

#### RESULT 14

AA048530  
 ID AA048530 standard; Peptide; 6 AA.

XX  
 AC AA048530;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 33.

XX Anti-inflammatory; antiaesthetic; cytostatic; antipsoriatic; nootropic;  
 XX antineumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 XX autoimmune disorder; multiple sclerosis; transplant rejection;  
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

PI May MJ, Ghosh S, Pindels MA, Phillips K;

DR WPI; 2002-121889/16.

PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 XX psoriasis -

PS Claim 6; Page 61; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially  
 CC AA048628-AA048645), comprising a membrane translocation domain  
 CC (AA048620-AA048627 or AA048646-AA048651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AA048525-AA048619). The antiinflammatory compounds have antiaesthetic,  
 CC cytostatic, antipsoriatic, antineumatic, antiarthritic, osteopathic,  
 CC antineurotic, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma;  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.

XX Sequence 6 AA;

Query Match 87.5%; Score 35; DB 23; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6  
 Db 1 LDMSWL 6

#### RESULT 15

AA048655  
 ID AA048655 standard; Peptide; 6 AA.

XX  
 AC AA048655;

DT 20-MAR-2002 (first entry)

DE NBD mutant peptide SEQ ID NO 2.

XX Anti-inflammatory; antiaesthetic; cytostatic; antipsoriatic; nootropic;  
 XX antineumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 XX autoimmune disorder; multiple sclerosis; transplant rejection;  
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

PA (UYVA ) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

DR Novel antiinflammatory compound comprising membrane translocation  
XX domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis -  
XX

PS Example 6; Page 47; 88pp; English.

XX  
XX The invention relates to an antiinflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain  
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NFKappaB  
CC activation by blocking interaction of IkkappaB kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of IkkappaB. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis,  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
XX

SQ Sequence 6 AA:

Query Match 87.5%; Score 35; DB 23; Length 6;

Best Local Similarity 83.3%; Pred. No. 9.3e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWSWL 6

DB 1 LDMWSWL 6

Search completed: February 18, 2004, 14:26:21  
Job time : 23.7763 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds  
(without alignments)  
75.239 Million cell updates/sec

Title: US-09-643-260-8

Perfect score: 39

Sequence: 1 LEWSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pubpaa/PTCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PTCT\_PUBCOMB.pep.\*  
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13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	39	100.0	6	10 US-09-847-940B-8	Sequence 8, Appli
2	39	100.0	6	10 US-09-847-946A-8	Sequence 8, Appli
3	36	92.3	6	10 US-09-847-940B-2	Sequence 2, Appli
4	36	92.3	6	11 US-09-847-946A-2	Sequence 2, Appli
5	36	92.3	6	11 US-09-847-946A-33	Sequence 33, Appli
6	36	92.3	7	11 US-09-847-946A-37	Sequence 37, Appli
7	36	92.3	8	11 US-09-847-946A-30	Sequence 30, Appli
8	36	92.3	8	11 US-09-847-946A-38	Sequence 38, Appli
9	36	92.3	9	11 US-09-847-946A-29	Sequence 29, Appli
10	36	92.3	9	11 US-09-847-946A-32	Sequence 32, Appli
11	36	92.3	9	11 US-09-847-946A-35	Sequence 35, Appli
12	36	92.3	9	11 US-09-847-946A-36	Sequence 36, Appli
13	36	92.3	10	11 US-09-847-946A-31	Sequence 31, Appli
14	36	92.3	10	11 US-09-847-946A-34	Sequence 34, Appli
15	36	92.3	11	11 US-09-847-946A-28	Sequence 28, Appli

16	36	92.3	11	11 US-09-847-946A-132	Sequence 132, App
17	36	92.3	11	11 US-09-847-946A-140	Sequence 140, App
18	36	92.3	11	11 US-09-847-946A-143	Sequence 143, App
19	36	92.3	11	11 US-09-847-946A-144	Sequence 144, App
20	36	92.3	11	11 US-09-847-946A-145	Sequence 145, App
21	36	92.3	11	11 US-09-847-946A-148	Sequence 148, App
22	36	92.3	11	11 US-09-847-946A-141	Sequence 141, App
23	36	92.3	11	11 US-09-847-946A-142	Sequence 142, App
24	36	92.3	11	11 US-09-847-946A-146	Sequence 146, App
25	36	92.3	17	11 US-09-847-946A-147	Sequence 147, App
26	36	92.3	18	11 US-09-847-946A-131	Sequence 131, App
27	36	92.3	18	11 US-09-847-946A-135	Sequence 135, App
28	36	92.3	18	11 US-09-847-946A-136	Sequence 136, App
29	36	92.3	22	11 US-09-847-946A-133	Sequence 133, App
30	36	92.3	22	11 US-09-847-946A-134	Sequence 134, App
31	36	92.3	22	11 US-09-847-946A-137	Sequence 137, App
32	36	92.3	22	11 US-09-847-946A-138	Sequence 138, App
33	36	92.3	22	11 US-09-847-946A-139	Sequence 139, App
34	36	92.3	28	11 US-09-847-946A-18	Sequence 18, Appli
35	36	92.3	28	11 US-09-847-946A-18	Sequence 18, Appli
36	36	92.3	22	10 US-09-771-161A-141	Sequence 2, Appli
37	36	92.3	745	9 US-09-796-872-2	Sequence 10, Appli
38	36	92.3	745	10 US-09-844-908-10	Sequence 10, Appli
39	36	92.3	745	10 US-09-844-908-10	Sequence 3, Appli
40	36	92.3	745	12 US-10-408-636-3	Sequence 32, Appli
41	36	92.3	745	12 US-10-394-322A-32	Sequence 4, Appli
42	36	92.3	745	15 US-10-243-408-4	Sequence 35, Appli
43	36	92.3	745	15 US-10-059-585-35	Sequence 10, Appli
44	36	92.3	745	15 US-10-338-462-10	Sequence 15, Appli
45	36	92.3	756	9 US-09-796-872-15	

#### ALIGNMENTS

RESULT 1  
US-09-847-940B-8  
; Sequence 8, Application US/09847940B  
; Patent No. US2002015600A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J.  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPT-117CP  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-8

Query Match 100.0%; Score 39; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEWSWL 6  
Db 1 LEWSWL 6

RESULT 2  
US-09-847-946A-8  
; Sequence 8, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J

```

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-8
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Query Match          100.0%; Score 39; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LEWSWL 6
        |||||
Db       1 LDMSWL 6
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RESULT 3
US-09-847-940B-2
; Sequence 2, Application US/09847940B
; Patent No. US2002015600A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-2
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Query Match          92.3%; Score 36; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LEWSWL 6
        |||||
Db       1 LDMSWL 6
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RESULT 4
US-09-847-946A-2
; Sequence 2, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
```

```

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-2
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Query Match          92.3%; Score 36; DB 11; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LEWSWL 6
        |||||
Db       1 LDMSWL 6
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RESULT 5
US-09-847-946A-33
; Sequence 33, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-33
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Query Match          92.3%; Score 36; DB 11; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LEWSWL 6
        |||||
Db       1 LDMSWL 6
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RESULT 6
US-09-847-946A-37
; Sequence 37, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
```



APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 37  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-37

Query Match 92.3%; Score 36; DB 11; Length 7;  
Best Local Similarity 83.3%; Pred. No. 7e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
|:||||  
DB 1 LDMSWL 6

RESULT 7  
US-09-847-946A-30  
Sequence 30, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findele, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 30  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-30

Query Match 92.3%; Score 36; DB 11; Length 8;  
Best Local Similarity 83.3%; Pred. No. 7e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
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DB 3 LDMSWL 8

RESULT 8  
US-09-847-946A-38  
Sequence 38, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:

APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findele, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 38  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-38

Query Match 92.3%; Score 36; DB 11; Length 8;  
Best Local Similarity 83.3%; Pred. No. 7e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
|:||||  
DB 1 LDMSWL 6

RESULT 9  
US-09-847-946A-29  
Sequence 29, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findele, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 29  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-29

Query Match 92.3%; Score 36; DB 11; Length 9;  
Best Local Similarity 83.3%; Pred. No. 7e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
|:||||  
DB 1 LDMSWL 6

RESULT 10  
US-09-847-946A-32

Sequence 32, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 32  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-32

Query Match 92.3%; Score 36; DB 11; Length 9;  
Best Local Similarity 83.3%; Pred. No. 7e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6  
|:||||  
Db 1 LDMSWL 6

RESULT 11  
US-09-847-946A-35  
Sequence 35, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 35  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-35

Query Match 92.3%; Score 36; DB 11; Length 9;  
Best Local Similarity 83.3%; Pred. No. 7e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6  
|:||||  
Db 3 LDMSWL 8

RESULT 12  
US-09-847-946A-36  
Sequence 36, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 36  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-36

Query Match 92.3%; Score 36; DB 11; Length 9;  
Best Local Similarity 83.3%; Pred. No. 7e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6  
|:||||  
Db 2 LDMSWL 7

RESULT 13  
US-09-847-946A-31  
Sequence 31, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 31  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-31

Query Match 92.3%; Score 36; DB 11; Length 10;  
Best Local Similarity 83.3%; Pred. No. 68;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6

Db 2 LDMSWL 7

RESULT 14  
US-09-847-946A-34  
Sequence 34, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Flindels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hamig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 34  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-34

Query Match 92.3%; Score 36; DB 11; Length 10;  
Best Local Similarity 83.3%; Pred. No. 68;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEMSWL 6  
Db 3 LDMSWL 8

RESULT 15  
US-09-847-946A-28  
Sequence 28, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Flindels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hamig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 28  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-28

Query Match 92.3%; Score 36; DB 11; Length 11;  
Best Local Similarity 83.3%; Pred. No. 73;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LEMSWL 6  
Db 3 LDMSWL 8

Search completed: February 18, 2004, 15:41:56  
Job time : 16.7529 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds

(without alignments)  
41.814 Million cell updates/sec

Title: US-09-643-260-8

Perfect score: 39

Sequence: 1 LEWSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	6	23	ABB08730
2	39	100.0	6	24	AAW08513
3	39	100.0	6	24	ABU08423
4	39	100.0	756	23	ABE77305
5	36	92.3	6	23	ABB08725
6	36	92.3	6	23	AAW08530
7	36	92.3	6	23	AAW08555
8	36	92.3	6	24	ABU08418
9	36	92.3	7	23	AAW08534

10	36	92.3	8	23	AAW08527	Anti-inflammatory
11	36	92.3	9	23	AAW08535	Anti-inflammatory
12	36	92.3	8	20	AAW06182	IKK-alpha polypept
13	36	92.3	9	23	AAW08526	Anti-inflammatory
14	36	92.3	9	23	AAW08529	Anti-inflammatory
15	36	92.3	9	23	AAW08532	Anti-inflammatory
16	36	92.3	10	23	AAW08533	Anti-inflammatory
17	36	92.3	10	23	ABE77313	IKKbeta NEMO bindi
18	36	92.3	10	23	AAW08528	Anti-inflammatory
19	36	92.3	10	23	AAW08531	Anti-inflammatory
20	36	92.3	11	23	ABE77311	Human NBD peptide
21	36	92.3	11	23	AAW08506	Human IKKbeta pept
22	36	92.3	11	23	AAW08525	Anti-inflammatory
23	36	92.3	11	23	AAW08553	NBD peptide, Synt
24	36	92.3	13	23	AAW08640	Anti-inflammatory
25	36	92.3	13	23	AAW08641	Anti-inflammatory
26	36	92.3	13	23	AAW08642	Anti-inflammatory
27	36	92.3	13	23	AAW08645	Anti-inflammatory
28	36	92.3	17	23	AAW08638	Anti-inflammatory
29	36	92.3	17	23	AAW08639	Anti-inflammatory
30	36	92.3	17	23	AAW08643	Anti-inflammatory
31	36	92.3	17	23	AAW08644	Anti-inflammatory
32	36	92.3	18	23	AAW08628	Anti-inflammatory
33	36	92.3	18	23	AAW08629	Anti-inflammatory
34	36	92.3	18	23	AAW08632	Anti-inflammatory
35	36	92.3	18	23	AAW08633	Anti-inflammatory
36	36	92.3	22	23	AAW08630	Anti-inflammatory
37	36	92.3	22	23	AAW08631	Anti-inflammatory
38	36	92.3	22	23	AAW08634	Anti-inflammatory
39	36	92.3	22	23	AAW08635	Anti-inflammatory
40	36	92.3	22	23	AAW08636	Anti-inflammatory
41	36	92.3	22	23	AAW08637	Anti-inflammatory
42	36	92.3	28	23	ABE08740	IKKbeta NEMO bindi
43	36	92.3	28	23	AAW08523	NBD peptide SEQ ID
44	36	92.3	28	24	ABU08434	wild-type human NE
45	36	92.3	36	23	AAW08652	IKKbeta mutated pe

#### ALIGNMENTS

RESULT 1	ABB08730	standard; peptide; 6 AA.
ID	ABB08730	
AC	ABB08730	
DT	14-JUN-2002	(first entry)
DE	Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 8.	
XX	IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;	
XX	kinase activation; leukocyte; inflammation; E-selectin; osteoclast;	
XX	autoimmune disease; transplant rejection; osteoporosis; cancer;	
XX	Alzheimer's disease; viral; infection; achma; anaphylaxis; psoriasis;	
XX	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;	
XX	corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;	
XX	osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;	
XX	antiartherosclerotic; virulence; antiasthmatic; antiallergic;	
XX	dermatological; antibacterial; antipruritic; antineumatic;	
XX	antiarthritic; osteopathic; antitumor; mutant; mutein.	
OS	Homo sapiens.	
XX	Synthetic.	
FT	Key	Location/Qualifiers
FT	Misc-difference 2	/note="Wildtype Asp substituted by Glu"
FT	WO200183547-A2.	
PN	08-NOV-2001.	
XX		
PD		
XX		

PF 02-MAY-2001; 2001WO-US40654.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S;  
 XX  
 DR WPI; 2002-179350/23.  
 XX  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 XX  
 PS Claim 23; Page 44; 82pp; English.  
 XX  
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprising contacting a cell with an anti-inflammatory compound  
 CC (AAB08725-AAB08742) comprising at least one NEMO binding domain  
 CC (AAB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of Ikapab. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC sporadic arthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
 CC binding domain of IKKbeta.  
 CC  
 SQ Sequence 6 AA;  
 OY  
 DB 1 LEMSWL 6  
 1 LEMSWL 6  
 Query Match 100.0%; Score 39; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 2  
 ID AAM48513 standard; Peptide; 6 AA.  
 AC AAM48513;  
 XX  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX NBD mutant peptide SEQ ID NO 8.  
 DE

XX  
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;  
 KW antineumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatologic; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; Ikapab kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammation; bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200183554-A2.  
 XX  
 XX 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRACIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 XX May MJ, Ghosh S, Flindeis MA, Phillips K;  
 PT WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Example 6; Page 47; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytostatic, antipsoriatic, antineumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatologic, neuroprotective,  
 CC neurotropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of Ikapab kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of Ikapab. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 SQ Sequence 6 AA;  
 OY  
 DB 1 LEMSWL 6  
 1 LEMSWL 6  
 Query Match 100.0%; Score 39; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 3  
 ID ABU08423 standard; peptide; 6 AA.  
 ABU08423

XX AC ABU08423;  
 XX XX 12-JUN-2003 (first entry)  
 XX DT  
 XX DE Human NEMO binding site (NBD) mutant peptide #6.  
 XX XX  
 KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;  
 KW IKKappab kinase-beta; IKKappab kinase-alpha; IKKalpha; NF-kappaB;  
 KW nuclear factor-kappaB induction; inflammatory disorder;  
 KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;  
 KW atherosclerosis; viral infection; Ataxia telangiectasia;  
 KW transplacental detection; immunosuppressive; osteopathic;  
 KW cytotropic; nocrotropic; neuroprotective; antitetherapeutic; virucide;  
 KW vasotropic; antineumatic; antitactile; mutant; mutain.  
 XX XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX XX  
 PN US2002156000-A1.  
 XX XX  
 PD 24-OCT-2002.  
 XX XX  
 PF 02-MAY-2001; 2001US-0847940.  
 XX XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX XX  
 PR 22-AUG-2000; 2000US-0643260.  
 XX XX  
 PA (MAYM/) MAY M J.  
 PA (GHOS/) GHOSH S.  
 XX XX  
 PI May MJ, Ghosh S;  
 XX XX  
 DR WPI; 2003-209142/20.  
 XX XX  
 PT Novel antiinflammatory peptide compounds comprising NEMO binding  
 PT domain, useful for modulating NF-kappaB induction in a cell and for  
 PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,  
 PT psoriasis, vasculitis -  
 XX XX  
 PS Claim 22; Page 17; 47pp; English.  
 XX XX  
 CC The present invention relates to antiinflammatory compounds comprising  
 CC NEMO binding domain (NBD) peptides. The NEMO binding domains are  
 CC found on Ikappab kinase-beta (IKKbeta) and Ikappab kinase-alpha  
 CC (IKKalpha) proteins. The antiinflammatory compounds of the invention  
 CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction  
 CC in a cell, where the compounds are capable of blocking the interaction  
 CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The  
 CC antiinflammatory compound further comprises at least one membrane  
 CC translocation domain. The compounds are useful for treating  
 CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia  
 CC telangiectasia, and for transplacental detection. The compounds of  
 CC the invention block NF-kappaB induction by IKK but do not inhibit  
 CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human  
 CC NBD mutant peptides.  
 XX XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 39; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LEWSWL 6  
 |||||  
 Db 1 LEWSWL 6  
 RESULT 4  
 ABB77305  
 ID ABB77305 standard; protein; 756 AA.  
 XX

AC ABB77305;  
 XX XX 14-JUN-2002 (first entry)  
 XX DT  
 XX DE Human IKKbeta mutant D738E.  
 XX XX  
 KW IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;  
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;  
 KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;  
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;  
 KW osteopathic; cytostatic; nocrotropic; neuroprotective; anti-HIV; human;  
 KW dermatolosclic; virucide; antitactile; antiallergic;  
 KW antitactile; antibacterial; antiporiatic; antineumatic;  
 KW antitactile; osteopathic; antitactile; mutant; mutain.  
 XX XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX XX  
 OS Key Location/Qualifiers  
 XX FH Misc-difference 738  
 XX FT /note= "Wildtype Asp substituted by Glu"  
 XX FT  
 XX PN WO200183547-A2.  
 XX XX  
 PD 08-NOV-2001.  
 XX XX  
 PF 02-MAY-2001; 2001WO-US40654.  
 XX XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX XX  
 PR 22-AUG-2000; 2000US-0643260.  
 XX XX  
 PA (UYVA ) UNIV YALB.  
 XX XX  
 PI May MJ, Ghosh S;  
 XX XX  
 DR WPI; 2002-179350/23.  
 XX XX  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 XX XX  
 PS Example 11; Page -; 82pp; English.  
 XX XX  
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprises contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of Ikappab. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,  
 CC sporadic arthritis, psoriatic arthritis, lupus and  
 CC polyomyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,

CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta  
 CC mutant, useful in examples of the invention.  
 CC Note: The present sequence is not given in the specification but is  
 CC derived from GenBank Accession No. 014920 (ABB77294).

SO Sequence 756 AA;  
 Query Match 100.0%; Score 39; DB 23; Length 756;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LEWSML 6  
 Db 737 LEWSML 742

RESULT 5  
 ID ABB08725 standard; peptide; 6 AA.  
 AC ABB08725;  
 XX 14-JUN-2002 (first entry)  
 DT XX  
 DE IKKbeta NEMO binding domain peptide SEQ ID NO 2.  
 XX  
 KW IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
 KW kinase activation; leukocyte; inflammation; B-selectin; osteopetrosis;  
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;  
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;  
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 KW corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;  
 KW osteopathic; cytoskeletal; nootropic; neuroprotective; anti-HIV; human;  
 KW antiarteriosclerotic; virucide; antiaesthetic; antiallergic;  
 KW dermatological; antibacterial; antiparasitic; antineumatic;  
 KW antiarthritic; osteopathic; antulcer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200183547-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US40654.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 PT May MJ, Ghosh S;  
 XX  
 DR WPI; 2002-179350/23.  
 XX  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain  
 XX  
 PS Claim 23; Page 44; 82pp; English.  
 XX  
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprises contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and

CC subsequent decreased phosphorylation of Ikbapp. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation. By down-regulating the  
 CC expression of B-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polyomyelitis, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of the NEMO  
 CC binding domain of IKKbeta.

SO Sequence 6 AA;  
 Query Match 92.3%; Score 36; DB 23; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LEWSML 6  
 Db 1 LEWSML 6

RESULT 6  
 ID AAM48530 standard; Peptide; 6 AA.  
 AC AAM48530;  
 XX  
 DT 20-MAR-2002 (first entry)  
 DE Anti-inflammatory peptide SEQ ID NO 33.  
 XX  
 KW Anti-inflammatory; antiaesthetic; cytoskeletal; antiparasitic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NF-kappaB; Ikbapp; kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX

PI	May MJ, Ghosh S, Firdels MA, Phillips K;
XX	
DR	WPI: 2002-121889/16.
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis -
XX	
PS	Claim 6; Page 61; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AAm48628-AAm48645), comprising a membrane translocation domain
CC	(AAm48620-AAm48637 or AAm48646-AAm48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AAm48625-AAm48619). The antiinflammatory compounds have antiasthmatic,
CC	cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	nootropic, antiatherosclerotic, virocidic and antiallergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of Ikappab kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of Ikappab. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
SQ	Sequence 6 AA;
OY	Query Match 92.3%; Score 36; DB 23; Length 6;
Dd	Best Local Similarity 83.3%; Pred. No. 9.3e+05;
	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
	1 LEMSWL 6
	:
	1 LDMSWL 6
RESULT 7	
AAm48655	
ID	AAm48655 standard; Peptide; 6 AA.
XX	
AC	AAm48655;
XX	
DT	20-MAR-2002 (first entry)
XX	
NBD	mutant peptide SEQ ID NO 2.
XX	
KM	Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KM	antiathermatic; antiarthritic; osteopathic; antibacterial; virocidic;
KM	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KM	antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KM	Cytokine; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;
KM	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KM	autoimmune disorder; multiple sclerosis; transplant rejection;
KM	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KM	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS	Synthetic.
XX	
PN	WO200183554-A2.
XX	
PD	08-NOV--2001.
XX	
FP	02-MAY-2001; 2001WO-US14346.
XX	

PR	02-MAY-2000; 2000US-201261P.
FR	22-AUG-2000; 2000US-064326O.
XX	
PA	(PRAE-) PRAECIS PHARM INC.
PA	(UTYA) UNIV YALE.
PI	May MJ, Ghosh S, Findels MA, Philippe K;
XX	
DR	WPI; 2002-121893/16.
XX	
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis -
XX	
PS	Example 6; Page 47; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AAM48628-AAM48645), comprising a membrane translocation domain
CC	(AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC	cycostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective, The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of IkkappaB kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of IkkappaB. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	relanglectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
SQ	Sequence 6 AA:
	Query Match 92.3%; Score 36; DB 23; Length 6;
	Best Local Similarity 83.3%; Pred. No. 9.3e+05;
	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Gy	1 LEWSNL 6
	:
Dd	1 LDMSWL 6
RESULT 8	
ID	ABU08418 standard; peptide; 6 AA.
XX	
AC	ABU08418;
XX	
DT	12-JUN-2003 (first entry)
DE	
XX	Human NEMO binding site (NBD) mutant peptide #1.
XX	
KV	Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
KV	IkkappaB kinase-beta; IkkappaB kinase-alpha; IKKalpha; NF-kappaB;
KV	nuclear factor-kappaB induction; inflammatory disorder;
KV	autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
KV	atherosclerosis; viral infection; Ataxia telangiectasia;
KV	transplantation detection; immunosuppressive; osteopathic;
KV	cycostatic; nocotropic; neuroprotective; antiatherosclerotic; vincloide;
KV	vaseotropic; antirheumatic; antiarthritic; mutant; mutcin.
OS	Homo sapiens.
OS	Synthetic.
XX	



PN US200215600-A1.  
XX  
XX 24-OCT-2002.  
XX  
XX 02-MAY-2001; 2001US-0847940.  
PF  
XX 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
XX  
XX (MAYM/) MAY M J.  
PA (GHOS/) GHOSH S.  
PI May MJ, Ghosh S;  
XX  
XX WPI; 2003-209142/20.  
DR N-PSDB; ABX94269, ABX94270.  
XX  
PT Novel antiinflammatory peptide compounds comprising NEMO binding  
PT domain, useful for modulating NF-kappaB induction in a cell and for  
PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,  
PT psoriasis, vasculitis -  
XX  
XX Claim 22; Page 17; 47pp; English.  
XX  
CC The present invention relates to antiinflammatory compounds comprising  
CC NEMO binding domain (NBD) peptides. The NEMO binding domains are  
CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha  
CC (IKKalpha) proteins. The antiinflammatory compounds of the invention  
CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction  
CC in a cell, where the compounds are capable of blocking the interaction  
CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The  
CC antiinflammatory compound further comprises at least one membrane  
CC translocation domain. The compounds are useful for treating  
CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,  
CC Alzheimer's disease, atherosclerosis, viral infection, Ataxia  
CC telangiectasia, and for transplantation detection. The compounds of  
CC the invention block NF-kappaB induction by IKK but do not inhibit  
CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human  
CC NBD mutant peptides.  
XX  
SQ Sequence 6 AA;  
Query Match 92.3%; Score 36; DB 24; Length 6;  
Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LEWSWL 6  
DB 1 LDMSWL 6  
RESULT 9  
AAM48534  
ID AAM48534 standard; Peptide; 7 AA.  
XX  
XX AAM48534;  
XX  
XX 20-MAR-2002 (first entry)  
XX  
XX Anti-inflammatory peptide SEQ ID NO 37.  
XX  
XX Antiinflammatory; antiaesthetic; cytostatic; antiproliferative; nootropic;  
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX autoimmune disorder; multiple sclerosis; transplant rejection;  
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
XX Synthetic.

PN WO200183554-A2.  
XX  
XX 08-NOV-2001.  
XX  
XX 02-MAY-2001; 2001WO-US14346.  
PF  
XX 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
XX  
XX (PRAE-) PRACIS PHARM INC.  
PA (UYVA) UNIV YALE.  
PI May MJ, Ghosh S, Finkels MA, Phillips K;  
XX  
XX WPI; 2002-121889/16.  
DR  
XX  
PT Novel antiinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis -  
XX  
XX Claim 6; Page 61; 88pp; English.  
XX  
CC The invention relates to an antiinflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain  
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
CC cytostatic, antiproliferative, antirheumatic, antarthritic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of IkappaB. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
XX  
XX SQ Sequence 7 AA;  
Query Match 92.3%; Score 36; DB 23; Length 7;  
Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LEWSWL 6  
DB 1 LDMSWL 6  
RESULT 10  
AAM48527  
ID AAM48527 standard; Peptide; 8 AA.  
XX  
XX AAM48527;  
XX  
XX 20-MAR-2002 (first entry)  
XX  
XX Anti-inflammatory peptide SEQ ID NO 30.  
XX  
XX Antiinflammatory; antiaesthetic; cytostatic; antiproliferative; nootropic;  
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

KW		autoimmune disorder; multiple sclerosis; transplant rejection;
KV		osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW		ataxia telangiectasia; allergy; amyotaxis; arthritis.
OS		Synthetic.
XX		
PN		WO200183554-A2.
PD		08-NOV-2001.
XX		
PF		02-MAY-2001; 2001WO-US14346.
XX		
PR		02-MAY-2000; 2000US-201261P.
PR		22-AUG-2000; 2000US-0643260.
XX		
PA		(PRAE-) PRAECTIS PHARM INC.
PA		(UYAA-) UNIV YALE.
XX		
PI		May MJ, Ghosh S, Finkelstein MA, Phillips K;
DR		WPI: 2002-121889/16.
XX		
PT		Novel antiinflammatory compound comprising membrane translocation
PT		domain fused to NEMO binding sequence, useful for blocking nuclear
PT		factor kappaB activation, and for treating asthma, lung inflammation,
PT		psoriasis -
XX		
PS		Claim 6; Page 61; 8pp; English.
CC		The invention relates to an antiinflammatory compound (especially
CC		AAM48628-AAM48645), comprising a membrane translocation domain
CC		(AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC		amino acid residues, fused to a NEMO binding sequence
CC		(AAM48525-AAM48519). The antiinflammatory compounds have antiaesthetic,
CC		cycostatic, antiprostaglandin, antirheumatic, antiarthritic, osteopathic,
CC		antibacterial, immunosuppressive, dermatological, neuroprotective,
CC		nootropic, antithrombotic, virucide and anti-allergic activity. The
CC		compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC		activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC		the NEMO binding domain that results in inhibition of IKKbeta kinase
CC		activation and subsequent decreased phosphorylation of IkappaB. The
CC		compounds are useful for treating inflammatory disorders, e.g. asthma,
CC		lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC		osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC		bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC		granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC		Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC		telangiectasia. The compounds are also useful for treating
CC		pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC		during or food sensitivity, eczema, dermatitis, sunburn, aging and
CC		arthritis.
XX		
SO		Sequence 8 AA;
Query Match		92.3%; Score 36; DB 23; Length 8;
Best Local Similarity		83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative		1; Mismatches 0; Indels 0; Gaps 0
OY		1 LEWSWL 6
		:
DB		3 LDWSWL 8
RESULT 11		
ID		AAM48535 standard; Peptide; 8 AA.
AC		AAM48535;
DT		20-MAR-2002 (first entry)
XX		
DE		Anti-inflammatory peptide SEQ ID NO 38.

KM	Antiinflammatory; antiasthmatic; cytoprotic; antiproliferative; neurotropic;
KW	antirheumatic; antiallergic; osteoprotic; antibacterial; virucide;
KX	immunosuppressive; dermatological; neuroprotective; antihypertensive;
KV	antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW	cyclokin; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KM	autoimmune disorder; multiple sclerosis; transplant rejection;
KM	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS	Synthetic.
XX	
PN	WO200183554-A2.
PD	08-NOV-2001.
PP	02-MAY-2001; 2001WO-US14346.
PR	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-0643260.
PA	(PRAE-) PRAECIS PHARM INC.
XX	(UYVA ) UNIV YALE.
PT	May MJ, Ghosh S, Findeis MA, Phillips K;
DR	WPI; 2002-121889/16.
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis -
PS	Claim 6; Page 61; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AAM48628-AAM48645), comprising a membrane translocation domain
CC	(AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC	cytoprotic, antiproliferative, antirheumatic, antiallergic, osteoprotic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	neurotropic, antihypertensive, virucide and antiallergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of IkappaB. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
SQ	Sequence 8 AA;
Query Match	92.3%; Score 36; DB 23; Length 8;
Best Local Similarity	83.3%; Pred. No. 9.3e+05;
Matches	5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY	1 LDMSWL 6
Dd	1 LDMSWL 6

AC AAM96182;  
 XX  
 DT 27-APR-1999 (first entry)  
 XX  
 DE IKK-alpha polypeptide with binding activity.  
 XX  
 KW I-kappa-B kinase; IKK-alpha; gene expression; modulation;  
 KM suppression; activation; tumour necrosis factor; TNF; interleukin-1;  
 KM IL-1; TNF receptor associated factor; TRAF.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO901541-A1.  
 XX  
 PD 14-JAN-1999.  
 XX  
 PF 01-JUL-1998; 98WO-US13782.  
 XX  
 PR 10-JUL-1997; 97US-0890854.  
 PR 01-JUL-1997; 97US-0887115.  
 XX  
 PA (TULSA-) TULARIX INC.  
 XX  
 PI Cao Z, Regnier C, Roche M,  
 DR WPI; 1999-106044/09.  
 XX  
 PT Newly isolated human kinase IkappaB Kinase (IKK- $\alpha$ ) polypeptides -  
 PT useful in screening for agents that modulate the interaction of an  
 PT IKK polypeptide to a binding target and for modulating signal  
 PT transduction involving IkappaB in a cell.  
 XX  
 PS Disclosure; Page -; 32pp; English.  
 XX  
 CC I-kappa-B kinase (AAM96182), deletion mutants of it retaining  
 CC I-kappa-B kinase activity and I-kappa-B polypeptides (comprising a  
 CC six residue domain of I-kappa-B containing one of Ser32 and Ser36,  
 CC and a candidate agent) can be used to screen for agents that  
 CC modulate the interaction of an IKK polypeptide to a binding target.  
 CC The modulation of the kinase activity of IKK-alpha forms a method  
 CC for modulating signal transduction involving I-kappa-B in a cell.  
 CC The IKK-alpha polypeptides are useful for generating oligonucleotide  
 CC primers and probes for use in the isolation of natural  
 CC IKK-alpha-encoding nucleic acids. The nucleic acids are useful as  
 CC translatable transcripts, hybridization probes, polymerase chain  
 CC reaction (PCR) probes and primers. Their diagnostic applications  
 CC include IKK-alpha hybridization probes for identifying wild-type and  
 CC mutant IKK-alpha alleles in clinical and laboratory samples.  
 CC Therapeutic application includes the use of IKK-alpha nucleic acids  
 CC for modulating cellular expression or intracellular  
 CC catalytically inactive IKK-alpha mutants suppress NF-kappa-B  
 CC activation induced by tissue necrosis factor (TNF), interleukin-1  
 CC (IL-1) stimulation, TNF receptor-associated factor (TRAF) and  
 CC NF-kappa-B-inducing kinase (NIK) overexpression. Polypeptides of  
 CC IKK-alpha showing exemplary binding activity are described in  
 CC AAM96182. These peptides all comprise one of Cys30, Glu54,  
 CC Leu60, Thr67, Ser68, Pro64, Thr66 or Ser67 of the full length  
 CC IKK-alpha described in AAM96157. Deletion mutants of the invention  
 CC comprise at least one of these regions.  
 CC N.B. The present sequence is not given in the present specification  
 CC but is derived from the sequence given in AAM96157 as specified.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 92.3%; Score 36; DB 20; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 13  
 AAM48526  
 ID AAM48526 Brandard; Peptide; 9 AA.  
 XX  
 AC AAM48526;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 29.  
 XX  
 KW Anti-inflammatory; antiaesthetic; cytosolic; antiproliferative; nocrotic;  
 KW antirheumatic; antiallergic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Rindels MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel anti-inflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Claim 6; Page 61; 89pp; English.  
 XX  
 CC The invention relates to an anti-inflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiaesthetic,  
 CC cytosolic, antiproliferative, antirheumatic, antiallergic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nocrotic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
 CC activation by blocking interaction of IkappaB Kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis, transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 92.3%; Score 36; DB 23; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 9.3e+05;

	Matches	5;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
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				:						
Db			1	LDMSWL 6						
RESULT 14										
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XX										
AC	AA048529;									
XX										
XX										
DT	20-MAR-2002	(first entry)								
DE	Anti-inflammatory peptide SEQ ID NO 32.									
KX	Anti-inflammatory; antiarthritic; cytopathic; antipsoriatic; neutrophic;									
KX	antiinflammatory; antiarthritic; osteopathic; antibacterial; virucide;									
KX	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;									
KX	antiatherogenic; membrane translocation domain; NEMO binding domain; eczema;									
KX	cytokine; NFkBpab; Ikappab kinase beta; IKKbeta; cancer; psoriasis;									
KX	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;									
KX	autoimmune disorder; multiple sclerosis; transplant rejection;									
KX	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;									
KX	ataxia telangiectasia; allergy; anaphylaxis; arthritis.									
XX										
OS	Synthetic.									
XX										
PN	WO200103554-A2.									
XX										
PD	08-NOV-2001.									
XX										
PF	02-MAY-2001; 2001WO-US14346.									
XX										
PR	02-MAY-2000; 2000US-201261P.									
XX										
PR	22-AUG-2000; 2000US-0643260.									
XX										
PA	(PRAE-) PRAECIS PHARM INC.									
XX										
PA	(UYYA ) UNIV YALE.									
XX										
PI	May MJ, Ghosh S, Finkelstein MA, Phillips K;									
XX										
DR	WPI; 2002-121889/16.									
XX										
PT	Novel antiinflammatory compound comprising membrane translocation									
PT	domain fused to NEMO binding sequence, useful for blocking nuclear									
PT	factor kappaB activation, and for treating asthma, lung inflammation,									
PT	psoriasis -									
XX										
PS	Claim 6; Page 61; 88pp; English.									
XX										
CC	The invention relates to an antiinflammatory compound (especially									
CC	AA048628-AA04645), comprising a membrane translocation domain									
CC	(AA048620-AA048637 or AA04646-AA048651) which comprises from 6-15									
CC	amino acid residues, fused to a NEMO binding sequence									
CC	(AA048625-AA048619). The antiinflammatory compounds have antiasthmatic,									
CC	cytopathic, antipsoriatic, antiinflammatory, antiarthritic, osteopathic,									
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,									
CC	neutrophic, antiatherosclerotic, virucide and anti-allergic activity. The									
CC	compounds act as selective inhibitors of cytokine-mediated NFkBpab									
CC	activation by blocking interaction of Ikappab kinase beta (IKKbeta) at									
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase									
CC	activation and subsequent decreased phosphorylation of Ikappab. The									
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,									
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,									
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,									

CC	arthritis.
XX	
SQ	Sequence    9 AA;
Query Match	92.3%; Score 36; DB 23; Length 9;
Best Local Similarity	83.3%; Pred. NO. 9.3e+05;
Matches    5; Conservative	1; Mismatches    0; Indels    0; Gaps    0.
OY	1 LEWSML 6  :     1 LDMSWL 6
DB	
RESULT 15	
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ID	AAM48532 standard; Peptide; 9 AA.
XX	
AC	AAM48532;
XX	
DT	20-MAR-2002 (first entry)
XX	
DE	Anti-inflammatory peptide SEQ ID NO 35.
XX	
KM	Antiinflammatory; antiseptic; cytosolic; antiposrotatic; noctropic; KM Antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; KM immunosuppressive; dermatological; neuroprotective; antithrombotic; KM anticancer; membrane translocation domain; NEMO binding domain; eczema; KM cytokine; NFkB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; KM autoimmunity disorder; multiple sclerosis; transplant rejection; KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; KM ataxia telangiectasia; allergy; anaphylaxis; arthritis. OS Synthetic. XX XX WO200183554-A2. XX XX PD 08-NOV-2001. XX XX PF 02-MAY-2001; 2001WO-US14346. XX XX PR 02-MAY-2000; 2000US-201261P. XX PR 22-AUG-2000; 2000US-0643260. XX XX PA (PRAE-) PRAECIS PHARM INC. XX PA (UYVA ) UNIV YALE. XX XX PI May MJ, Ghosh S, Findele MA, Phillips K; XX DR WPI; 2002-121889/16. XX XX PT Novel antiinflammatory compound comprising membrane translocation PT domain fused to NEMO binding sequence, useful for blocking nuclear PT factor kappaB activation, and for treating asthma, lung inflammation, PT psoriasis - XX XX PS Claim 6; Page 61; 88pp; English. XX XX CC The invention relates to an antiinflammatory compound (especially CC AAM48628-AAM48645), comprising a membrane translocation domain CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 CC amino acid residues, fused to a NEMO binding sequence CC (AAM48525-AAM48619). The antiinflammatory compounds have antiseptic, CC cytosolic, antiposrotatic, antirheumatic, antiarthritic, osteopathic, CC antibacterial, immunosuppressive, dermatological, neuroprotective, CC noctropic, antithrombotic, virucide and anticancer activity. The CC compounds act as selective inhibitors of cytokine-mediated NFkB CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at CC the NEMO binding domain that results in inhibition of IKKbeta kinase CC activation and subsequent decreased phosphorylation of IkappaB. The CC compounds are useful for treating inflammatory disorders, e.g. asthma, CC lung inflammation or cancer, psoriasis, rheumatoid arthritis, CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,

CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.

XX  
SQ Sequence 9 AA;

Query Match 92.3%; Score 36; DB 23; Length 9;  
Best Local Similarity 83.3%; Pred. No. 9.3e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
|:|:|:|  
Db 3 LDWSWL 8

Search completed: February 18, 2004, 14:26:20  
Job time : 22.7763 secs

Wb ant

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds  
(without alignments)  
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Title: US-09-643-260-7

Perfect score: 38

Sequence: 1 LAMSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/pubppa/PCF\_NEW\_PUB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

## SUMMARIES

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2	38	100.0	6	11 US-09-847-946A-7	Sequence 7, Appli
3	38	100.0	6	12 US-10-369-493-20896	Sequence 20896, A
4	38	100.0	1217	12 US-10-104-047-2283	Sequence 2263, Ap
5	35	92.1	196	16 US-10-080-170-120	Sequence 120, App
6	35	92.1	210	16 US-10-080-170-548	Sequence 548, App
7	35	92.1	1055	9 US-09-759-667A-3	Sequence 3, Appli
8	34	89.5	56	12 US-09-933-767-359	Sequence 359, App
9	34	89.5	56	15 US-10-023-282-359	Sequence 359, App
10	34	89.5	64	9 US-09-864-761-39808	Sequence 39808, A
11	34	89.5	170	12 US-10-104-047-2210	Sequence 2210, Ap
12	34	89.5	449	15 US-10-156-761-7842	Sequence 7842, Ap
13	34	89.5	493	12 US-10-147-324-2	Sequence 2, Appli
14	34	89.5	544	12 US-10-257-378-17	Sequence 17, Appli
15	34	89.5	544	15 US-10-067-668-8	Sequence 8, Appli

16	34	89.5	544	15	US-10-175-686-8	Sequence 8, Appli
17	34	89.5	659	12	US-10-369-493-12634	Sequence 12634, A
18	34	89.5	821	12	US-10-369-493-7850	Sequence 7850, Ap
19	33	86.8	6	10	US-09-847-940B-8	Sequence 8, Appli
20	33	86.8	6	11	US-09-847-946A-8	Sequence 8, Appli
21	33	86.8	186	15	US-10-106-698-8201	Sequence 8201, Ap
22	33	86.8	328	9	US-09-820-893-74	Sequence 74, Appli
23	33	86.8	283	9	US-09-820-893-131	Sequence 131, Appli
24	33	86.8	323	12	US-10-264-237-1765	Sequence 1765, Ap
25	33	86.8	350	9	US-09-820-893-132	Sequence 132, App
26	33	86.8	355	10	US-09-712-363-161	Sequence 161, App
27	33	86.8	355	12	US-10-084-843-79	Sequence 79, Appli
28	33	86.8	355	12	US-10-193-002-80	Sequence 80, Appli
29	33	86.8	355	12	US-10-096-732A-2	Sequence 2, Appli
30	33	86.8	433	16	US-10-080-170-547	Sequence 547, App
31	33	86.8	440	16	US-10-080-170-164	Sequence 164, App
32	33	86.8	828	12	US-10-369-493-20660	Sequence 20660, A
33	33	86.8	1053	12	US-10-369-493-22733	Sequence 22733, A
34	33	86.8	1569	14	US-10-108-605-303	Sequence 303, App
35	32	84.2	6	10	US-09-847-940B-2	Sequence 2, Appli
36	32	84.2	6	10	US-09-847-940B-9	Sequence 9, Appli
37	32	84.2	6	11	US-09-847-946A-2	Sequence 2, Appli
38	32	84.2	6	11	US-09-847-946A-9	Sequence 9, Appli
39	32	84.2	6	11	US-09-847-946A-33	Sequence 33, Appli
40	32	84.2	7	11	US-09-847-946A-37	Sequence 37, Appli
41	32	84.2	8	11	US-09-847-946A-30	Sequence 30, Appli
42	32	84.2	8	11	US-09-847-946A-38	Sequence 38, Appli
43	32	84.2	9	11	US-09-847-946A-29	Sequence 29, Appli
44	32	84.2	9	11	US-09-847-946A-32	Sequence 32, Appli
45	32	84.2	9	11	US-09-847-946A-35	Sequence 35, Appli

## ALIGNMENTS

RESULT 1  
US-09-847-940B-7  
; Sequence 7, Application US/09847940B  
; Patent No. US20020156000A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J.  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-117CP  
; CURRENT APPLICATION NUMBER: US/09/847,940B  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; TYPE: PRT  
; LENGTH: 6  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-7

Query Match 100.0%; Score 38; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
Db 1 LAMSWL 6

RESULT 2  
US-09-847-946A-7  
; Sequence 7, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar  
APPLICANT: Firdels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NBD peptide  
US-09-847-946A-7

Query Match 100.0%; Score 38; DB 11; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
Db 1 LAMSWL 6

RESULT 3  
US-10-369-493-20896  
Sequence 20896, Application US/10369493  
Publication No. US20030233675A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Goldman, Barry S.  
APPLICANT: Chen, Xianfeng  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
FILE REFERENCE: 38-10(52052)B  
CURRENT APPLICATION NUMBER: US/10/369,493  
PRIOR FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360,039  
PRIOR FILING DATE: 2002-02-21  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 20896  
LENGTH: 872  
TYPE: PRT  
ORGANISM: SYNECHOCOCCUS SP. WH 8102  
US-10-369-493-20896

Query Match 100.0%; Score 38; DB 12; Length 872;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
Db 692 LAMSWL 697

RESULT 4  
US-10-104-047-2263  
Sequence 2263, Application US/10104047  
Publication No. US20030236392A1  
GENERAL INFORMATION:  
APPLICANT: HELIX RESEARCH INSTITUTE  
TITLE OF INVENTION: NO. US20030236392A1 full length cDNA  
FILE REFERENCE: H1-A0105  
CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT FILING DATE: 2002-03-25  
PRIOR APPLICATION NUMBER:  
PRIOR FILING DATE:  
NUMBER OF SEQ ID NOS: 4096  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2263  
LENGTH: 1217  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-104-047-2263

Query Match 100.0%; Score 38; DB 12; Length 1217;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
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QY 1 LAMSWL 6  
Db 590 LAMSWL 595

RESULT 5  
US-10-080-170-120  
Sequence 120, Application US/10080170  
Publication No. US20030129601A1  
GENERAL INFORMATION:  
APPLICANT: COLE, S.T.  
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR  
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR  
FILE REFERENCE: 03495.0218  
CURRENT APPLICATION NUMBER: US/10/080,170  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: 60/270,123  
PRIOR FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 652  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 120  
LENGTH: 196  
TYPE: PRT  
ORGANISM: Mycobacterium leprae  
US-10-080-170-120

Query Match 92.1%; Score 35; DB 16; Length 196;  
Best Local Similarity 83.3%; Pred. No. 9.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
Db 109 LAMSWL 114

RESULT 6  
US-10-080-170-548  
Sequence 548, Application US/10080170  
Publication No. US20030129601A1  
GENERAL INFORMATION:  
APPLICANT: COLE, S.T.  
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR  
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR  
FILE REFERENCE: 03495.0218  
CURRENT APPLICATION NUMBER: US/10/080,170  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: 60/270,123  
PRIOR FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 652  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 548  
LENGTH: 210  
TYPE: PRT  
ORGANISM: Mycobacterium tuberculosis  
US-10-080-170-548

Query Match 92.1%; Score 35; DB 16; Length 210;  
Best Local Similarity 83.3%; Pred. No. 9.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
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Db 123 VAMSWL 128

RESULT 7  
US-09-759-667A-3  
; Sequence 3, Application US/09759667A  
; Patent No. US20020064777A1  
; GENERAL INFORMATION:  
; APPLICANT: Mengiste, Teesaye  
; APPLICANT: Paszkowski, Jerzy  
; TITLE OF INVENTION: Recombination Repair Gene, MIM, from Arabidopsis thaliana  
; FILE REFERENCE: S-30568A  
; CURRENT APPLICATION NUMBER: US/09/759,667A  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 9815485.9  
; PRIOR FILING DATE: 1998-07-16  
; PRIOR APPLICATION NUMBER: 9900760.1  
; PRIOR FILING DATE: 1999-01-14  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 3  
; LENGTH: 1055  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-759-667A-3

Query Match 92.1%; Score 35; DB 9; Length 1055;  
Best Local Similarity 83.3%; Pred. No. 3.3e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
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Db 248 LAMSWV 253

RESULT 8  
US-09-933-767-359  
; Sequence 359, Application US/09933767  
; Publication No. US20030181692A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P2  
; CURRENT APPLICATION NUMBER: US/09/933,767  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: PCT/US01/05614  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: 60/184,836  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/193,170  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 09/205,258  
; PRIOR FILING DATE: 1998-12-04  
; PRIOR APPLICATION NUMBER: PCT/US98/11422  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/048,885  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,375  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,881  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,880  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,896  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,020  
; PRIOR FILING DATE: 1997-06-06

; PRIOR APPLICATION NUMBER: 60/048,876  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,895  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,884  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,894  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,971  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,964  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,882  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,899  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,893  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,900  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,901  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,892  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,915  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,019  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,970  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,972  
; PRIOR FILING DATE: 1997-06-06  
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; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,373  
; PRIOR FILING DATE: 1997-06-06  
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; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,374  
; PRIOR FILING DATE: 1997-06-06  
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; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,949  
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; PRIOR FILING DATE: 1997-06-06  
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; PRIOR FILING DATE: 1997-06-06  
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; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,877  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,878  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/068,054  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/068,064  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/068,053  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/070,923  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/073,160  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/073,159  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/073,165



;; PRIOR FILING DATE: 1998-01-30  
;; PRIOR APPLICATION NUMBER: 60/073,164  
;; PRIOR FILING DATE: 1998-01-30  
;; PRIOR APPLICATION NUMBER: 60/085,925  
;; PRIOR FILING DATE: 1998-05-18  
;; PRIOR APPLICATION NUMBER: 60/085,921  
;; PRIOR FILING DATE: 1998-05-18  
;; PRIOR APPLICATION NUMBER: 60/085,923  
;; PRIOR FILING DATE: 1998-05-18  
;; PRIOR APPLICATION NUMBER: 60/085,922  
;; PRIOR FILING DATE: 1998-05-18  
;; PRIOR APPLICATION NUMBER: 60/092,921  
;; PRIOR FILING DATE: 1998-07-15  
;; PRIOR APPLICATION NUMBER: 60/094,657  
;; PRIOR FILING DATE: 1998-07-30  
;; NUMBER OF SEQ ID NOS: 1245  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 359  
;; LENGTH: 56  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: SITE  
;; LOCATION: (56)  
;; OTHER INFORMATION: Xaa equals stop translation  
US-09-933-767-359

Query Match 89.5%; Score 34; DB 12; Length 56;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSM 5  
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Db 9 LAWSM 13

RESULT 9  
US-10-023-282-359  
;; Sequence 359, Application US/10023282  
;; Publication No. US2003002893A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Young et al.  
;; TITLE OF INVENTION: 207 Human Secreted Proteins  
;; FILE REFERENCE: P2007P1  
;; CURRENT FILING DATE: 2001-12-20  
;; EARLIER FILING DATE: 1998-12-04  
;; EARLIER APPLICATION NUMBER: 09/205,258  
;; EARLIER FILING DATE: 1998-12-04  
;; EARLIER APPLICATION NUMBER: PCT/US98/11422  
;; EARLIER FILING DATE: 1998-06-04  
;; EARLIER APPLICATION NUMBER: 60/048,885  
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;; EARLIER FILING DATE: 1997-06-06  
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;; EARLIER FILING DATE: 1997-06-06  
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;; EARLIER APPLICATION NUMBER: 60/048,878  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/070,923  
;; EARLIER FILING DATE: 1997-12-18  
;; EARLIER APPLICATION NUMBER: 60/092,921  
;; EARLIER FILING DATE: 1998-07-15  
;; EARLIER APPLICATION NUMBER: 60/094,657  
;; EARLIER FILING DATE: 1998-07-30  
;; NUMBER OF SEQ ID NOS: 1227  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 359  
;; LENGTH: 56  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: SITE  
;; LOCATION: (56)  
;; OTHER INFORMATION: Xaa equals stop translation  
US-10-023-282-359

Query Match 89.5%; Score 34; DB 15; Length 56;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSM 5  
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Db 9 LAWSW 13

RESULT 10

US-09-864-761-39808

; Sequence 39808, Application US/09864761

; Patent No. US20020046763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; FILE REFERENCE: Aeonica-X-1

; CURRENT FILING DATE: 2001-05-23

; PRIOR FILING DATE: 2000-02-04

; PRIOR FILING DATE: 2000-02-04

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-08-03

; PRIOR FILING DATE: 2000-10-04

; PRIOR FILING DATE: 2000-09-27

; PRIOR FILING DATE: 2001-01-30

; PRIOR FILING DATE: 2001-01-30

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Best Local Similarity 100.0%; Pred. No. 5.3e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 33 LAWSW 37

RESULT 11

US-10-104-047-2210

; Sequence 2210, Application US/10104047

; Publication No. US20030236392A1

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: NO. US20030236392A1e1 full length cDNA

; FILE REFERENCE: H1-A0105

; CURRENT FILING DATE: US/10/104,047

; PRIOR FILING DATE: 2002-03-25

; PRIOR FILING DATE:

; NUMBER OF SEQ ID NOS: 4096

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2210

; LENGTH: 170

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-104-047-2210

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Best Local Similarity 83.3%; Pred. No. 1.1e+03; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 162 LAWSW 167

RESULT 12

US-10-156-761-7842

; Sequence 7842, Application US/10156761

; Publication No. US20030115018A1

; GENERAL INFORMATION:

; APPLICANT: OKEDA, HARUO

; APPLICANT: ISHIKAWA, JUN

; APPLICANT: HORIKAWA, HIROSHI

; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIYUKI

; APPLICANT: HATTORI, MASAHIRA

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-262

; CURRENT FILING DATE: US/10/156,761

; PRIOR FILING DATE: 2002-05-29

; PRIOR FILING DATE: JP 2001-204089

; PRIOR FILING DATE: 2001-05-10

; PRIOR FILING DATE: JP 2001-272697

; PRIOR FILING DATE: 2001-08-02

; NUMBER OF SEQ ID NOS: 15109

; SEQ ID NO 7842

; LENGTH: 449

; TYPE: PRT

; ORGANISM: Streptomyces avermitilis

US-10-156-761-7842

Query Match 89.5%; Score 34; DB 15; Length 449;

Best Local Similarity 83.3%; Pred. No. 2.3e+03; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LAWSW 6

Db 42 LAWSW 47

RESULT 13  
US-10-147-324-2  
; Sequence 2, Application US/10147324  
; Publication No. US20030215812A1  
; GENERAL INFORMATION:  
; APPLICANT: MA, YAN-HE  
; APPLICANT: XUE, YAN-PEN  
; TITLE OF INVENTION: GENE ENCODING B-MANNANASE, ENZYME PREPARATION AND USES  
; FILE REFERENCE: 0304-0001  
; CURRENT APPLICATION NUMBER: US/10/147,324  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 493  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-10-147-324-2

Query Match 89.5%; Score 34; DB 12; Length 493;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSW 5  
DB 280 LAMSW 284

RESULT 14  
US-10-257-378-17  
; Sequence 17, Application US/10257378  
; Publication No. US20030190642A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Glenville  
; APPLICANT: Peckovich, P. Martin  
; APPLICANT: White, Jay  
; APPLICANT: Ramshaw, Heather A.  
; APPLICANT: Stangle, Wayne A.  
; TITLE OF INVENTION: A Thymus Expressed Human Cytochrome P450 (P450TEC)  
; FILE REFERENCE: 11812-65  
; CURRENT APPLICATION NUMBER: US/10/257,378  
; CURRENT FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: US 60/208,785  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/198,617  
; PRIOR FILING DATE: 2000-04-20  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 544  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-257-378-17

Query Match 89.5%; Score 34; DB 12; Length 544;  
Best Local Similarity 83.3%; Pred. No. 2.7e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LAMSW 6  
DB 46 LAMSW 51

RESULT 15  
US-10-067-668-8  
; Sequence 8, Application US/10067668  
; Publication No. US20030022334A1  
; GENERAL INFORMATION:  
; APPLICANT: Glucksmann, Maria Alexandra  
; TITLE OF INVENTION: 33312, 33303, 32579, NOVEL HUMAN  
; TITLE OF INVENTION: CYTOCHROME P450 FAMILY MEMBERS AND USES THEREOF  
; FILE REFERENCE: 10448-136001

; CURRENT APPLICATION NUMBER: US/10/067,668  
; CURRENT FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 60/266,140  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 544  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-067-668-8

Query Match 89.5%; Score 34; DB 15; Length 544;  
Best Local Similarity 83.3%; Pred. No. 2.7e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 46 LAMSW 51

Search completed: February 18, 2004, 15:41:56  
Job time : 17.7529 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds  
(without alignment)  
41.814 Million cell updates/sec

Title: US-09-643-260-7  
Sequence: 1 LAMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_19Jun03:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	6	23	ABR08729
2	38	100.0	6	23	AAW48512
3	38	100.0	6	24	ABU08432
4	38	100.0	7	23	ABR77303
5	35	92.1	196	22	AAU62777
6	35	92.1	196	23	ABU05469
7	35	92.1	210	23	ABU05897
8	35	92.1	321	22	ABR64219
9	35	92.1	329	22	ABR71850

10	35	92.1	1055	21	AAV44787	Arabidopsis thaliana
11	34	89.5	13	20	AAV78379	Human papillomavirus
12	34	89.5	56	20	AAW88644	Secreted protein e
13	34	89.5	56	22	ABG55011	Human secreted pro
14	34	89.5	64	22	ABG55123	Human liver peptid
15	34	89.5	64	22	ABR33983	Peptide #7489 enco
16	34	89.5	64	22	ABR24510	Human bone marrow
17	34	89.5	64	22	AAW60730	Human brain exper
18	34	89.5	64	22	AAW73401	Human bone marrow
19	34	89.5	64	22	AAW33604	Peptide #7641 enco
20	34	89.5	64	23	ABG43260	Human peptide enco
21	34	89.5	93	22	AAO03124	Human polypeptide
22	34	89.5	123	22	AAO08298	Human polypeptide
23	34	89.5	138	20	AAV42442	Novel amino acid s
24	34	89.5	140	20	AAV42443	Extended novel ami
25	34	89.5	164	22	ABG28076	Novel human diagn
26	34	89.5	170	21	AAV87324	Human signal pepti
27	34	89.5	199	22	ABG07731	Novel human diagn
28	34	89.5	320	21	AAV54132	Amino acid sequenc
29	34	89.5	331	21	AAV54127	Amino acid sequenc
30	34	89.5	369	21	AAV54129	Amino acid sequenc
31	34	89.5	432	22	AAU48985	Propionibacterium
32	34	89.5	468	21	AAV44496	Bacillus agardher
33	34	89.5	468	21	AAV54125	Amino acid sequenc
34	34	89.5	468	23	ABR82020	Bacillus mannanase
35	34	89.5	476	21	AAV54123	A mannanase-linker
36	34	89.5	487	22	ABR60890	Drosophila melanog
37	34	89.5	490	21	AAV54122	Amino acid sequenc
38	34	89.5	493	21	AAV44495	Bacillus agardher
39	34	89.5	493	21	AAV54124	Amino acid sequenc
40	34	89.5	493	23	ABG71218	Bacillus alkaline
41	34	89.5	493	23	ABR82019	B. agardherens ma
42	34	89.5	544	23	AAK21061	Human drug metabo
43	34	89.5	544	23	AAU91320	Human P450TEC prot
44	34	89.5	720	22	ABR66438	Drosophila melanog
45	34	89.5	2311	23	ABG95034	Human translocatio

## ALIGNMENTS

RESULT 1  
ID ABR08729 standard; peptide; 6 AA.  
XX  
AC ABR08729;  
XX  
DT 14-JUN-2002 (first entry)  
XX  
DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 7.  
XX  
KW IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;  
KW autoimmune disease; transplant rejection; osteoporosis; cancer;  
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;  
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
KW corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;  
KW osteopathic; cytotoxic; nocotopic; neuroprotective; anti-HIV; human;  
KW antileukemic; vituicide; antineoplastic; antileukemic;  
KW dermatological; antibacterial; antiparasitic; antineoplastic;  
KW antileukemic; osteopathic; antileukemic; antileukemic; mutant; mutain.  
XX  
OS Homo sapiens.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 2 /note="Wildtype Asp substituted by Ala"  
FT  
PN WO200183547-A2.  
XX  
PD 08-NOV-2001.  
XX

No art.

PF 02-MAY-2001; 2001WO-US40654.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (UYTA ) UNITV YALE.  
 XX  
 PI May MJ, Ghosh S;  
 XX  
 DR WPI; 2002-179350/23.  
 XX  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 XX  
 PS Claim 23; Page 44; 82pp; English.  
 XX  
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprising contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB07313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of IkkappaB. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC sporadic arthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polyarthritis, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
 CC binding domain of IKKbeta.  
 XX  
 SO Sequence 6 AA;  
 QY Query Match 100.0%; Score 38; DB 23; Length 6;  
 Db Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LAWSWL 6  
 Db 1 LAWSWL 6  
 XX  
 XX  
 AC AAM48512;  
 XX  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX NBD mutant peptide SEQ ID NO 7.  
 DE

XX  
 XX Antiinflammatory; antiaesthetic; cytostatic; antipsoriatic; neurotropic;  
 XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 XX autoimmune disorder; multiple sclerosis; transplant rejection;  
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200183554-A2.  
 PN  
 XX  
 PD 08-NOV-2001.  
 PD  
 XX  
 PP 02-MAY-2001; 2001WO-US14346.  
 PP  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYTA ) UNITV YALE.  
 XX  
 PI May MJ, Ghosh S, Fandels MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 DR  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Example 6; Page 47; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC neurotropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX  
 SO Sequence 6 AA;  
 QY Query Match 100.0%; Score 38; DB 23; Length 6;  
 Db Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LAWSWL 6  
 Db 1 LAWSWL 6  
 XX  
 XX  
 AC AAM48422;  
 XX  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX AAM48422 standard; peptide; 6 AA.  
 DE

[illegible]

AC	ABB77303;	
AD		
AE	14-JUN-2002 (first entry)	
AF		
AG	Human IKKbeta mutant D738A.	
AH		
AI	IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;	
AJ	kinase activation; leukocyte; inflammation; E-selectin; osteoclast;	
AK	autoimmune disease; transplant rejection; osteoporosis; cancer;	
AL	Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;	
AM	retinoid acid arthritis; Crohn's disease; multiple sclerosis; HIV;	
AN	corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;	
AO	osteopathic; cytotoxic; nootropic; neuroprotective; anti-HIV; human;	
AP	antiarteriosclerotic; virucide; antiasthmatic; antiallergic;	
AQ	dermatological; antibacterial; antipruritic; antirhumatic;	
AR	antiarthritic; osteopathic; antitumor; mutant; mutein.	
AS		
AT	Homo sapiens.	
AV	Synthetic.	
AW		
AX	Key	Location/Qualifiers
AY	Misc-difference 738	/note= "wildtype Asp substituted by Ala"
AZ		
BA	WO200183547-A2.	
BB		
BC	08-NOV-2001.	
BD		
BE	02-MAY-2001; 2001WO-US40654.	
BF		
BG	02-MAY-2000; 2000US-201261P.	
BH	22-AUG-2000; 2000US-0643260.	
BI		
BJ	(UYVA ) UNITV YALB.	
BK		
BL	May MJ, Ghosh S;	
BM		
BN	WPI, 2002-179350/23.	
BO		
BP		
BQ		
BR		
BS		
BT		
BU		
BV		
BW		
BX		
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CA		
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CJ		
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CL		
CM		
CN		
CO		
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CQ		
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CQ		
CR		
CS		
CT		
CU		
CV		
CW		
CX		
CY		
CA		
CB		
CC		
CD		
CE		
CF		
CG		
CH		
CI		
CJ		
CK		
CL		

CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of an IkB $\beta$   
 CC mutant, useful in examples of the invention.  
 CC Note: The present sequence is not given in the specification but is  
 CC derived from GenBank Accession No. O14920 (ABB71294).

SO Sequence 756 AA;

Query Match 100.0%; Score 38; DB 23; Length 756;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6  
 DB 737 LAWSWL 742

#### RESULT 5

ID AAU62777 standard; Protein; 196 AA.

AC AAU62777;

DT 27-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #23673.

KX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
 KM uveitis; endophthalmitis; bone; joint; central nervous system; EISA;  
 KM inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
 KM dermatological; osteopathic; neuroprotectant.

OS Propionibacterium acnes.

PN WO200181581-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US12865.

XX 21-APR-2000; 2000US-199047P.

PR 02-JUN-2000; 2000US-208841P.

PR 07-JUL-2000; 2000US-216747P.

PA (CORI-) CORIXA CORP.

PI Skelly YAM, Persing DH, Mitcham JL, Wang SS, Bhacia A;  
 PI L.malonneuve J, Zhang Y, Jen S, Carter D;

DR WPI; 2001-616774/71.

DR N-PSDB; AAS59629.

XX Propionibacterium acnes polypeptides and nucleic acids useful for  
 PT vaccinating against and diagnosing infections, especially useful for  
 PT treating acne vulgaris -

XX Example 1; SEQ ID No 23972; 10699P; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic  
 CC polypeptides. The proteins and their associated DNA sequences are used in  
 CC the treatment, prevention and diagnosis of medical conditions caused by  
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,  
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.  
 CC P. acnes is also involved in infections of bone, joints and the central  
 CC nervous system, however it is particularly involved in the inflammatory  
 CC lesions associated with acne vulgaris. A method for detecting the  
 CC presence or absence of P. acnes in a patient comprises contacting a  
 CC sample with a binding agent that binds to the proteins of the invention  
 CC and determining the amount of bound protein in the sample. The

CC polypeptides may be used as antigens in the production of antibodies  
 CC specific for P. acnes proteins. These antibodies can be used to  
 CC downregulate expression and activity of P. acnes polypeptides and  
 CC therefore treat P. acnes infections. The antibodies may also be used as  
 CC diagnostic agents for determining P. acnes presence, for example, by  
 CC enzyme linked immunosorbent assay (ELISA).  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

SO Sequence 196 AA;

Query Match 92.1%; Score 35; DB 22; Length 196;  
 Best Local Similarity 83.3%; Pred. No. 4.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6  
 DB 102 VAMSWL 107

#### RESULT 6

ID ABU05469 standard; Protein; 196 AA.

AC ABU05469;

DT 08-APR-2003 (first entry)

DE M. tuberculosis and M. leprae marker protein #120.

KX Mycobacterioses; survival; virulence; protective antigen; vaccine;  
 KM mycobacterial disease; tuberculosis; leprosy.

OS Mycobacterium tuberculosis.

PN WO200274903-A2.

XX 26-SEP-2002.

XX 22-FEB-2002; 2002WO-IB01973.

XX 22-FEB-2001; 2001US-270123P.

PA (INSP ) INST PASTEUR.

XX Cole S;

PI WPI; 2002-759685/82.

DR Identifying and selecting genes for survival or virulence of  
 PT mycobacteria by a comparative genomic analysis of the sequences of  
 PT Mycobacterium tuberculosis and M. leprae -

XX Claim 17; Page 288-289; 8749P; English.

XX This invention relates to a novel method for identifying essential genes  
 CC for survival or virulence of mycobacteria species. The method comprises  
 CC aligning the genomic sequence of a first mycobacterium species on a  
 CC genomic sequence of a second mycobacterium species and selecting a  
 CC polynucleotide sequence that is highly conserved in both genomes with no  
 CC counterparts in other bacterial genomic sequences and that corresponds  
 CC to an essential gene for the survival or virulence of mycobacterium  
 CC species. The method of the invention is useful for detecting M.  
 CC tuberculosis or M. leprae infection. The method reduces the number of  
 CC potential new targets and protective antigens for new drugs and vaccine  
 CC compositions to treat and prevent mycobacterial diseases, particularly  
 CC tuberculosis and leprosy. The present sequence represents a marker  
 CC protein from Mycobacterium tuberculosis and Mycobacterium leprae  
 CC identified using the method of the invention.

SO Sequence 196 AA;

Query Match 92.1%; Score 35; DB 23; Length 186;  
 Best Local Similarity 83.3%; Pred. No. 4.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
 :|||||  
 DB 109 VAMSWL 114

## RESULT 7

ABU05897  
 ID ABU05897 standard; Protein; 210 AA.

AC ABU05897;

DT 08-APR-2003 (first entry)

DE M. tuberculosis and M. leprae marker protein #548.

KM Mycobacterioses; survival; virulence; protective antigen; vaccine;  
 KW Mycobacterial disease; tuberculosis; leprosy.

OS Mycobacterium tuberculosis.

OS Mycobacterium leprae.

PN WO200274903-A2.

PD 26-SEP-2002.

PF 22-FEB-2002; 2002WO-1B01973.

PR 22-FEB-2001; 2001US-270123P.

PA (INSP ) INST PASTEUR.

PI Cole S;

DR WPI; 2002-759885/82.

PT Identifying and selecting genes for survival or virulence of  
 PT mycobacteria by a comparative genomic analysis of the sequences of  
 PT Mycobacterium tuberculosis and M. leprae -

PS Claim 17; Page 763-764; 874pp; English.

CC This invention relates to a novel method for identifying essential genes  
 CC for survival or virulence of mycobacteria species. The method comprises  
 CC aligning the genomic sequence of a first mycobacterium species on a  
 CC genomic sequence of a second mycobacterium species and selecting a  
 CC polynucleotide sequence that is highly conserved in both genomes with no  
 CC counterparts in other bacterial genomic sequences and that corresponds  
 CC to an essential gene for the survival or virulence of mycobacterium  
 CC species. The method of the invention is useful for detecting M.  
 CC tuberculosis or M. leprae infection. The method reduces the number of  
 CC potential new targets and protective antigens for new drugs and vaccine  
 CC compositions to treat and prevent mycobacterial diseases, particularly  
 CC tuberculosis and leprosy. The present sequence represents a marker  
 CC protein from Mycobacterium tuberculosis and Mycobacterium leprae  
 CC identified using the method of the invention.

SO Sequence 210 AA;

Query Match 92.1%; Score 35; DB 23; Length 210;  
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
 :|||||  
 DB 123 VAMSWL 128

## RESULT 8

ABB64219  
 ID ABB64219 standard; Protein; 321 AA.

AC ABB64219;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 19449.

KM Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE ) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI; 2001-656860/75.

DR N-PSDB; ABL08322.

PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -

PS Disclosure; SEQ ID NO 19449; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA  
 CC sequences (ABU01840-ABU16175) and the encoded proteins  
 CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

SO Sequence 321 AA;

Query Match 92.1%; Score 35; DB 22; Length 321;  
 Best Local Similarity 83.3%; Pred. No. 7.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
 :|||||  
 DB 64 LMSWML 69

## RESULT 9

ABB71850  
 ID ABB71850 standard; Protein; 329 AA.

AC ABB71850;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 42342.

KM Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.

OS Drosophila melanogaster.



XX PN WO200171042-A2.  
 XX PD 27-SEP-2001.  
 XX PF 23-MAR-2001; 2001WO-US09231.  
 XX PR 23-MAR-2000; 2000US-191637P.  
 XX PR 11-JUL-2000; 2000US-0614150.  
 XX PA (BEKE ) PE CORP NY.  
 XX PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX DR WPI; 2001-656860/75.  
 XX DR N-PSDB; ABL15953.  
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT gene from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX PS Disclosure; SEQ ID NO 42342; 21pp + Sequence Listing; English.  
 XX CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL10511), expressed DNA  
 CC sequences (ABL101840-ABL16175) and the encoded proteins  
 CC (ABBS7733-ABBS72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 329 AA;  
 XX  
 XX Query Match 92.1%; Score 35; DB 22; Length 329;  
 XX Best Local Similarity 83.3%; Pred. No. 7.8e+02;  
 XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 LAMSWL 6  
 XX 17 LAMTWL 22  
 XX DB

RESULT 10  
 AAY44787  
 ID AAY44787 standard; Protein; 1055 AA.  
 AC AAY44787;  
 XX  
 DT 04-MAY-2000 (first entry)  
 XX  
 DE Arabidopsis thaliana recombination repair protein, MIM.  
 XX  
 KW MIM; recombination; plant; DNA repair; hypersensitivity;  
 KM SMC protein family; Structural Maintenance of Chromosomes; MIM;  
 KM methyl methanesulphonate; irradiation; mitomycin C.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 XX Key Location/Qualifiers  
 XX Binding-site 49..56  
 FT /label= NTP\_binding\_domain  
 FT Region 184..442  
 FT /label= Coiled\_coil\_region-I  
 FT Region 443..627  
 FT /label= Hinge/spacer  
 FT Region 628..909  
 FT /label= Coiled\_coil\_region-II  
 FT 971..1007  
 FT Domain /label= DA-box

FT FT /note= "conserved motif which harbours a Walker B type  
 FT FT NTP binding domain"  
 XX PN WO200004174-A1.  
 XX PD 27-JAN-2000.  
 XX PF 14-JUL-1999; 99WO-EP04984.  
 XX PR 16-JUL-1998; 98GB-0015485.  
 XX PR 14-JAN-1999; 99GB-0000760.  
 XX PA (NOVS ) NOVARTIS AG.  
 XX PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
 XX PI Mengler T, Paszkowski J;  
 XX DR WPI; 2000-182437/16.  
 XX DR N-PSDB; AA250145; AA250146.  
 XX PT New Arabidopsis polynucleotide encoding protein useful for assisting  
 PT recombinant repair of DNA damage in plants -  
 XX PS Claim 1; Pages 22-25; 30pp; English.  
 XX CC The present sequence is a MIM protein from Arabidopsis thaliana, which  
 CC contributes to recombination repair of DNA damage in plant cells.  
 CC The protein was tracked down with the help of a T-DNA tagged Arabidopsis  
 CC mutant showing hypersensitivity to methyl methanesulphonate (MMS). It  
 CC shows homology to a member of SMC (Structural Maintenance of Chromosomes)  
 CC protein family and confers hypersensitivity to treatment with MMS,  
 CC X-rays, UV light or mitomycin C. The present sequence is useful for DNA  
 CC repair in plant cells.  
 XX SQ Sequence 1055 AA;  
 XX  
 XX Query Match 92.1%; Score 35; DB 21; Length 1055;  
 XX Best Local Similarity 83.3%; Pred. No. 2.6e+03;  
 XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 LAMSWL 6  
 XX 248 LAMSWV 253  
 XX DB

RESULT 11  
 AAY78379  
 ID AAY78379 standard; peptide; 13 AA.  
 AC AAY78379;  
 XX  
 DT 08-MAY-2000 (first entry)  
 XX  
 DE Human papillomavirus E7 protein inhibiting peptide SEQ ID NO.5.  
 XX  
 KW HPV; E7 protein; inhibition; virucide; carcinoma.  
 KM Human papillomavirus.  
 OS Synthetic.  
 OS  
 PN EP969013-A1.  
 XX  
 PD 05-JAN-2000.  
 XX  
 PF 30-JUN-1998; 98EP-0112047.  
 XX  
 PR 30-JUN-1998; 98EP-0112047.  
 XX  
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX  
 PI Jansen-Duerr P, Zwerschke W;  
 XX  
 DR WPI; 2000-149116/14.

```

XX  New peptides used for the prevention and treatment of human papilloma
PT  virus associated disease .
XX
XX  Claim 1, Page 22, 26pp; English.
XX
CC  AAY78375 to AAY78415 represent peptide capable of inhibiting the human
CC  papillomavirus (HPV) E7 protein. The peptides have virucide activity.
CC  The peptides can be used in pharmaceutical compositions to inhibit
CC  HPV E7 protein, which allows the prevention and/or treatment of HPV
CC  associated diseases, which may comprise carcinomas.
XX
SQ  Sequence 13 AA;

Query Match      89.5%; Score 34; DB 21; Length 13;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 LAMSW 5
    |||||
    3 LAMSW 7

Db

RESULT 12
AAW8644
ID  AAW8644 standard; Protein; 56 AA.
XX
AC  AAW8644;
XX
DT  01-MAR-1999 (first entry)
XX
DE  Secreted protein encoded by gene 111 clone HTMBY29.
XX
XX  Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX  diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
XX  developmental abnormality; foetal deficiency; allergy; renal;
XX  immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX  inflammation; ischaemic shock; Alzheimer's disease; reostosis; AIDS;
XX  cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX  osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX  endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS  Homo sapiens.
XX
XX  WO9854963-A2.
XX
PD  10-DEC-1998.
XX
XX  04-JUN-1998; 98WC-US11422.
XX
XX  18-DEC-1997; 97US-0070923.
XX  06-JUN-1997; 97US-0048877.
XX  06-JUN-1997; 97US-0048881.
XX  06-JUN-1997; 97US-0048884.
XX  06-JUN-1997; 97US-0048893.
XX  06-JUN-1997; 97US-0048896.
XX  06-JUN-1997; 97US-0048899.
XX  06-JUN-1997; 97US-0048915.
XX  06-JUN-1997; 97US-0048949.
XX  06-JUN-1997; 97US-0048964.
XX  06-JUN-1997; 97US-0048972.
XX  06-JUN-1997; 97US-0049020.
XX  06-JUN-1997; 97US-0049375.
XX  05-SEP-1997; 97US-0057628.
XX  05-SEP-1997; 97US-0057635.
XX  05-SEP-1997; 97US-0057644.
XX  05-SEP-1997; 97US-0057647.
XX  05-SEP-1997; 97US-0057650.
XX  05-SEP-1997; 97US-0057661.
XX  05-SEP-1997; 97US-0057667.
XX  05-SEP-1997; 97US-0057761.
XX  05-SEP-1997; 97US-0057764.
XX  05-SEP-1997; 97US-0057770.

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PR  05-SEP-1997; 97US-0057775.
PR  05-SEP-1997; 97US-0057778.
PR  06-JUN-1997; 97US-0048875.
PR  06-JUN-1997; 97US-0048878.
PR  06-JUN-1997; 97US-0048882.
PR  06-JUN-1997; 97US-0048885.
PR  06-JUN-1997; 97US-0048894.
PR  06-JUN-1997; 97US-0048897.
PR  06-JUN-1997; 97US-0048900.
PR  06-JUN-1997; 97US-0048916.
PR  06-JUN-1997; 97US-0048962.
PR  06-JUN-1997; 97US-0048970.
PR  06-JUN-1997; 97US-0048974.
PR  06-JUN-1997; 97US-0049373.
PR  05-SEP-1997; 97US-0057584.
PR  05-SEP-1997; 97US-0057629.
PR  05-SEP-1997; 97US-0057642.
PR  05-SEP-1997; 97US-0057645.
PR  05-SEP-1997; 97US-0057648.
PR  05-SEP-1997; 97US-0057651.
PR  05-SEP-1997; 97US-0057662.
PR  05-SEP-1997; 97US-0057668.
PR  05-SEP-1997; 97US-0057762.
PR  05-SEP-1997; 97US-0057765.
PR  05-SEP-1997; 97US-0057771.
PR  05-SEP-1997; 97US-0057776.
PR  06-JUN-1997; 97US-0048876.
PR  06-JUN-1997; 97US-0048880.
PR  06-JUN-1997; 97US-0048883.
PR  06-JUN-1997; 97US-0048892.
PR  06-JUN-1997; 97US-0048895.
PR  06-JUN-1997; 97US-0048898.
PR  06-JUN-1997; 97US-0048901.
PR  06-JUN-1997; 97US-0048917.
PR  06-JUN-1997; 97US-0048963.
PR  06-JUN-1997; 97US-0048971.
PR  06-JUN-1997; 97US-0049019.
PR  06-JUN-1997; 97US-0049374.
PR  05-SEP-1997; 97US-0057627.
PR  05-SEP-1997; 97US-0057634.
PR  05-SEP-1997; 97US-0057643.
PR  05-SEP-1997; 97US-0057646.
PR  05-SEP-1997; 97US-0057649.
PR  05-SEP-1997; 97US-0057654.
PR  05-SEP-1997; 97US-0057666.
PR  05-SEP-1997; 97US-0057760.
PR  05-SEP-1997; 97US-0057763.
PR  05-SEP-1997; 97US-0057769.
PR  05-SEP-1997; 97US-0057774.
PR  05-SEP-1997; 97US-0057777.
XX
XX  (HUMA-) HUMAN GENOME SCI INC.
XX
XX  Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA;
XX  Pan P, Feng P, Ferris AM, Fischer CL, Florence C;
XX  Florence K, Greene JM, Hu J, Kyaw H, Latleur DW;
XX  Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM;
XX  Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
XX  WPI, 1999-059665/05.
XX  N-PSDB; AAW84521.
XX
DR  New isolated human genes and the secreted polypeptides they encode -
PT  useful for diagnosis and treatment of e.g. cancer, neurological
PT  disorders, immune diseases, inflammation or blood disorders
XX
XX  Claim 11, Page 542; 772pp; English.
XX
XX  The invention relates to nucleic acid sequences (AAV84411 to AAV84633)
XX  encoding human secreted proteins (AAW88534 to AAW88756). The secreted
XX  protein gene sequences are deposited with the ATCC under deposit numbers
XX  ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,
XX  209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. HORT

```

cells comprising recombinant vectors contain the nucleic acid sequences are used for the recombinant production of the secreted proteins. The polynucleotide and amino acid sequences are useful for a variety of purposes. For example, the polynucleotide and amino acid sequences are useful for preventing, creating or ameliorating medical conditions e.g. by protein or gene therapy. Pathological conditions can be also diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, tumours, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, ischaemic shock, Alzheimer's and cognitive disorders, schizophrenia, osteoporosis, prostatic diseases, obesity disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseases of testes, lung or thymus, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The present sequence represents human secreted protein (see descriptor line for gene number and clone identification).

**5Q Sequence 56 AA;**

Query Match	89.54; Score 34; DB 20; Length 56;
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Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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QY	1	LAWSW	5
Db	9	LAWSW	13

## RESULT 13

ID ABB50411 standard; Protein; 56 AA.

AC ABB50411

DT 07-FEB-2002 (first entry)

DE Human secreted protein encoded by gene 111 SEQ ID NO:359.

KM Human, secreted protein; immunomodulatory; antisclerotic; anti-HIV.  
 KM dermatological; immunosuppressive; antiinflammatory; immunostimulant;  
 KM cytostatic; cardiac; vascular; anti-angiogenic; ophthalmological;  
 KM neuroprotective; nontropic; anticonvulsant; antiallergens; vulnerability;  
 KM antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;  
 KM multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;  
 KM human immunodeficiency virus; hyperproliferative disorder; wound healing  
 KM Gaucher's disease; cardiovascular disease; Schmidt's syndrome; chemoat-  
 KM Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder;  
 KM corneal graft neovascularisation; diabetic retinopathy; regeneration;  
 KM neurological disorder; Huntington's chorea; Alzheimer's disease;  
 KM Parkinson's disease; infectious disease; chromosome 10.

## OS Homo sapiens

PN WO200162891-A2.

PD 30-AUG-2001

PF 21-FEB-2001; 2001WO-US05614.

PR 24-FEB-2000; 2000US-184836P.

XX XX

100

PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;  
PI Florence C, Hu J, Li Y, Kwaw H, Fletcher CL, Ferris AM, Fan P  
PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;  
PI Zeng Z, Greene JM;

XX WPI; 2001-625724/72  
DR N-PSDB; ABA83304.  
DR

**PT** Nucleic acids and

PT disease and diabetic retinopathy -

PS Claim 11; Page 1140; 1533pp; English

CC ABB5030 to ABB51287 and ABA8319 to ABA8341 represent human secreted  
CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various  
CC activities based on the tissues and cells the genes are expressed in.  
CC Example of these activities include: immunomodulatory; antileukemic;  
CC dermatological; immunosuppressive; anti-inflammatory; immunostimulant;  
CC anti-HIV; cytostatic; cardiant; anti-angiogenic; ophthalmological;  
CC neuroprotective; nootropic; anticonvulsant; anti-Alzheimer's vascular;  
CC antiParkinsonian; antimicrobial; and vulnerable. (I) and (II) can be used  
CC in gene therapy and vaccine production. (I) and (II) can be used in the  
CC prevention, diagnosis and treatment of immune disorders (e.g. multiple  
CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus  
CC (HIV) infections), hyperproliferative disorders (e.g. cancers and  
CC Gaucher's disease), cardiovascular diseases (e.g. Schmitzer syndrome,  
CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic  
CC disorders (e.g. corneal graft neovascularisation and diabetic  
CC retinopathy), neurological disorders (e.g. Huntington's chorea,  
CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or  
CC for promoting wound healing, regeneration and/or chemotaxis. ABA8318 to  
CC ABA83193 and ABB50300 represent sequences used in the exemplification of  
CC the present invention.

**SQ Sequence 56 AA;**

Query Match	89.5%	Score 34	DB 22	Length 56
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Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

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QY	1	LAWSW	5
Db	9	LAWSW	13

## RESULT 14

ID ABG55123 standard; Peptide; 64 AA

AC ABG55123

DT 25-FEB-2003 (first entry)

Human liver peptide, SEQ ID No 33771.

KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia  
KW hypercholesterolaemia; coronary heart disease.

**OS Homo sapiens.**

PN WO200157273-A2

PD 09-AUG-2001

PF 30-JAN-2001; 2001WO-US00664

PR 04-FEB-2000; 2000US-0180312

PR 30-JUN-2000; 2000US-0608408

PR 21-SEP-2000; 2000US-0234687

PR 04-OCT-2000; 2000GB-0024263

PA (MOLE-) MOLECULAR DYNAMICS :

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-488898/53.  
 XX Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human adult liver -  
 XX  
 PS Claim 27; SEQ ID No 33771; 658bp; English.  
 CC The invention relates to a single exon nucleic acid probe (SENP) (I) for  
 CC measuring human gene expression in a sample derived from human adult  
 CC liver, comprising one of 13109 defined nucleotide sequences given in the  
 CC specification (or complements/ fragments). The probe hybridizes at high  
 CC stringency to a nucleic acid molecule expressed in the human adult  
 CC liver. (I) may be used for predicting, measuring and displaying gene  
 CC expression in samples derived from human adult liver. The genes  
 CC identified may be involved in genetic liver diseases such as cirrhosis,  
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which  
 CC is associated with coronary heart disease. ABG47348-ABG5930 represent  
 CC human liver single exon encoded peptides of the invention.  
 CC Note: The sequence information for this patent does not appear in the  
 CC printed specification but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 SQ Sequence 64 AA;

Query Match 89.5%; Score 34; DB 22; Length 64;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5  
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 DB 33 LAMSW 37

RESULT 15  
 ABB39983  
 ID ABB39983 standard; Peptide; 64 AA.  
 XX  
 AC ABB39983;  
 XX  
 DT 04-FEB-2002 (first entry)  
 XX  
 DE Peptide #7489 encoded by human foetal liver single exon probe.  
 XX  
 KW Human; foetal liver; gene expression; single exon nucleic acid probe.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157277-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00669.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 XX WPI; 2001-483447/52.  
 DR  
 XX Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human fetal liver -  
 XX  
 PS Claim 27; SEQ ID NO 32618; 639pp + sequence listing; English.

XX  
 CC The invention relates to a single exon nucleic acid probe for  
 CC measuring human gene expression in a sample derived from human foetal  
 CC liver. The single exon nucleic acid probes may be used for predicting,  
 CC measuring and displaying gene expression in samples derived from human  
 CC foetal liver. The present sequence is a peptide encoded by a single exon  
 CC nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 64 AA;

Query Match 89.5%; Score 34; DB 22; Length 64;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5  
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 DB 33 LAMSW 37

Search completed: February 18, 2004, 14:26:20  
 Job time : 23.7763 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds  
(without alignments)  
75.239 Million cell updates/sec

Title: US-09-643-260-6  
Perfect score: 40  
Sequence: 1 ADMSWA 6

Scoring table: BLAST62  
Gapop 10.0, Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database:

Published Applications AA.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	6	11 US-09-847-946A-41	Sequence 41, Appl
2	40	100.0	6	11 US-09-847-946A-73	Sequence 73, Appl
3	40	100.0	7	11 US-09-847-946A-77	Sequence 77, Appl
4	40	100.0	8	11 US-09-847-946A-70	Sequence 70, Appl
5	40	100.0	8	11 US-09-847-946A-78	Sequence 78, Appl
6	40	100.0	9	11 US-09-847-946A-69	Sequence 69, Appl
7	40	100.0	9	11 US-09-847-946A-72	Sequence 72, Appl
8	40	100.0	9	11 US-09-847-946A-75	Sequence 75, Appl
9	40	100.0	9	11 US-09-847-946A-76	Sequence 76, Appl
10	40	100.0	10	11 US-09-847-946A-71	Sequence 71, Appl
11	40	100.0	10	11 US-09-847-946A-74	Sequence 74, Appl
12	40	100.0	11	11 US-09-847-946A-68	Sequence 68, Appl
13	37	92.5	12	11 US-10-441-625-17	Sequence 17, Appl
14	37	92.5	885	9 US-09-815-242-5090	Sequence 5090, Ap
15	36	90.0	6	10 US-09-847-940B-4	Sequence 4, Appl

16	36	90.0	6	10 US-09-847-940B-5	Sequence 5, Appl
17	36	90.0	6	11 US-09-847-946A-4	Sequence 4, Appl
18	36	90.0	6	11 US-09-847-946A-5	Sequence 5, Appl
19	36	90.0	6	11 US-09-847-946A-39	Sequence 39, Appl
20	36	90.0	6	11 US-09-847-946A-40	Sequence 40, Appl
21	36	90.0	6	11 US-09-847-946A-51	Sequence 51, Appl
22	36	90.0	6	11 US-09-847-946A-62	Sequence 62, Appl
23	36	90.0	7	11 US-09-847-946A-55	Sequence 55, Appl
24	36	90.0	7	11 US-09-847-946A-66	Sequence 66, Appl
25	36	90.0	8	11 US-09-847-946A-48	Sequence 48, Appl
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27	36	90.0	8	11 US-09-847-946A-59	Sequence 59, Appl
28	36	90.0	8	11 US-09-847-946A-67	Sequence 67, Appl
29	36	90.0	9	11 US-09-847-946A-47	Sequence 47, Appl
30	36	90.0	9	11 US-09-847-946A-50	Sequence 50, Appl
31	36	90.0	9	11 US-09-847-946A-53	Sequence 53, Appl
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35	36	90.0	9	11 US-09-847-946A-64	Sequence 64, Appl
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38	36	90.0	10	11 US-09-847-946A-52	Sequence 52, Appl
39	36	90.0	10	11 US-09-847-946A-57	Sequence 57, Appl
40	36	90.0	10	11 US-09-847-946A-60	Sequence 60, Appl
41	36	90.0	10	11 US-09-847-946A-63	Sequence 63, Appl
42	36	90.0	11	11 US-09-847-946A-66	Sequence 66, Appl
43	36	90.0	173	15 US-10-156-761-15045	Sequence 15045, A
44	36	90.0	174	15 US-10-219-220-163	Sequence 163, App
45	36	90.0	225	15 US-10-219-220-162	Sequence 162, App

## ALIGNMENTS

RESULT 1  
US-09-847-946A-41  
; Sequence 41, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Fingels, Mark A  
; APPLICANT: Phillips, Kathryn  
; TITLE OF INVENTION: Anti-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 41  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: NEMO binding  
; OTHER INFORMATION: Sequence  
US-09-847-946A-41

Query Match 100.0%; Score 40; DB 11; Length 6;

Best Local Similarity 100.0%; Pred. No. 7e+05; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||||  
Db 1 ADMSWA 6

No 4-7

RESULT 2  
US-09-847-946A-73  
Sequence 73, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hamnig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 73  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-73

Query Match  
Best Local Similarity 100.0%; Score 40; DB 11; Length 6;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
DB 1 ADMSWA 6

RESULT 3  
US-09-847-946A-77  
Sequence 77, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hamnig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 77  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-77

Query Match  
Best Local Similarity 100.0%; Score 40; DB 11; Length 7;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
DB 1 ADMSWA 6

DB 1 ADMSWA 6

RESULT 4  
US-09-847-946A-70  
Sequence 70, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hamnig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 70  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-70

Query Match  
Best Local Similarity 100.0%; Score 40; DB 11; Length 8;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
DB 3 ADMSWA 8

RESULT 5  
US-09-847-946A-78  
Sequence 78, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hamnig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 78  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-78

Query Match  
Best Local Similarity 100.0%; Score 40; DB 11; Length 8;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
Db 1 ADMSWA 6

## RESULT 6

US-09-847-946A-69  
; Sequence 69, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 69  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding  
US-09-847-946A-69

Query Match 100.0%; Score 40; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
Db 1 ADMSWA 6

## RESULT 7

US-09-847-946A-72  
; Sequence 72, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 72  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding  
US-09-847-946A-72

Query Match 100.0%; Score 40; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
Db 1 ADMSWA 6

## RESULT 8

US-09-847-946A-75  
; Sequence 75, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 75  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding  
US-09-847-946A-75

Query Match 100.0%; Score 40; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
Db 3 ADMSWA 8

## RESULT 9

US-09-847-946A-76  
; Sequence 76, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 76  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding

```
OTHER INFORMATION: sequence
US-09-847-946A-76

Query Match          100.0%; Score 40; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
   |||||
Db 2 ADMSWA 7

RESULT 10
US-09-847-946A-71
; Sequence 71, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-71

Query Match          100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
   |||||
Db 2 ADMSWA 7

RESULT 11
US-09-847-946A-74
; Sequence 74, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
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ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-74

Query Match          100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
   |||||
Db 3 ADMSWA 8

RESULT 12
US-09-847-946A-68
; Sequence 68, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-68

Query Match          100.0%; Score 40; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
   |||||
Db 3 ADMSWA 8

RESULT 13
US-10-441-626-17
; Sequence 17, Application US/10441626
; Publication No. US20030186418A1
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. US20030186418A1e1 Variant EGIII-Like Cellulase
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/10/441,626
; CURRENT FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Glisocladium roseum (3)
US-10-441-626-17
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Query Match 92.5%; Score 37; DB 12; Length 236;  
 Best Local Similarity 83.3%; Pred. No. 3.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSMA 6  
 |||||  
 DB 63 ADWSMS 68

RESULT 14  
 US-09-815-242-5090  
 ; Sequence 5090, Application US/09815242  
 ; Patent No. US20020061569A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Haselbeck, Robert  
 ; APPLICANT: Ohlsen, Karl L.  
 ; APPLICANT: Zyskind, Judith W.  
 ; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John D.  
 ; APPLICANT: Carr, Grant J.  
 ; APPLICANT: Yamamoto, Robert T.  
 ; APPLICANT: Xu, H. Howard  
 ; TITLE OF INVENTION: Identification of Essential Genes in  
 ; FILE OF INVENTION: Prokaryotes  
 ; FILE REFERENCE: ELITRA.011A  
 ; CURRENT APPLICATION NUMBER: US/09/815,242  
 ; CURRENT FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/191,078  
 ; PRIOR FILING DATE: 2000-03-21  
 ; PRIOR APPLICATION NUMBER: 60/206,848  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 60/207,727  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/242,578  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: 60/253,625  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/257,931  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 60/269,308  
 ; PRIOR FILING DATE: 2001-02-16  
 ; NUMBER OF SEQ ID NOS: 14110  
 ; SOFTWARE: PastSeq for Windows Version 4.0  
 ; SEQ ID NO 5090  
 ; LENGTH: 885  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-815-242-5090

Query Match 92.5%; Score 37; DB 9; Length 885;  
 Best Local Similarity 83.3%; Pred. No. 1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSMA 6  
 |||||  
 DB 563 ADWAMA 568

RESULT 15  
 US-09-847-940B-4  
 ; Sequence 4, Application US/09847940B  
 ; Patent No. US2002015600A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: May, Michael J.  
 ; APPLICANT: Ghosh, Sankar  
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
 ; FILE REFERENCE: PPI-117CP  
 ; CURRENT APPLICATION NUMBER: US/09/847,940B  
 ; CURRENT FILING DATE: 2001-05-02  
 ; PRIOR APPLICATION NUMBER: 09/643,260  
 ; PRIOR FILING DATE: 2000-08-22  
 ; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
 US-09-847-940B-4

Query Match 90.0%; Score 36; DB 10; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 7e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5  
 |||||  
 DB 1 ADWSW 5

Search completed: February 18, 2004, 15:41:55  
 Job time : 16.7529 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds  
(without alignments)  
41.814 Million cell updates/sec

Title: US-09-643-260-6  
Perfect score: 40  
Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	AAW48538	Anti-Inflammatory
2	40	100.0	6	AAW48570	Anti-Inflammatory
3	40	100.0	7	AAW48574	Anti-Inflammatory
4	40	100.0	8	AAW48567	Anti-Inflammatory
5	40	100.0	8	AAW48575	Anti-Inflammatory
6	40	100.0	9	AAW48566	Anti-Inflammatory
7	40	100.0	9	AAW48569	Anti-Inflammatory
8	40	100.0	9	AAW48572	Anti-Inflammatory
9	40	100.0	9	AAW48573	Anti-Inflammatory

10	40	100.0	10	23	AAW48568	Anti-Inflammatory
11	40	100.0	10	23	AAW48571	Anti-Inflammatory
12	40	100.0	11	23	AAW48576	Anti-Inflammatory
13	37	92.5	33	22	AAW48565	Human novel foetal
14	37	92.5	103	20	AAU21305	Gliocladium roseum
15	37	92.5	236	20	AAU06332	Gliocladium roseum
16	37	92.5	236	21	AAU06363	Gliocladium roseum
17	37	92.5	236	21	AAU14876	Gliocladium roseum
18	37	92.5	236	21	AAU84341	Antio acid sequenc
19	37	92.5	236	23	AAU77428	Gliocladium roseum
20	37	92.5	274	23	AAU7584	G. roseum EGII-11
21	37	92.5	597	22	ABP65718	Bifidobacterium 10
22	37	92.5	885	22	AAU3594	Drosophila melanog
23	36	90.0	6	23	ABU08727	Pseudomonas aerugi
24	36	90.0	6	23	ABU08728	Mutated IKKbeta NE
25	36	90.0	6	23	AAW48509	NBD mutant peptide
26	36	90.0	6	23	AAW48510	NBD mutant peptide
27	36	90.0	6	23	AAW48536	Anti-Inflammatory
28	36	90.0	6	23	AAW48537	Anti-Inflammatory
29	36	90.0	6	23	AAW48548	Anti-Inflammatory
30	36	90.0	6	23	AAW48559	Anti-Inflammatory
31	36	90.0	6	24	ABU08420	Human NEMO binding
32	36	90.0	6	24	ABU08421	Human NEMO binding
33	36	90.0	7	23	AAW48552	Anti-Inflammatory
34	36	90.0	7	23	AAW48563	Anti-Inflammatory
35	36	90.0	8	23	AAW48545	Anti-Inflammatory
36	36	90.0	8	23	AAW48553	Anti-Inflammatory
37	36	90.0	8	23	AAW48556	Anti-Inflammatory
38	36	90.0	8	23	AAW48564	Anti-Inflammatory
39	36	90.0	9	23	AAW48544	Anti-Inflammatory
40	36	90.0	9	23	AAW48547	Anti-Inflammatory
41	36	90.0	9	23	AAW48550	Anti-Inflammatory
42	36	90.0	9	23	AAW48551	Anti-Inflammatory
43	36	90.0	9	23	AAW48555	Anti-Inflammatory
44	36	90.0	9	23	AAW48558	Anti-Inflammatory
45	36	90.0	9	23	AAW48561	Anti-Inflammatory

#### ALIGNMENTS

RESULT 1	AAW48538	standard; Peptide; 6 AA.
ID	AAW48538	
AC	AAW48538;	
XX		
DT	20-MAR-2002 (first entry)	
XX		
DB	Anti-inflammatory peptide SEQ ID NO 41.	
XX		
XX	Anti-inflammatory; antiaesthetic; cytopathic; antipeptidic; nootropic;	
KW	antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;	
KW	immunopressive; dermatological; neuroprotective; antihemorrhagic;	
KW	antiallergic; membrane translocation domain; NEMO binding domain; eczema;	
KW	cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;	
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;	
KW	autoimmune disorder; multiple sclerosis; transplant rejection;	
KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;	
KW	ataxia telangiectasia; allergy; anaphylaxis; arthritis.	
OS	Synthetic.	
XX		
XX		
PN	WO200183554-A2.	
PD	08-NOV-2001.	
XX		
PP	02-MAY-2001; 2001WO-US14346.	
XX		
PR	02-MAY-2000; 2000US-201261P.	
PR	22-AUG-2000; 2000US-0643260.	
XX		
PA	(PRAE-) PRAECIS PHARM INC.	

PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 XX  
 XX WPI, 2002-121889/16.  
 DR  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Claim 6; Page 61; 88pp; English.  
 XX  
 XX The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of Ikkappa kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of Ikkappa. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis, transplant rejection, osteoporosis,  
 CC Alzheimer's disease, atherosclerosis, viral infections, and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 40; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADMSWA 6  
 DB 1 ADMSWA 6  
 AC  
 XX  
 AC AAM48570;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 73.  
 XX  
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;  
 KM antiinflammatory; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; Ikkappa kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX

PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECTIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 XX  
 XX WPI, 2002-121889/16.  
 DR  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
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 PT psoriasis -  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 XX The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of Ikkappa kinase beta (IKKbeta) at  
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 CC granulomatosis, multiple sclerosis, transplant rejection, osteoporosis,  
 CC Alzheimer's disease, atherosclerosis, viral infections, and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 40; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADMSWA 6  
 DB 1 ADMSWA 6  
 AC  
 XX  
 AC AAM48574;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 77.  
 XX  
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;  
 KM antiinflammatory; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; Ikkappa kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX

OS Synthetic.  
 XX WO200183554-A2.  
 PN  
 XX 08-NOV-2001.  
 PD  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 PF  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
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 XX May MJ, Ghosh S, Finkel MA, Phillips K;  
 PI WPI; 2002-121889/16.  
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 XX Claim 6; Page 62; 88pp; English.  
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 CC granulomatosis, multiple sclerosis, transplant rejection; osteoporosis;  
 CC Alzheimer's disease, atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 CC Sequence 7 AA;  
 SQ  
 Query Match 100.0%; Score 40; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 ADMSWA 6  
 |||||  
 Db 1 ADMSWA 6  
 RESULT 4  
 ID AAM48567 standard; Peptide; 8 AA.  
 XX  
 XX AAM48567;  
 AC  
 XX  
 XX 20-MAR-2002 (first entry)  
 DE  
 XX Anti-inflammatory peptide SEQ ID NO 70.  
 XX  
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;

KW cytokine; NFkappaB; IkkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 XX Synthetic.  
 OS  
 XX WO200183554-A2.  
 PN  
 XX 08-NOV-2001.  
 PD  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 PF  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 XX May MJ, Ghosh S, Finkel MA, Phillips K;  
 PI WPI; 2002-121889/16.  
 DR  
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 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 XX Claim 6; Page 62; 88pp; English.  
 PS  
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 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 CC Sequence 8 AA;  
 SQ  
 Query Match 100.0%; Score 40; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 ADMSWA 6  
 |||||  
 Db 3 ADMSWA 8  
 RESULT 5  
 ID AAM48575 standard; Peptide; 8 AA.  
 XX  
 XX AAM48575;  
 AC  
 XX  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX

DE Anti-Inflammatory peptide SEQ ID NO 78.  
 XX  
 XX Antinflammatory; antiaesthetic; cytostatic; antiproliferative; nootropic;  
 XX antineumatic; antiallergic; osteopathic; antibacterial; virucide;  
 XX immunosuppressive; dermatological; neuroprotective; antihypertensive;  
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 XX autoimmune disorder; multiple sclerosis; transplant rejection;  
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 OS Synthetic.  
 XX WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001MO-US14346.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 XX PR 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 XX (UYTA ) UNIT YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
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 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antinflammatory compounds have antiaesthetic,  
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 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
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 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX  
 XX Sequence 8 AA;  
 SO  
 Query Match 100.0%; Score 40; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADMSWA 6  
 Db 1 ADMSWA 6  
 RESULT 6  
 AAM48566

ID AAM48566 standard; peptide, 9 AA.  
 XX  
 XX AC AAM48566;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-Inflammatory peptide SEQ ID NO 69.  
 XX  
 XX Antinflammatory; antiaesthetic; cytostatic; antiproliferative; nootropic;  
 XX antineumatic; antiallergic; osteopathic; antibacterial; virucide;  
 XX immunosuppressive; dermatological; neuroprotective; antihypertensive;  
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 XX autoimmune disorder; multiple sclerosis; transplant rejection;  
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 OS Synthetic.  
 XX WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001MO-US14346.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 XX PR 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 XX (UYTA ) UNIT YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
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 PT psoriasis -  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
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 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
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 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
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 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX  
 XX Sequence 9 AA;  
 SO  
 Query Match 100.0%; Score 40; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADMSWA 6

DB 1 ADMSWA 6

RESULT 7  
ID AAM48569 standard; Peptide; 9 AA.

AC AAM48569;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 72.

XX Anti-inflammatory; antiaesthetic; cyostatic; antiporiatic; nootropic;  
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
XX anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX autoimmune disorder; multiple sclerosis; transplant rejection;  
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX WO200183554-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US14346.

XX PR 02-MAY-2000; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

XX PA (PRAE-) PRAECTIS PHARM INC.  
(UYTA ) UNIT YALE.

XX PI May MJ, Ghosh S, Findeis MA, Phillips K;  
XX WPI; 2002-121889/16.

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XX PT domain fused to NEMO binding sequence, useful for blocking nuclear  
XX PT factor kappaB activation, and for treating asthma, lung inflammation,  
XX PT psoriasis -

XX PS Claim 6; Page 62; 88pp; English.

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XX CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
XX CC arthritis.

XX CC Sequence 9 AA;

Query Match 100.0%; Score 40; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6

DB 1 ADMSWA 6

RESULT 8  
ID AAM48572 standard; Peptide; 9 AA.

AC AAM48572;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 75.

XX Anti-inflammatory; antiaesthetic; cyostatic; antiporiatic; nootropic;  
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
XX anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX autoimmune disorder; multiple sclerosis; transplant rejection;  
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX WO200183554-A2.

XX PN 08-NOV-2001.

XX PD 02-MAY-2001; 2001WO-US14346.

XX PF 02-MAY-2000; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

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XX  
SQ Sequence 9 AA;  
Query Match 100.0%; Score 40; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ADMSWA 6  
DB 3 ADMSWA 8  
RESULT 9  
ID AAM48573 standard; Peptide; 9 AA.  
XX  
AC AAM48573;  
XX  
DT 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 76.  
XX  
XX Anti-inflammatory; antiaesthetic; cytoskeletal; antiporiatic; nootropic;  
XX anti-rheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
XX allergic; membrane translocation domain; NEMO binding domain; eczema;  
XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX autoimmune disorder; multiple sclerosis; transplant rejection;  
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
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XX  
OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US14346.  
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PR 02-MAY-2000; 2000US-201261P.  
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XX (PRAE-) PRAECIS PHARM INC.  
PA (UYVA ) UNIV YALE.  
PI May MJ, Ghosh S, Findeis MA, Phillips K;  
PI WPI; 2002-121889/16.  
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CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
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CC arthritis.  
XX  
SQ Sequence 9 AA;  
Query Match 100.0%; Score 40; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ADMSWA 6  
DB 2 ADMSWA 7  
RESULT 10  
ID AAM48568 standard; Peptide; 10 AA.  
XX  
XX AAM48568;  
XX  
DT 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 71.  
XX  
XX Anti-inflammatory; antiaesthetic; cytoskeletal; antiporiatic; nootropic;  
XX anti-rheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
XX allergic; membrane translocation domain; NEMO binding domain; eczema;  
XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX autoimmune disorder; multiple sclerosis; transplant rejection;  
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US14346.  
XX  
XX  
PR 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
XX  
XX (PRAE-) PRAECIS PHARM INC.  
PA (UYVA ) UNIV YALE.  
PI May MJ, Ghosh S, Findeis MA, Phillips K;  
PI WPI; 2002-121889/16.  
DR  
XX  
PT Novel anti-inflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis  
XX  
PS Claim 6; Page 62; 88pp; English.  
XX  
CC The invention relates to an anti-inflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain  
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiaesthetic,  
CC cytoskeletal, antiporiatic, antirheumatic, antiarthritic, osteopathic,

CC antibacterial, immunosuppressive, dermatological, neuroprotective, CC  
 CC nootropic, antithrombotic, virucide and anti-allergic activity. The CC  
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappa B CC  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at CC  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase CC  
 CC activation and subsequent decreased phosphorylation of IkappaB. The CC  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma, CC  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis, CC  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, CC  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, CC  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; CC  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia CC  
 CC telangiectasia. The compounds are also useful for treating CC  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis, CC  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and CC  
 CC arthritis.

SO Sequence 10 AA;

Query Match 100.0%; Score 40; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 |||||  
 Db 2 ADMSWA 7

RESULT 11  
 AAM48571  
 ID AAM48571 standard; Peptide; 10 AA.

AC AAM48571;  
 XX  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 74.

KW Anti-inflammatory; antiaesthetic; cyostatic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antithrombotic;  
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

XX  
 XX 08-NOV-2001.

PD  
 XX 02-MAY-2001; 2001WO-US14346.

XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.

XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.

XX  
 XX May MJ, Ghosh S, Findeis MA, Phillips K;  
 PI WPI; 2002-121889/16.

XX  
 XX Novel anti-inflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 XX  
 XX Claim 6; Page 62; 88pp; English.

CC The invention relates to an anti-inflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiaesthetic,  
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective, CC  
 CC nootropic, antithrombotic, virucide and anti-allergic activity. The CC  
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappa B CC  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at CC  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase CC  
 CC activation and subsequent decreased phosphorylation of IkappaB. The CC  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma, CC  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis, CC  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, CC  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, CC  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; CC  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia CC  
 CC telangiectasia. The compounds are also useful for treating CC  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis, CC  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and CC  
 CC arthritis.

SO Sequence 10 AA;

Query Match 100.0%; Score 40; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 |||||  
 Db 3 ADMSWA 8

RESULT 12  
 AAM48565  
 ID AAM48565 standard; Peptide; 11 AA.

AC AAM48565;  
 XX  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 68.

KW Anti-inflammatory; antiaesthetic; cyostatic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antithrombotic;  
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

XX  
 XX 08-NOV-2001.

PD  
 XX 02-MAY-2001; 2001WO-US14346.

XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.

XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.

XX  
 XX May MJ, Ghosh S, Findeis MA, Phillips K;  
 PI WPI; 2002-121889/16.

XX  
 XX Novel anti-inflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 XX  
 XX Claim 6; Page 62; 88pp; English.



PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis -  
XX  
PS Claim 6; Page 62; 88pp; English.  
XX  
CC The invention relates to an antiinflammatory compound (especially  
CC AA48628-AA48645), comprising a membrane translocation domain  
CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,  
CC cytobacterial, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC nootropic, antithrombotic, virucide and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
CC activation by blocking interaction of Ikkappa kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of Ikkappa. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC relapsing. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
XX  
SQ Sequence 11 AA:  
  
Query Match 100.0%; Score 40; DB 23; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ADWSMA 6  
|||  
3 ADWSMA 8  
  
Db  
  
RESULT 13  
AAU21305  
ID AAU21305 standard; Protein: 33 AA.  
XX  
AC AAU21305;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Human novel foetal antigen, SEQ ID NO 1549.  
XX  
XX Human; foetal tissue antigen; antiinflammatory; neuroprotective;  
XX immunomodulator; cardiovascular; cytosolic; nephroprotective;  
XX cardiovascular; autoimmune disease; rheumatoid arthritis;  
XX hyperproliferative disorder; breast neoplasm; cancer;  
XX cardiovascular disorder; cardiac arrest; cerebrovascular disorder;  
XX cerebral ischaemia; angiogenesis; nervous system disorder;  
XX Alzheimer's disease; infection; ocular disorder; corneal infection;  
XX wound healing; epithelial cell proliferation; food additive.  
OS Homo sapiens.  
XX  
FN WO200155312-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-0901321.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
XX 04-FEB-2000; 2000US-0180628.  
XX 24-FEB-2000; 2000US-0184664.  
XX 02-MAR-2000; 2000US-0186350.  
XX 16-MAR-2000; 2000US-0189874.  
XX 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220963.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225457.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228824.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235634.  
PR 27-SEP-2000; 2000US-0235636.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.



CC AAY06331-70). Also provided by the invention are vectors, host  
 CC cells and methods for the recombinant production of such enzymes,  
 CC which can be used in the treatment of cellulose-containing textiles,  
 CC as feed additives, in the treatment of wood pulp, in the reduction  
 CC of biomass to glucose, in the stone washing of indigo dyed denim,  
 CC or as laundry detergent components (all claimed).

XX Sequence 103 AA;

Query Match 92.5%; Score 37; DB 20; Length 103;

Best Local Similarity 83.3%; Pred. No. 63;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6

DB 29 ADMSWS 34

# RESULT 15

AY06363 ID AAY06363 standard; Protein; 236 AA.

XX AC AAY06363;

XX DT 06-SEP-1999 (first entry)

DE Glucosylidum roseum EGIII-like cellulase.

XX Cellulase; endoglucanase; EGIII; textile; feed additive; baking;

XX food processing; grain wet milling; pulp; paper.

OS Glucosylidum roseum.

XX PN WO931255-A2.

XX PD 24-JUN-1999.

XX PF 14-DEC-1998; 98MO-US26552.

XX PR 16-DEC-1997; 97US-0991720.

XX PA (GEMV ) GENENCOR INT INC.

PI Bower BS, Fowler T, Phillips JT;

XX DR WPI; 1999-395187/33.

XX PT EGIII like cellulase

XX PS Example; Fig 6; 47pp; English.

XX CC The present polypeptide represents a full-length sequence of a  
 CC novel EGIII-like cellulase of Glucosylidum roseum. It was deduced  
 CC from a gene sequence isolated from genomic DNA using PCR  
 CC primers (see AAY59180-91) based on conserved motifs (see AAY06325-29)  
 CC of Trichoderma reesei EGIII cellulase and related enzymes. PCR  
 CC has been used to identify novel EGIII-like enzymes, including the  
 CC present protein, from bacterial and fungal sources (see AAY06331-70).  
 CC The sequence shows homology to T. reesei EGIII (see AAY06330). Also  
 CC provided by the invention are vectors, host cells and methods  
 CC for the recombinant production of such enzymes, which can be used  
 CC in the treatment of cellulose-containing textiles, as feed  
 CC additives, in the treatment of wood pulp, in the reduction of  
 CC biomass to glucose, in the stone washing of indigo dyed denim, or  
 CC as laundry detergent components (all claimed).

XX SQ Sequence 236 AA;

Query Match 92.5%; Score 37; DB 20; Length 236;

Best Local Similarity 83.3%; Pred. No. 1.5e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6

DB 63 ADMSWS 68

Search completed: February 18, 2004, 14:26:19  
 Job time : 22.7763 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds  
(without alignments)  
35.929 Million cell updates/sec

Title: US-09-643-260-5  
Perfect score: 40  
Sequence: 1 LDMSMA 6

Scoring table: BL0SUM62  
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	242	US-09-345-236B-3	Sequence 3, App11
2	38	95.0	245	US-09-252-991A-22368	Sequence 22368, A
3	37	92.5	316	US-09-252-991A-17312	Sequence 17312, A
4	36	90.0	68	US-09-252-991A-18367	Sequence 18367, A
5	36	90.0	100	US-08-241-853-28	Sequence 28, App1
6	36	90.0	100	US-08-241-853-29	Sequence 29, App1
7	36	90.0	100	US-08-850-917-28	Sequence 28, App1
8	36	90.0	100	US-08-850-917-29	Sequence 29, App1
9	36	90.0	462	US-09-252-991A-21704	Sequence 21704, A
10	36	90.0	745	US-08-887-518-3	Sequence 3, App11
11	36	90.0	745	US-09-023-321-3	Sequence 3, App11
12	36	90.0	745	US-08-890-853-4	Sequence 4, App11
13	36	90.0	745	US-09-032-475-3	Sequence 3, App11
14	36	90.0	745	US-09-099-125A-4	Sequence 4, App11
15	36	90.0	745	US-09-099-124A-4	Sequence 4, App11
16	36	90.0	745	US-09-032-476-4	Sequence 4, App11
17	36	90.0	745	US-08-890-854-4	Sequence 4, App11
18	36	90.0	745	US-09-023-324-4	Sequence 4, App11
19	36	90.0	745	US-09-168-629-2	Sequence 2, App11
20	36	90.0	745	US-08-910-820-10	Sequence 10, App1
21	36	90.0	745	US-08-910-820-12	Sequence 2, App11
22	36	90.0	745	US-09-109-886-4	Sequence 4, App11
23	36	90.0	745	US-09-844-908-10	Sequence 10, App1
24	36	90.0	745	US-09-868-758-3	Sequence 3, App11
25	36	90.0	756	US-08-887-518-4	Sequence 4, App11
26	36	90.0	756	US-09-023-321-4	Sequence 4, App11
27	36	90.0	756	US-08-890-853-2	Sequence 2, App11

28	36	90.0	756	2	US-09-032-475-4	Sequence 4, App11
29	36	90.0	756	2	US-09-099-125A-2	Sequence 2, App11
30	36	90.0	756	2	US-09-099-124A-2	Sequence 2, App11
31	36	90.0	756	3	US-09-032-476-2	Sequence 2, App11
32	36	90.0	756	3	US-08-890-854-2	Sequence 2, App11
33	36	90.0	756	3	US-09-023-324-2	Sequence 2, App11
34	36	90.0	756	3	US-09-168-629-15	Sequence 15, App1
35	36	90.0	756	3	US-08-910-820-9	Sequence 9, App11
36	36	90.0	756	4	US-09-109-986-2	Sequence 2, App11
37	36	90.0	756	4	US-09-844-908-9	Sequence 9, App11
38	36	90.0	756	4	US-09-868-758-4	Sequence 4, App11
39	36	90.0	983	2	US-08-673-789-4	Sequence 4, App11
40	36	90.0	983	1	US-08-162-809-16	Sequence 16, App1
41	36	90.0	983	1	US-08-167-919A-10	Sequence 10, App1
42	36	90.0	983	1	US-08-449-645A-21	Sequence 21, App1
43	36	90.0	983	2	US-08-702-367A-21	Sequence 21, App1
44	36	90.0	983	3	US-08-715-106-10	Sequence 10, App1
45	36	90.0	983	5	PCT-US95-04681-21	Sequence 21, App1

## ALIGNMENTS

RESULT 1  
US-09-345-236B-3  
Sequence 3, Application US/09345236B  
Patent No. 6521454  
GENERAL INFORMATION:  
APPLICANT: Becnel, James J.  
APPLICANT: Tuhuo, Fukuda  
APPLICANT: Moser, Bettina  
APPLICANT: Cockburn, Andrew  
APPLICANT: White, Susan B.  
APPLICANT: Undeen, Albert H.  
TITLE OF INVENTION: No. 6521454el Baculoviruses, Insecticidal  
TITLE OF INVENTION: Compositions, and Methods for Control of Invertebrates  
FILE REFERENCE: 21042.0004  
CURRENT APPLICATION NUMBER: US/09/345,236B  
CURRENT FILING DATE: 1999-06-30  
NUMBER OF SEQ ID NOS: 148  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 242  
TYPE: PRT  
ORGANISM: mosquito baculovirus  
US-09-345-236B-3

Query Match  
Best Local Similarity 100.0%; Score 40; DB 4; Length 242;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSMA 6  
|||||  
Db 79 LDMSMA 84

RESULT 2  
US-09-252-991A-22368  
Sequence 22368, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 22368

LENGTH: 445  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-22368

Query Match 95.0%; Score 38; DB 4; Length 445;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6  
| | | | |  
DB 303 MDMSWA 308

RESULT 3  
US-09-252-991A-17312  
Sequence 17312, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252.991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 17312  
LENGTH: 316  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-17312

Query Match 92.5%; Score 37; DB 4; Length 316;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6  
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DB 271 LDMSWA 276

RESULT 4  
US-09-252-991A-18367  
Sequence 18367, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252.991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 18367  
LENGTH: 68  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18367

Query Match 90.0%; Score 36; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
| | | | |

DB 2 DMSWA 6

RESULT 5  
US-08-241-853-28  
Sequence 28, Application US/08241853  
Patent No. 5693468  
GENERAL INFORMATION:  
APPLICANT: Fang, Kathy S.  
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/241.853  
FILING DATE: 12-MAY-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-078  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 100 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-241-853-28

Query Match 90.0%; Score 36; DB 1; Length 100;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5  
| | | | |  
DB 19 LDMSW 23

RESULT 6  
US-08-241-853-29  
Sequence 29, Application US/08241853  
Patent No. 5693468  
GENERAL INFORMATION:  
APPLICANT: Fang, Kathy S.  
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA

ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/241,853  
FILING DATE: 12-MAY-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-078  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 100 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-241-853-29

Query Match 90.0%; Score 36; DB 1; Length 100;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5  
|||||  
DB 19 LDMSW 23

RESULT 7  
US-08-850-917-28  
Sequence 28, Application US/08850917  
Patent No. 5854045  
GENERAL INFORMATION:  
APPLICANT: Fang, Kathy S.  
APPLICANT: Hanafusa, Hideaburo  
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE  
TITLE OF INVENTION: AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/850,917  
FILING DATE: 02-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/241,853  
FILING DATE: 12-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-078  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 100 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-850-917-28

Query Match 90.0%; Score 36; DB 2; Length 100;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5  
|||||  
DB 19 LDMSW 23

RESULT 8  
US-08-850-917-29  
Sequence 29, Application US/08850917  
Patent No. 5854045  
GENERAL INFORMATION:  
APPLICANT: Fang, Kathy S.  
APPLICANT: Hanafusa, Hideaburo  
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE  
TITLE OF INVENTION: AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/850,917  
FILING DATE: 02-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/241,853  
FILING DATE: 12-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-078  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 100 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-850-917-29

Query Match 90.0%; Score 36; DB 2; Length 100;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5  
|||||  
Db 19 LDMSW 23

RESULT 9  
US-09-252-991A-21704  
; Sequence 21704, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 21704  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-21704

Query Match 90.0%; Score 36; DB 4; Length 462;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
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Db 169 DMSWA 173

RESULT 10  
US-08-887-518-3  
; Sequence 3, Application US/0887518  
; Patent No. 5843721  
; GENERAL INFORMATION:  
; APPLICANT: Roche, Mike  
; APPLICANT: Wu, Lin  
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,518  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A.  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: T97-008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 745 amino acids  
; TYPE: amino acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-887-518-3

Query Match 90.0%; Score 36; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSW 5  
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Db 738 LDMSW 742

RESULT 11  
US-09-023-321-3  
; Sequence 3, Application US/09023321  
; Patent No. 5844073  
; GENERAL INFORMATION:  
; APPLICANT: Roche, Mike  
; APPLICANT: Wu, Lin  
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,321  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,518  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A.  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: T97-008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 745 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-023-321-3

Query Match 90.0%; Score 36; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSW 5  
|||||  
Db 738 LDMSW 742

RESULT 12  
US-08-890-853-4  
; Sequence 4, Application US/08890853  
; Patent No. 5851812  
; GENERAL INFORMATION:  
; APPLICANT: Goeddel, David V.

APPLICANT: Moronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-853-4

Query Match 90.0%; Score 36; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5  
DB 738 LDMSW 742

RESULT 13  
US-09-032-475-3  
Sequence 3, Application US/09032475  
Patent No. 5854003  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Wu, Lin  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,475  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/887,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-032-475-3

Query Match 90.0%; Score 36; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5  
DB 738 LDMSW 742

RESULT 14  
US-09-099-125A-4  
Sequence 4, Application US/09099125A  
Patent No. 5916760  
GENERAL INFORMATION:  
APPLICANT: Goedel, David V.  
APPLICANT: Moronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,125A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-099-125A-4

Query Match 90.0%; Score 36; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5



Db 738 LDMSW 742

RESULT 15  
US-09-099-124A-4  
Sequence 4, Application US/09099124A  
Patent No. 5939302  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Moronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,124A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-099-124A-4

Query Match 90.0%; Score 36; DB 2; Length 745;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5  
Db 738 LDMSW 742

Search completed: February 18, 2004, 14:41:46  
Job time: 7.06579 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds  
(without alignments)  
41.814 Million cell updates/sec

Title: US-09-643-260-5

Perfect score: 40  
Sequence: 1 LDMSWA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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6: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1985.DAT.\*  
7: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1986.DAT.\*  
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12: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1991.DAT.\*  
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22: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT.\*  
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24: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	ABB08728	Mutated IKKbeta NE
2	40	100.0	6	AA048510	NBD mutant peptide
3	40	100.0	6	AA048537	Anti-inflammatory
4	40	100.0	6	AA048559	Anti-inflammatory
5	40	100.0	6	ABU08421	Human NEMO binding
6	40	100.0	7	AA048563	Anti-inflammatory
7	40	100.0	8	AA048556	Anti-inflammatory
8	40	100.0	8	AA048564	Anti-inflammatory
9	40	100.0	9	AA048555	Anti-inflammatory

10	40	100.0	9	AA048558	Anti-inflammatory
11	40	100.0	9	AA048561	Anti-inflammatory
12	40	100.0	9	AA048562	Anti-inflammatory
13	40	100.0	10	AA048554	Anti-inflammatory
14	40	100.0	10	AA048557	Anti-inflammatory
15	40	100.0	10	AA048560	Anti-inflammatory
16	40	100.0	745	AB077292	Human IKKalpha mut
17	40	100.0	756	AB077309	Human IKKbeta muta
18	36	90.0	6	AB080725	IKKbeta NEMO bindi
19	36	90.0	6	AA048530	Anti-inflammatory
20	36	90.0	6	AA048538	Anti-inflammatory
21	36	90.0	6	AA048570	Anti-inflammatory
22	36	90.0	6	AA048555	NBD mutant peptide
23	36	90.0	6	ABU08418	Human NEMO binding
24	36	90.0	7	AA048534	Anti-inflammatory
25	36	90.0	7	AA048574	Anti-inflammatory
26	36	90.0	8	AA048527	Anti-inflammatory
27	36	90.0	8	AA048535	Anti-inflammatory
28	36	90.0	8	AA048567	Anti-inflammatory
29	36	90.0	8	AA048575	Anti-inflammatory
30	36	90.0	9	AA0485182	IKK-alpha polypept
31	36	90.0	9	AA048526	Anti-inflammatory
32	36	90.0	9	AA048529	Anti-inflammatory
33	36	90.0	9	AA048532	Anti-inflammatory
34	36	90.0	9	AA048533	Anti-inflammatory
35	36	90.0	9	AA048566	Anti-inflammatory
36	36	90.0	9	AA048569	Anti-inflammatory
37	36	90.0	9	AA048572	Anti-inflammatory
38	36	90.0	9	AA048573	Anti-inflammatory
39	36	90.0	10	AB077313	IKKbeta NEMO bindi
40	36	90.0	10	AA048528	Anti-inflammatory
41	36	90.0	10	AA048531	Anti-inflammatory
42	36	90.0	10	AA048568	Anti-inflammatory
43	36	90.0	10	AA048571	Anti-inflammatory
44	36	90.0	11	AB077311	Human NBD peptide
45	36	90.0	11	AA048506	Human IKKbeta pept

## ALIGNMENTS

RESULT 1	AB08728	standard; peptide; 6 AA.
ID	AB08728	
XX	AB08728	
AC	AB08728	
XX	AB08728	
DT	14-JUN-2002	(first entry)
DE	Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 5.	
KW	IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;	
KW	kinase activation; leukocyte; inflammation; B-selectin; osteoclast;	
KW	autoimmune disease; transplant rejection; osteoporosis; cancer;	
KW	Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;	
KW	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;	
KW	corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;	
KW	osteopathic; cyclostatic; neotropic; neuroprotective; anti-HIV; human;	
KW	antiarteriosclerotic; vincristine; antiasthmatic; antiallergic;	
KW	dermatological; antibacterial; antipruritic; antirheumatic;	
KW	antiarthritic; osteopathic; anticancer; mutant; muteln.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 6	/note= "Wildtype Leu substituted by Ala"
PN	WO200183547-A2.	
PD	08-NOV-2001.	
XX		

PF 02-MAY-2001; 2001WO-US40654.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (UYTA ) UNIV YALE.  
 PI May MJ, Ghosh S;  
 XX  
 DR WPI; 2002-179350/23.  
 XX  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 XX  
 XX Claim 23; Page 44; 82pp; English.  
 XX  
 XX The invention relates to modulating NF-kappaB (NF-KB) induction in a cell  
 CC comprising contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB077313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-KB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of Ikbppab. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-KB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC polyarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polyarthritis, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections,  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
 CC binding domain of IKKbeta.  
 XX  
 SQ Sequence 6 AA;  
 QY  
 DB 1 LDMSWA 6  
 1 LDMSWA 6  
 Query Match 100.0%; Score 40; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 2  
 AAM48510  
 ID AAM48510 standard; Peptide: 6 AA.  
 XX  
 AC AAM48510;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE NBD mutant peptide SEQ ID NO 5.

XX  
 XX Antiinflammatory; antiaesthetic; cyostatic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; vitruclide;  
 KW immunosuppressive; dermatological; neuroprotective; antiheterosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200183554-A2.  
 PN  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYTA ) UNIV YALE.  
 PI May MJ, Ghosh S, Fandels MA, Phillips K;  
 XX  
 DR WPI; 2002-121869/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 XX Example 6; Page 47; 88pp; English.  
 PS  
 XX The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiheterosclerotic, vitruclide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease, atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 6 AA;  
 QY  
 DB 1 LDMSWA 6  
 1 LDMSWA 6  
 Query Match 100.0%; Score 40; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 3  
 AAM48537  
 ID AAM48537 standard; Peptide: 6 AA.

XX AAM48537;  
 AC AAM48537;  
 XX 20-MAR-2002 (first entry)  
 DT 20-MAR-2002 (first entry)  
 XX Anti-inflammatory peptide SEQ ID NO 40.  
 DE Anti-inflammatory peptide SEQ ID NO 40.  
 XX  
 KW Antinflammatory; antiaesthetic; cyostatic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virocidic;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200183554-A2.  
 XX  
 XX 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 XX  
 XX 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 XX (UYTA) UNIV YALE.  
 XX  
 XX May MJ, Ghosh S, Findeis MA, Phillips K,  
 PI WPI; 2002-121889/16.  
 XX  
 XX Novel antinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 XX Claim 6; Page 61; 88pp; English.  
 PS  
 XX The invention relates to an antinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antinflammatory compounds have antiaesthetic,  
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virocidic and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX Sequence 6 AA;  
 SO  
 Query Match 100.0%; Score 40; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 LDMSWA 6  
 RESULT 4  
 ID AAM48559  
 XX AAM48559 standard; Peptide; 6 AA.  
 AC AAM48559;  
 XX 20-MAR-2002 (first entry)  
 DT 20-MAR-2002 (first entry)  
 XX Anti-inflammatory peptide SEQ ID NO 62.  
 DE Anti-inflammatory peptide SEQ ID NO 62.  
 XX  
 KW Antinflammatory; antiaesthetic; cyostatic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virocidic;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200183554-A2.  
 XX  
 XX 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 XX  
 XX 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 XX (UYTA) UNIV YALE.  
 XX  
 XX May MJ, Ghosh S, Findeis MA, Phillips K,  
 PI WPI; 2002-121889/16.  
 XX  
 XX Novel antinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 XX Claim 6; Page 62; 88pp; English.  
 PS  
 XX The invention relates to an antinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antinflammatory compounds have antiaesthetic,  
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virocidic and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX Sequence 6 AA;  
 SO

Query Match 100.0%; Score 40; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6  
 DB 1 LDMSWA 6

## RESULT 5

ABU08421  
 ID ABU08421 standard; peptide; 6 AA.

AC ABU08421;

DT 12-JUN-2003 (first entry)

DE Human NEMO binding site (NBD) mutant peptide #4.

XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;  
 KM IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;  
 KM nuclear factor-kappaB induction; inflammatory disorder;  
 KM autoimmune disease; osteoporosis; cancer; Alzheimer's disease;  
 KM atherosclerosis; viral infection; Ataxia telangiectasia;  
 KM translocation detection; immunosuppressive; osteopathic;  
 KM cytosolic; neutrotropic; antineoplastic; antineurotic; virucide;  
 KM vascotropic; antirheumatic; antichronic; mutant; muten.

OS Homo sapiens.  
 OS Synthetic.

PN US2002156000-A1.

PD 24-OCT-2002.

PF 02-MAY-2001; 2001US-0847940.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

PA (MAYM/) MAY M J.

PA (GHOSH/) GHOSH S.

PI May MJ, Ghosh S;

PI May MJ, Ghosh S;

PI May MJ, Ghosh S;

PI May MJ, Ghosh S;

PI May MJ, Ghosh S;

PI May MJ, Ghosh S;

PI May MJ, Ghosh S;

PI May MJ, Ghosh S;

PI May MJ, Ghosh S;

PI May MJ, Ghosh S;

PI May MJ, Ghosh S;

PI May MJ, Ghosh S;

PI May MJ, Ghosh S;

PI May MJ, Ghosh S;

PI May MJ, Ghosh S;

PI May MJ, Ghosh S;

PI May MJ, Ghosh S;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6  
 DB 1 LDMSWA 6

## RESULT 6

AAM48563  
 ID AAM48563 standard; Peptide; 7 AA.

AC AAM48563;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 66.

XX Antiinflammatory; antiaesthetic; cytosolic; antiprotective; neutrotropic;  
 KM antirheumatic; antichronic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neutrotropic; antineurotic; eczema;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; cancer;  
 KM cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.  
 OS WO200183554-A2.

PN 08-NOV-2001.

PD 02-MAY-2001; 2001WO-US14346.

PF 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

PA (PRAE-) PRAEIS PHARM INC.

PA (UYVA) UNIV YALE.

PI May MJ, Ghosh S, Pindels MA, Phillips K;

PI May MJ, Ghosh S, Pindels MA, Phillips K;

PI May MJ, Ghosh S, Pindels MA, Phillips K;

PI May MJ, Ghosh S, Pindels MA, Phillips K;

PI May MJ, Ghosh S, Pindels MA, Phillips K;

PI May MJ, Ghosh S, Pindels MA, Phillips K;

PI May MJ, Ghosh S, Pindels MA, Phillips K;

PI May MJ, Ghosh S, Pindels MA, Phillips K;

PI May MJ, Ghosh S, Pindels MA, Phillips K;

PI May MJ, Ghosh S, Pindels MA, Phillips K;

PI May MJ, Ghosh S, Pindels MA, Phillips K;

PI May MJ, Ghosh S, Pindels MA, Phillips K;

PI May MJ, Ghosh S, Pindels MA, Phillips K;

PI May MJ, Ghosh S, Pindels MA, Phillips K;

PI May MJ, Ghosh S, Pindels MA, Phillips K;

PI May MJ, Ghosh S, Pindels MA, Phillips K;

PI May MJ, Ghosh S, Pindels MA, Phillips K;

PI May MJ, Ghosh S, Pindels MA, Phillips K;

Claim 6; Page 62; 88pp; English.

The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
 CC cytosolic, antiprotective, antirheumatic, antichronic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC neutrotropic, antineurotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis, autoimmune diseases such as lupus, polyarthritis, scleroderma,  
 CC granulomatosis, multiple sclerosis, transplant rejection, osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

Query Match 100.0%; Score 40; DB 24; Length 6;

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 XX  
 SQ Sequence 7 AA;  
 Query Match 100.0%; Score 40; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6  
 |||||  
 Db 1 LDMSWA 6

RESULT 7  
 AAM48556  
 ID AAM48556 standard; Peptide; 8 AA.  
 XX  
 XX AAM48556;  
 AC  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 59.  
 XX  
 KM Antiinflammatory; antiasthmatic; cytostatic; antiportiatric; nootropic;  
 KM antineumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX  
 PR 22-AUG-2000; 2000US-0643260.  
 PA  
 PA (PRAE-) PRAECTIS PHARM INC.  
 PA (UYVA) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytostatic, antiportiatric, antineumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 40; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6  
 |||||  
 Db 3 LDMSWA 8

RESULT 8  
 AAM48564  
 ID AAM48564 standard; Peptide; 8 AA.  
 XX  
 XX AAM48564;  
 AC  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 67.  
 XX  
 KM Antiinflammatory; antiasthmatic; cytostatic; antiportiatric; nootropic;  
 KM antineumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX  
 PR 22-AUG-2000; 2000US-0643260.  
 PA  
 PA (PRAE-) PRAECTIS PHARM INC.  
 PA (UYVA) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytostatic, antiportiatric, antineumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of IkappaB. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis; multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
CC  
SQ Sequence 8 AA;  
Query Match 100.0%; Score 40; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSMA 6  
DB 1 LDMSMA 6  
RESULT 9  
ID AAM48555 standard; Peptide; 9 AA.  
XX  
AC AAM48555;  
XX  
DT 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 58.  
XX  
KW Anti-inflammatory; antiasthmatic; cytosstatic; antipsoriatic; neutropic;  
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US14346.  
XX  
PR 02-MAY-2000; 2000US-201261P.  
XX  
PR 22-AUG-2000; 2000US-0643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
XX  
PA (UYVA) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Findeis MA, Phillips K;  
XX  
DR WPI; 2002-121889/16.  
XX  
PT Novel antiinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis -  
XX  
PS Claim 6; Page 62; 88pp; English.  
XX  
CC The invention relates to an antiinflammatory compound (especially  
CC AAM48528-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
CC cytosstatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC neutropic, antiatherosclerotic, virucide and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of IkappaB. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis; multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
CC  
SQ Sequence 9 AA;  
Query Match 100.0%; Score 40; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSMA 6  
DB 1 LDMSMA 6  
RESULT 10  
ID AAM48558 standard; Peptide; 9 AA.  
XX  
AC AAM48558;  
XX  
DT 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 61.  
XX  
KW Anti-inflammatory; antiasthmatic; cytosstatic; antipsoriatic; neutropic;  
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US14346.  
XX  
PR 02-MAY-2000; 2000US-201261P.  
XX  
PR 22-AUG-2000; 2000US-0643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
XX  
PA (UYVA) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Findeis MA, Phillips K;  
XX  
DR WPI; 2002-121889/16.  
XX  
PT Novel antiinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,

PT		psooriasis -
XX		Claim 6; Page 62; 89pp; English.
XX		The invention relates to an antiinflammatory compound (especially
CC		AA048628-AA048645), comprising a membrane translocation domain
CC		(AA048620-AA048627 or AA048646-AA048651) which comprises from 6-15
CC		amino acid residues, fused to a NEMO binding sequence
CC		(AA048625-AA048619). The antiinflammatory compounds have antiasthmatic,
CC		cytostatic, antipsoaritic, antirheumatic, antiallergic, osteopathic,
CC		antibacterial, immunosuppressive, dermatological, neuroprotective,
CC		nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
CC		compounds act as selective inhibitors of cytokine-mediated NF-kappa B
CC		activation by blocking interaction of Ikappa B kinase beta (IKKbeta) at
CC		the NEMO binding domain that results in inhibition of IKKbeta kinase
CC		activation and subsequent decreased phosphorylation of Ikappa B. The
CC		compounds are useful for treating inflammatory disorders, e.g., asthma,
CC		lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC		osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC		bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,
CC		granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC		Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC		telangectasia. The compounds are also useful for treating
CC		pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC		drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC		arthritis.
XX		
SQ		Sequence 9 A/;
Query Match:	100.0%;	Score 40; DB 23; Length 9;
Best Local Similarity	100.0%;	Pred. No. 9.3e+05;
Matches 6; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Oy	1 LDMSWA 6	
Db	1 LDMSWA 6	
RESULT 11		
AAM48561		
ID	AAM48561 standard; Peptide; 9 A.	
AC	AAM48561;	
DT	20-MAR-2002 (first entry)	
DE	Anti-inflammatory peptide SEQ ID NO 64.	
KM	Antiinflammatory; antiasthmatic; cytostatic; antipsoaritic; nootropic;	
KM	antirheumatic; antiallergic; osteopathic; antibacterial; virucide;	
KM	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;	
KM	anti-allergic; membrane translocation domain; NEMO binding domain; eczema;	
KM	cyclokin; NFkappaB; Ikappa B kinase beta; IKKbeta; cancer; psoriasis;	
KM	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;	
KM	autoimmune disorder; multiple sclerosis; transplant rejection;	
KM	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;	
KM	ataxia telangectasia; allergy; anapylaxis; arthritis.	
OS	Synthetic.	
XX		
PN	WO200183554-A2.	
PD	08-NOV-2001.	
PE	02-MAY-2001; 2001MO-US14346.	
XX		
XX	02-MAY-2000; 2000US-201261P.	
PR	22-AUG-2000; 2000US-0643260.	
PA	(PRAE-) PRAECIS PHARM INC.	
XX	(UYTA ) UNIV YALE.	
PI	May MJ, Ghosh S, Rindels MA, Phillips K,	

XX	WP1; 2002-121899/16.
XX	
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis
XX	-
PS	Claim 6; Page 62; 8pp; English.
CC	The invention relates to an antiinflammatory compound (especially
CC	(AAM48628-AAM48645), comprising a membrane translocation domain
CC	(AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,
CC	cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	nootropic, antithrombotic, virucide and antiallergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of IkappaB. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	bursitis; autoimmune diseases such as lupus, polyaralgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
SQ	Sequence 9 AA:
OY	Query Match 100.0%; Score 40; DB 23; Length 9;
Db	Best Local Similarity 100.0%; Pred. No. 9.3e+05;
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
	1 LDMSMA 6
	3 LDMSMA 8
RESULT 12	
AAM48562	
ID AAM48562 standard; Peptide: 9 AA.	
AC AAM48562;	
XX	
DT 20-MAR-2002 (first entry)	
XX	
DE Anti-inflammatory peptide SEQ ID NO 65.	
XX	
KM Antiflammatory; antiaesthetic; cytostatic; antipsoriatic; nootropic;	
KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;	
KM immunosuppressive; dermatological; neuroprotective; antithrombotic;	
KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;	
KM cyclokin; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;	
KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;	
KM autoimmune disorder; multiple sclerosis; transplant rejection;	
KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;	
KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.	
XX	
OS Synthetic.	
XX	
PN WO200183554-A2.	
XX	
PD 08-NOV-2001.	
XX	
PE 02-MAY-2001; 2001WO-US4346.	
XX	
PR 02-MAY-2000; 2000US-201261P.	
XX	



PR	22-AUG-2000; 2000US-0643260.
PA	(PRAE-) PRAECIS PHARM INC.
PA	(UYTA ) UNIV YALE.
XX	
P1	May MJ, Ghosh S, Findeis MA, Phillips K;
XX	
DR	WPI; 2002-12189/16.
XX	
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis -
XX	
PS	Claim 6; Page 62; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AAM48628-AAM48645), comprising a membrane translocation domain
CC	(AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AAM48625-AAM48619). The antiinflammatory compounds have antiaesthetic,
CC	cytostatic, antiproliferative, antiarthritic, antiallergic, osteoprotective,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective, The
CC	neotropic, antihypertensive, virocidic and antiallergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of IkappaB. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	during or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
SQ	Sequence 9 AA;
	Query Match 100.0%; Score 40; DB 23; Length 9;
	Best Local Similarity 100.0%; Pred. No. 9.3e+05;
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY	1 LDMSWA 6 
DB	2 LDMSWA 7
	RESULT 13
	AAM48554
ID	AAM48554 standard; Peptide; 10 AA.
XX	
XX	AAM48554;
XX	
DT	20-MAR-2002 (first entry)
DE	
XX	Anti-inflammatory peptide SEQ ID NO 57.
KM	Antifluorescent; antiaesthetic; cytotoxic; antiproliferative; neurotoxic;
KM	antiimmunogenic; antiallergic; osteoprotective; antibacterial; virucide;
KM	immunosuppressive; dermatological; neuroprotective; antihypertensive;
KM	antiallergic, membrane translocation domain, NEMO binding domain; eczema;
KM	cystokine; NFkappaB; IkappaB kinase beta; IKKdelta; cancer; psoriasis;
KM	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KM	autoimmune disorder; multiple sclerosis; transplant rejection;
KM	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KM	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX	
OS	Synthetic.
XX	
PN	WO200103554-A2.

XX	08-NOV-2001.
PD	
XX	
XX	02-MAY-2001; 2001WO-US14346.
FP	
XX	
PR	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-0643260.
XX	
PA	(PRAE-) PRACIS PHARM INC.
PA	(UYTA ) UNIV YALE.
PI	
P1	May MJ, Ghosh S, Findeis MA, Phillips K,
DR	WPI, 2002-12189/16.
XX	
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis -
XX	
PS	Claim 6; Page 62; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AAM48628-AA448645), comprising a membrane translocation domain
CC	(AAM48620-AA448627 or AAM48646-AA448651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AAM48525-AA448619). The antiinflammatory compounds have antiasthmatic,
CC	cycostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	nootropic, antihistseroleptic, virucide and antiallergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of Ikappab kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of Ikappab. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
XX	
SQ	Sequence 10 AA:
	Query Match 100.0%; Score 40; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 2,6; Mismatches 0; Gaps 0;
	Matches 6; Conservative 0; Indels 0; Gaps 0;
OY	1 LDMSWA 6 
DB	2 LDMSWA 7
RESULT 14	
AAM48557	
ID	AAM48557 standard; Peptide; 10 AA.
XX	
AC	AAM48557;
XX	
DT	20-MAR-2002 (first entry)
DE	
XX	Anti-inflammatory peptide SEQ ID NO 60.
XX	
KW	Antiinflammatory; antiasthmatic; cycostatic; antipsoriatic; nootropic;
KW	antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW	immunosuppressive; dermatologic; neuroprotective; antiatherosclerotic;
KW	antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW	cytokine; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW	autoimmune disorder; multiple sclerosis; transplant rejection;

KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX Synthetic.  
 OS  
 XX WO200183554-A2.  
 PN  
 XX 08-NOV-2001.  
 PD  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Finkelstein MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC (AAW48628-AAW48645), comprising a membrane translocation domain  
 CC (AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAW48625-AAW48619). The antiinflammatory compounds have antiasthmatic,  
 CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nocotropic, antiatherosclerotic, virucide and anti-allergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 CC  
 SQ Sequence 10 AA;  
 QY  
 DB Query Match 100.0%; Score 40; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSWA 6  
 |||||  
 DB 2 LDMSWA 7  
 |||||  
 RESULT 15  
 AAW48560  
 ID AAW48560 standard; Peptide; 10 AA.  
 XX  
 AC AAW48560;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 63.  
 XX  
 KM Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; nocotropic;

KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX Synthetic.  
 OS  
 XX WO200183554-A2.  
 PN  
 XX 08-NOV-2001.  
 PD  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Finkelstein MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC (AAW48628-AAW48645), comprising a membrane translocation domain  
 CC (AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAW48625-AAW48619). The antiinflammatory compounds have antiasthmatic,  
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 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nocotropic, antiatherosclerotic, virucide and anti-allergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 CC  
 SQ Sequence 10 AA;  
 QY  
 DB Query Match 100.0%; Score 40; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSWA 6  
 |||||  
 DB 3 LDMSWA 8  
 |||||  
 Search completed: February 18, 2004, 14:26:19  
 Job time : 23.7763 secs

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OM protein - protein search, using SW model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds

(without alignments)  
41.814 Million cell updates/sec

Title: US-09-643-260-4

Perfect score: 40

Sequence: 1 ADMSWL 6

Scoring table: BLOSUM62

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A\_Geneseq\_19jun03.\*

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
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6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
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9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
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16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	23	AB08727
2	40	100.0	6	23	AA048509
3	40	100.0	6	23	AA048536
4	40	100.0	6	23	AA048548
5	40	100.0	6	24	AB08420
6	40	100.0	7	23	AA048552
7	40	100.0	8	23	AA048545
8	40	100.0	8	23	AA048553
9	40	100.0	9	23	AA048544

10	40	100.0	9	23	AA048547	Anti-inflammatory
11	40	100.0	9	23	AA048550	Anti-inflammatory
12	40	100.0	9	23	AA048551	Anti-inflammatory
13	40	100.0	10	23	AA048546	Anti-inflammatory
14	40	100.0	10	23	AA048549	Anti-inflammatory
15	40	100.0	11	23	AA048543	Anti-inflammatory
16	40	100.0	11	23	AA048544	Anti-inflammatory
17	40	100.0	11	23	AA048545	Anti-inflammatory
18	40	100.0	11	23	AA048546	Anti-inflammatory
19	40	100.0	11	23	AA048547	Anti-inflammatory
20	40	100.0	11	23	AA048548	Anti-inflammatory
21	40	100.0	11	23	AA048549	Anti-inflammatory
22	40	100.0	11	23	AA048550	Anti-inflammatory
23	40	100.0	11	23	AA048551	Anti-inflammatory
24	40	100.0	11	23	AA048552	Anti-inflammatory
25	40	100.0	11	23	AA048553	Anti-inflammatory
26	40	100.0	11	23	AA048554	Anti-inflammatory
27	40	100.0	11	23	AA048555	Anti-inflammatory
28	40	100.0	11	23	AA048556	Anti-inflammatory
29	40	100.0	11	23	AA048557	Anti-inflammatory
30	40	100.0	11	23	AA048558	Anti-inflammatory
31	40	100.0	11	23	AA048559	Anti-inflammatory
32	40	100.0	11	23	AA048560	Anti-inflammatory
33	40	100.0	11	23	AA048561	Anti-inflammatory
34	40	100.0	11	23	AA048562	Anti-inflammatory
35	40	100.0	11	23	AA048563	Anti-inflammatory
36	40	100.0	11	23	AA048564	Anti-inflammatory
37	40	100.0	11	23	AA048565	Anti-inflammatory
38	40	100.0	11	23	AA048566	Anti-inflammatory
39	40	100.0	11	23	AA048567	Anti-inflammatory
40	40	100.0	11	23	AA048568	Anti-inflammatory
41	40	100.0	11	23	AA048569	Anti-inflammatory
42	40	100.0	11	23	AA048570	Anti-inflammatory
43	40	100.0	11	23	AA048571	Anti-inflammatory
44	40	100.0	11	23	AA048572	Anti-inflammatory
45	40	100.0	11	23	AA048573	Anti-inflammatory

## ALIGNMENTS

RESULT 1  
ID ABB08727 standard; peptide; 6 AA.

XX ABB08727;

DT 14-JUN-2002 (first entry)

DB Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 4.

IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
kinase activator; leukocyte; inflammation; E-selectin; osteoclast;  
autoimmune disease; transplant rejection; osteoporosis; cancer;  
Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;  
rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
osteoporosis; cytostatic; neoplastic; neuroprotective; anti-HIV; human;  
antiartherosclerotic; viral; anti-inflammatory; antiproliferative;  
dermatological; antibacterial; antiparasitic; antipneumatic;  
antiarthritic; osteopathic; antitumor; mutant; mutein.

OS Homo sapiens.  
OS Synthetic.

Key Location/Qualifiers  
Misc-difference 1 /note="Wildtype Leu substituted by Ala"

PN WO200183547-A2.

PD 08-NOV-2001.

NO CNT

PF	02-MAY-2001; 2001MO-US40654.
XX	
XX	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-0643260.
XX	
XX	(UYVA ) UNIV YALE.
PA	
PI	May MJ, Ghosh S;
XX	
DR	WPI; 2002-1179350/23.
XX	
PT	Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT	inflammatory disorders, osteoporosis and cancer, comprises contacting a
PT	cell with an anti-inflammatory compound comprising at least one NEMO
XX	binding domain -
PS	Claim 23; Page 44; 82pp; English.
XX	
XX	The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC	comprises contacting a cell with an anti-inflammatory compound
CC	(AB808725-AB808742) comprising at least one NEMO binding domain
CC	(AB877313). The compound has acts through selective inhibition of
CC	cytokine-mediated NF-kB activation by blocking the interaction of NEMO
CC	with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC	interaction results in inhibition of IKKbeta kinase activation and
CC	subsequent decreased phosphorylation of Ikbppab. The compound may also
CC	act (directly or indirectly) by blocking the recruitment of leukocytes
CC	into sites of acute and chronic inflammation, by down-regulating the
CC	expression of E-selectin on leukocytes or by blocking osteoclast
CC	differentiation. The compound is useful in treating NF-kB mediated
CC	conditions, where the condition is an inflammatory disorder, an
CC	autoimmune disease, transplant rejection, osteoporosis, cancer,
CC	Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC	relanguectasia. The inflammatory disorder is asthma, allergies,
CC	urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
CC	rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
CC	bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC	burnsitis. The inflammatory disorder may also be dermatitis, eczema,
CC	psoriasis, osteoarthritis, psoriatic arthritis, lupus and
CC	spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC	polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC	cryoglobulinemia or multiple sclerosis. For chronic viral infections
CC	caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
CC	diseases include HIV and influenza. The compound may also be useful for
CC	treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC	sunburn or aging. The compound may be used to replace corticosteroids in
CC	any application in which corticosteroids are used, including
CC	immunosuppression in transplants and cancer therapy. Also for identifying
CC	antiinflammatory compounds and for diagnosis of an inflammatory disorder.
CC	The compound may be administered alone or in combination with other known
CC	anti-inflammatory agents. The present sequence is that of a mutated NEMO
CC	binding domain of IKKbeta.
XX	
XX	Sequence 6 AA;
XX	
QY	1 ADMSWTL 6
DB	1 ADMSWTL 6
XX	
XX	Query Match 100.0%; Score 40; DB 23; Length 6;
XX	Beet Local Similarity 100.0%; Pred. NO. 9.3e+05; Indels 0; Gaps 0;
XX	Matches 6; Conservative 0; Mismatches 0;
XX	
XX	RESULT 2
XX	AA048509
XX	AA048509 standard; peptide; 6 AA.
XX	AA048509;
XX	20-MAR-2002 (first entry)
XX	NBD mutant peptide SEQ ID NO 4.
XX	

XX Antinflammatory; antiasthmatic; cytostatic; antiportatic; nootropic;  
KW antineumatic; antiarthritic; osteopathic; antibacterial; virutide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW allergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
OS Synthetic.  
XX  
XX WO200183554-A2.  
PN  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US14346.  
XX  
XX 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
PP (UYA ) UNIV YALE.  
PI May MJ, Ghosh S, Findeis MA, Phillips K,  
DR WPI; 2002-121889/16.  
XX  
PT Novel antinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis -  
PS Example 6; Page 47; 88pp; English.

The invention relates to an antinflammatory compound (especially  
AAW48628-AAW4865), comprising a membrane translocation domain  
(AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15  
amino acid residues, fused to a NEMO binding sequence  
(AAW48525-AAW48619). The antinflammatory compounds have antiasthmatic,  
cyostatic, antiportartic, antirheumatic, antiarthritic, osteopathic,  
antibacterial, immunosuppressive, dermatological, neuroprotective,  
nootropic, antiatherosclerotic, virutide and anti-allergic activity. The  
compounds act as selective inhibitors of cytokine-mediated NFkappaB  
activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
the NEMO binding domain that results in inhibition of IKKbeta kinase  
activation and subsequent decreased phosphorylation of IkappaB. The  
compounds are useful for treating inflammatory disorders, e.g. asthma,  
lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
telangiectasia. The compounds are also useful for treating  
pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
arthritis.

Sequence 6 AA;

Query Match 100.0%; Score 40; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ADMSWL 6  
| | | | |  
1 ADMSWL 6

RESULT 3  
AAW48536  
ID AAW48536 standard; Peptide; 6 AA.

XX  
AC AAM48536;  
XX  
DT 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 39.  
XX  
KW Anti-inflammatory; antiasthmatic; cytosolic; antiproliferative; neurotrophic;  
KW antitumor; antidiabetic; osteoporosis; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US14346.  
XX  
PR 02-MAY-2000; 2000US-201261P.  
XX  
PR 22-AUG-2000; 2000US-0643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
XX  
PA (UYVA ) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Finkelstein MA, Phillips K,  
XX  
DR WPI; 2002-121889/16.  
XX  
PT Novel anti-inflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis -  
XX  
PS Claim 6; Page 61; 88pp; English.  
XX  
XX The invention relates to an anti-inflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain  
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,  
CC cytosolic, antiproliferative, antineoplastic, antidiabetic, osteoporotic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC neurotrophic, antiatherosclerotic, virucide and anti-allergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of IkappaB. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
XX  
SO Sequence 6 AA;  
XX  
Query Match 100.0%; Score 40; DB 23; Length 6;  
Best Local Similarity 100.0%; Pctd. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
1 ADMSWL 6  
|||||

DB 1 ADMSWL 6  
RESULT 4  
AAM48548  
ID AAM48548 standard; Peptide; 6 AA.  
XX  
XX AAM48548;  
XX  
DT 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 51.  
XX  
KW Anti-inflammatory; antiasthmatic; cytosolic; antiproliferative; neurotrophic;  
KW antitumor; antidiabetic; osteoporosis; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US14346.  
XX  
PR 02-MAY-2000; 2000US-201261P.  
XX  
PR 22-AUG-2000; 2000US-0643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
XX  
PA (UYVA ) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Finkelstein MA, Phillips K,  
XX  
DR WPI; 2002-121889/16.  
XX  
PT Novel anti-inflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis -  
XX  
PS Claim 6; Page 62; 88pp; English.  
XX  
XX The invention relates to an anti-inflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain  
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,  
CC cytosolic, antiproliferative, antineoplastic, antidiabetic, osteoporotic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC neurotrophic, antiatherosclerotic, virucide and anti-allergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of IkappaB. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
XX  
SO Sequence 6 AA;  
XX

Query Match 100.0%; Score 40; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ADMSWL 6  
1 ADMSWL 6  
Db 1 ADMSWL 6

RESULT 5  
ABU08420  
ID ABU08420 standard; peptide; 6 AA.

XX AC ABU08420;  
XX DT 12-JUN-2003 (first entry)  
XX XX

DE Human NEMO binding site (NBD) mutant peptide #3.

XX Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;  
XX IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;  
XX nuclear factor-kappaB induction; inflammatory disorder;  
XX autoimmune disease; osteoporosis; cancer; Alzheimer's disease;  
XX atherosclerosis; viral infection; Ataxia telangiectasia;  
XX transplantation detection; immunosuppressive; osteopathic;  
XX transostatic; neutrotropic; antirheumatic; antithrombotic; virucide;  
XX cyostatic; antirheumatic; antithrombotic; mutant; muten.

XX OS Homo sapiens.  
XX OS Synthetic.

XX PN US2002156000-A1.

XX PD 24-OCT-2002.

XX PF 02-MAY-2001; 2001US-0847940.

XX PR 02-MAY-2000; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

XX PA (MAYM/) MAY M J.

XX PA (GHOSH/) GHOSH S.

XX PI May MJ, Ghosh S;

XX DR WPI; 2003-209142/20.

XX PT Novel antiinflammatory peptide compounds comprising NEMO binding  
PT domain, useful for modulating NF-kappaB induction in a cell and for  
PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,  
PT psoriasis, vasculitis -

XX PS Claim 22; Page 17; 47pp; English.

XX CC The present invention relates to antiinflammatory compounds comprising  
CC NEMO binding domain (NBD) peptides. The NEMO binding domains are  
CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha  
CC (IKKalpha) proteins. The antiinflammatory compounds of the invention  
CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction  
CC in a cell, where the compounds are capable of blocking the interaction  
CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The  
CC antiinflammatory compound further comprises at least one membrane  
CC translocation domain. The compounds are useful for treating  
CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,  
CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia  
CC telangiectasia, and for transplantation detection. The compounds of  
CC the invention block NF-kappaB induction by IKK but do not inhibit  
CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human  
CC NBD mutant peptides.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 40; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ADMSWL 6  
1 ADMSWL 6  
Db 1 ADMSWL 6

RESULT 6  
AAM48552  
ID AAM48552 standard; peptide; 7 AA.

XX AC AAM48552;  
XX DT 20-MAR-2002 (first entry)  
XX XX

DE Anti-inflammatory peptide SEQ ID NO 55.

XX Antiinflammatory; antiaesthetic; cytostatic; antiproliferic; neutrotropic;  
XX antithrombotic; antithrombotic; osteopathic; antibacterial; virucide;  
XX immunosuppressive; dermatological; neutrotropic; antithrombotic;  
XX anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
XX cytokine; NF-kappaB; IkappaB kinase-beta; IKKbeta; cancer; psoriasis;  
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX autoimmune disorder; multiple sclerosis; transplant rejection;  
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.

XX PN WO200183554-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US14346.

XX PR 02-MAY-2000; 2000US-201261P.

XX PR 22-AUG-2000; 2000US-0643260.

XX PA (PRAE-) PRAECIS PHARM INC.

XX PA (UYVA ) UNIV YALE.

XX PI May MJ, Ghosh S, Finkel MA, Phillips K;

XX DR WPI; 2002-121889/16.

XX PT Novel antiinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis -

XX PS Claim 6; Page 62; 88pp; English.

XX CC The invention relates to an antiinflammatory compound (especially  
CC AAM48528-AAM48645), comprising a membrane translocation domain  
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
CC cytostatic, antiproliferic, antithrombotic, antithrombotic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neutrotropic,  
CC neutrotropic, antithrombotic, virucide and anti-allergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
CC activation by blocking interaction of IkappaB kinase-beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of IkappaB. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 100.0%; Score 40; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWL 6  
 Db 1 ADMSWL 6

RESULT 7  
 AAM48545 standard; Peptide; 8 AA.  
 XX  
 AC AAM48545;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 48.  
 XX  
 KW Antiinflammatory; antiaesthetic; cytostatic; antiproliferative; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
 CC cytostatic, antiproliferative, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis.

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infection; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 40; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWL 6  
 Db 3 ADMSWL 8

RESULT 8  
 AAM48553 standard; Peptide; 8 AA.  
 XX  
 AC AAM48553;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 56.  
 XX  
 KW Antiinflammatory; antiaesthetic; cytostatic; antiproliferative; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
 CC cytostatic, antiproliferative, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of IkappaB. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
CC  
SQ Sequence 8 AA;  
  
Query Match 100.0%; Score 40; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 ADMSWL 6  
DB 1 ADMSWL 6  
  
RESULT 9  
ID AAM48544 standard; Peptide: 9 AA.  
XX AAM48544;  
XX  
XX 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 47.  
XX  
XX Antinflammatory; antiaesthetic; cytostatic; antipsoriatic; nootropic;  
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX autoimmune disorder; multiple sclerosis; transplant rejection;  
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
OS Synthetic.  
XX  
XX WO200183554-A2.  
XX  
XX 08-NOV-2001.  
XX  
XX 02-MAY-2001; 2001WO-US14346.  
XX  
XX 02-MAY-2000; 2000US-201261P.  
XX 22-AUG-2000; 2000US-0643260.  
XX  
XX (PRAE-) PRAECIS PHARM INC.  
XX (UYVA ) UNIV YALE.  
XX  
XX May MJ, Ghosh S, Findeis MA, Phillips K;  
XX  
XX WPI, 2002-121889/16.  
XX  
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XX domain fused to NEMO binding sequence, useful for blocking nuclear  
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XX psoriasis -  
XX  
XX Claim 6; Page 62; 88pp; English.  
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XX The invention relates to an antinflammatory compound (especially  
XX AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
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CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
CC  
SQ Sequence 9 AA;  
  
Query Match 100.0%; Score 40; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 ADMSWL 6  
DB 1 ADMSWL 6  
  
RESULT 10  
ID AAM48547  
XX AAM48547 standard; Peptide: 9 AA.  
XX  
XX AAM48547;  
XX  
XX 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 50.  
XX  
XX Antinflammatory; antiaesthetic; cytostatic; antipsoriatic; nootropic;  
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX autoimmune disorder; multiple sclerosis; transplant rejection;  
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
OS Synthetic.  
XX  
XX WO200183554-A2.  
XX  
XX 08-NOV-2001.  
XX  
XX 02-MAY-2001; 2001WO-US14346.  
XX  
XX 02-MAY-2000; 2000US-201261P.  
XX 22-AUG-2000; 2000US-0643260.  
XX  
XX (PRAE-) PRAECIS PHARM INC.  
XX (UYVA ) UNIV YALE.  
XX  
XX May MJ, Ghosh S, Findeis MA, Phillips K;  
XX  
XX WPI, 2002-121889/16.  
XX  
XX Novel antinflammatory compound comprising membrane translocation  
XX domain fused to NEMO binding sequence, useful for blocking nuclear  
XX factor kappaB activation, and for treating asthma, lung inflammation,  
XX psoriasis -  
XX



PT psoriasis -

XX Claim 6, Page 62; 88pp; English.

CC The invention relates to an antiinflammatory compound (especially

CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15

CC amino acid residues, fused to a NEMO binding sequence

CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,

CC cytoostatic, antipsoriatic, antirheumatic, antiarthritic, osteoprotic,

CC antibacterial, immunosuppressive, dermatological, neuroprotective,

CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The

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CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at

CC the NEMO binding domain that results in inhibition of IKKbeta kinase

CC activation and subsequent decreased phosphorylation of IkappaB. The

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CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,

CC burstitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,

CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;

CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia

CC telangiectasia. The compounds are also useful for treating

CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and

CC arthritis.

XX Sequence 9 AA;

SQ

Query Match 100.0%; Score 40; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6

DB 1 ADMSWL 6

RESULT 11

AAM48550

ID AAM48550 standard; Peptide; 9 AA.

XX

AC AAM48550;

XX

DT 20-MAR-2002 (first entry)

XX

DE Anti-inflammatory peptide SEQ ID NO 53.

XX

XX Antiinflammatory; antiasthmatic; cytoostatic; antipsoriatic; nootropic;

KM antiinflammatory; antiarthritic; osteoprotic; antibacterial; virucide;

KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;

KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;

KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

KM autoimmune disorder; multiple sclerosis; transplant rejection;

KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;

KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX

OS Synthetic.

XX

PN WO200183554-A2.

XX

PD 08-NOV-2001.

XX

XX 02-MAY-2001; 2001WO-US14346.

XX

XX 02-MAY-2000; 2000US-201261P.

XX

XX 22-AUG-2000; 2000US-0643260.

XX

PA (PRAE-) PRAECTIS PHARM INC.

XX

XX (UYVA ) UNIV YALE.

XX

PI May MJ, Ghosh S, Findels MA, Phillips K;

XX

DR WPI; 2002-121889/16.

XX

PT Novel antiinflammatory compound comprising membrane translocation

PT domain fused to NEMO binding sequence, useful for blocking nuclear

PT factor kappaB activation, and for treating asthma, lung inflammation,

PT psoriasis -

XX

PS Claim 6, Page 62; 88pp; English.

XX

CC The invention relates to an antiinflammatory compound (especially

CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15

CC amino acid residues, fused to a NEMO binding sequence

CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,

CC cytoostatic, antipsoriatic, antirheumatic, antiarthritic, osteoprotic,

CC antibacterial, immunosuppressive, dermatological, neuroprotective,

CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB

CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at

CC the NEMO binding domain that results in inhibition of IKKbeta kinase

CC activation and subsequent decreased phosphorylation of IkappaB. The

CC compounds are useful for treating inflammatory disorders, e.g. asthma,

CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,

CC burstitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,

CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;

CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia

CC telangiectasia. The compounds are also useful for treating

CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and

CC arthritis.

XX Sequence 9 AA;

SQ

Query Match 100.0%; Score 40; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6

DB 3 ADMSWL 8

RESULT 12

AAM48551

ID AAM48551 standard; Peptide; 9 AA.

XX

AC AAM48551;

XX

DT 20-MAR-2002 (first entry)

XX

DE Anti-inflammatory peptide SEQ ID NO 54.

XX

XX Antiinflammatory; antiasthmatic; cytoostatic; antipsoriatic; nootropic;

KM antiinflammatory; antiarthritic; osteoprotic; antibacterial; virucide;

KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;

KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;

KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

KM autoimmune disorder; multiple sclerosis; transplant rejection;

KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;

KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX

OS Synthetic.

XX

PN WO200183554-A2.

XX

PD 08-NOV-2001.

XX

XX 02-MAY-2001; 2001WO-US14346.

XX

XX 02-MAY-2000; 2000US-201261P.

Pt	XX	22-AUG-2000; 2000US-0643260.
Pa	XX	(PRAE-) PRAECTIS PHARM INC.
Pa	XX	(UYTA ) UNIV YALE.
Pt	XX	May MJ, Ghosh S, Findels MA, Phillips K;
Dr	XX	WPI; 2002-121889/16.
Pt	XX	Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation, psoriasis -
Pt	PS	Claim 6; Page 62; 88pp; English.
Cc	XX	The invention relates to an antiinflammatory compound (especially AAM48620-AAM48645), comprising a membrane translocation domain CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cycostatic, antipsoriatic, antirheumatic, antiarthritic, osteoprotic, antibacterial, immunosuppressive, dermatologic, neuroprotective, CC nocotropic, antidiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of Ikappab kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase CC activation and subsequent decreased phosphorylation of Ikappab. These CC compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, CC divertitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia CC telangiectasia. The compounds are also useful for treating CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and CC arthritis.
Cc	XX	Sequence 9 AA;
SQ		
Query Match		100.0%; Score 40; DB 23; Length 9;
Best Local Similarity		100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative		0; Mismatches 0; Indels 0; Gaps 0
Dy		1 ADMSWL 6 
Db		2 ADMSWL 7
RESULT 13		
ID	AAM48546	
AA	AAM48546 standard; Peptide; 10 AA.	
AA	AAM48546;	
DT	20-MAR-2002 (first entry)	
DE	Anti-Inflammatory peptide SEQ ID NO 49.	
KV	Antinflammatory; antiaesthetic; cytosolic; antipsoriatic; nocotropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antidiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; rheumekine; NFkappab; Ikappab kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmunne disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.	
OS	Synthetic.	
PN	WO200183554-A2.	

XX	08-NOV-2001.
PD	
XX	02-MAY-2001; 2001WO-US14346.
PF	
XX	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-0643260.
XX	
PA	(PRAE-) PRACIS PHARM INC.
PA	(DTYA ) UNIV YALE.
PI	May MJ, Ghosh S, Findels MA, Phillips K,
PI	WPI; 2002-121889/16.
DR	
XX	
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis
XX	
PS	Claim 6; Page 62; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AAW48628-AAW48651), comprising a membrane translocation domain
CC	(AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AAW48523-AAW48619). The antiinflammatory compounds have antiasthmatic,
CC	cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	nocotropic, antiatherosclerotic, virocidic and antiangiogenic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of IkappaB. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	burialis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	relangitactasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
XX	
SQ	Sequence 10 AA;
	Query Match 100.0%; Score 40; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 2,5; Mismatches 0; Gaps 0;
	Matches 6; Conservative 0; Indels 0;
QY	1 ADMSWL 6
DB	2 ADMSWL 7
RESULT 14	
AAW48543	
ID	AAW48549 standard; Peptide; 10 AA.
XX	
XX	AAW48549;
XX	
XX	20-MAR-2002 (first entry)
DT	
XX	
DE	Anti-inflammatory peptide SEQ ID NO 52.
XX	
KW	Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nocotropic;
KW	antiinflammatory; antiarthritic; osteopathic; antibacterial; virocidic;
KW	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW	antiangiogenic; membrane translocation domain; NEMO binding domain; eczema;
KW	cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW	autoimmune disorders; multiple sclerosis; transplant rejection;

KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX Synthetic.  
 OS  
 XX WO200183554-A2.  
 PN  
 PD 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 PF  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
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 PA (UYVA ) UNIV YALE.  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
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 PT psoriasis -  
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 CC  
 SQ Sequence 10 AA;  
 XX  
 XX  
 Query Match 100.0%; Score 40; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.5; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0;  
 QY 1 ADMSWL 6  
 |||||  
 DB 3 ADMSWL 8  
 XX  
 RESULT 15  
 AA48543  
 ID AA48543 standard; Peptide; 11 AA.  
 XX  
 AC AA48543;  
 XX  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX Anti-inflammatory peptide SEQ ID NO 46.  
 DE  
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;  
 KM

KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 PF  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 DR WPI; 2002-121889/16.  
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 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 SQ Sequence 11 AA;  
 XX  
 XX  
 Query Match 100.0%; Score 40; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.7; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0;  
 QY 1 ADMSWL 6  
 |||||  
 DB 3 ADMSWL 8  
 XX

Search completed: February 18, 2004, 14:26:18  
 Job time : 22.7763 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 16.5769 Seconds  
(without alignments)  
79.423 Million cell updates/sec

Title: US-09-643-260-19  
Perfect score: 148  
Sequence: 1 DRQIKIFQNRBMKMKKTALDASALQTE 28

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	103	69.6	224 1 HXB6_HUMAN	P17509 homo sapien
2	103	69.6	224 1 HXB6_MOUSE	P09023 mus musculu
3	100	67.6	105 1 HXAY_RAT	P09634 rattus norv
4	100	67.6	229 1 HXAY_MOUSE	P02830 mus musculu
5	99	66.9	75 1 HXSA_SALSA	P09636 galus gall
6	98	66.2	84 1 HXB6_CHICK	P14839 gallus gall
7	96.5	65.2	96 1 HXCG_BRARE	P15862 brachydantio
8	96	64.9	208 1 HXAY_HERTR	Q91825 heterodontu
9	96	64.9	234 1 HXCG_XENTLA	P09925 xenopus lae
10	95	64.2	153 1 HXCG_SHEEP	P1268 homo sapien
11	95	64.2	230 1 HXAY_HUMAN	P09019 xenopus lae
12	95	64.2	230 1 HXB5_XENTLA	P14858 notophthalm
13	95	64.2	234 1 HXCG_NOTVI	P09630 homo sapien
14	95	64.2	235 1 HXCG_HUMAN	P10629 mus musculu
15	95	64.2	242 1 HXAY_MOUSE	P24061 coturnix co
16	95	64.2	242 1 HXAY_COTJA	P09013 brachydantio
17	94.5	63.9	81 1 HXB5_BRARE	P09067 homo sapien
18	94.5	63.9	269 1 HXB5_HUMAN	P09079 mus musculu
19	94.5	63.9	269 1 HXB5_MOUSE	P09012 brachydantio
20	94.5	63.9	275 1 HXB5_BRARE	P09012 brachydantio
21	94	63.5	48 1 HXB6_XENTLA	P12636 xenopus lae
22	94	63.5	49 1 HXAS_SHEEP	Q28609 ovis aries
23	94	63.5	71 1 HXAY_SHEEP	Q28609 ovis aries
24	94	63.5	71 1 HXCS_NOTVI	P1262 notophthalm
25	94	63.5	71 1 HX90_APTME	P15860 apis mellif
26	94	63.5	76 1 HXCG_RAT	P18865 rattus norv
27	94	63.5	78 1 HXAS_SALSA	P09637 galus gall
28	94	63.5	80 1 HXAY_LINSA	P09112 linus sang
29	94	63.5	82 1 HXB5_CHICK	P14839 gallus gall
30	94	63.5	86 1 SCR_APTME	P15865 apis mellif
31	94	63.5	87 1 HXCS_XENTLA	P09020 xenopus lae
32	94	63.5	93 1 HXB6_PIG	P09078 sus scrofa
33	94	63.5	105 1 HXB4_BRARE	P22574 brachydantio

34	94	63.5	112 1 HXB7_RAT	P18864 rattus norv
35	94	63.5	148 1 HXAS_LAMBME	P50208 ambystoma m
36	94	63.5	209 1 HXAY_XENTLA	P09071 xenopus lae
37	94	63.5	217 1 HXB7_BOVIN	Q91838 bos taurus
38	94	63.5	217 1 HXB7_HUMAN	P09629 homo sapien
39	94	63.5	217 1 HXB7_MOUSE	P09024 mus musculu
40	94	63.5	220 1 HX7A_XENTLA	Q91771 xenopus lae
41	94	63.5	220 1 HXB7_XENTLA	P04476 xenopus lae
42	94	63.5	222 1 HXCS_HUMAN	Q00444 homo sapien
43	94	63.5	222 1 HXCS_MOUSE	P32043 mus musculu
44	94	63.5	225 1 HXAY_MORSA	Q9pw44 morone saxa
45	94	63.5	228 1 HXB6_BRARE	P15861 brachydantio

## ALIGNMENTS

RESULT 1  
ID HXB6\_HUMAN STANDARD; PRT; 224 AA.  
AC P17509; P09068; Q9HB11; Q9UGH2;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Homeobox protein Hox-B6 (Hox-2b) (Hox-2.2) (HU-2).  
GN HOXB6 OR HOXB2B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OC NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RC TISSUE=Placenta;  
RX MEDLINE=91187672; PubMed=1672751;  
RA Shen W.-F., Delmer K., Simonitch-Eason T.A., Lawrence H.J.,  
LA Laryman C.;  
RT "Alternative splicing of the HOX 2.2 homeobox gene in human  
hematopoietic cells and murine embryonic and adult tissues.";  
RL Nucleic Acids Res. 19:539-545(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Frezza D., D'Esposito M., Migliaccio E., Santini S.M., Fruscalzo A.;  
RT "Expression of HOX genes in T lymphocytes and hairy leukemia cell  
lines.";  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Kidd K.R., Bueygina V., Demille M.M.C., Speed W.C., Ruggieri V.,  
RT "Overall linkage disequilibrium in 33 populations for highly  
informative multistate haplotypes spanning the HOXB gene cluster.";  
RL Am. J. Hum. Genet. 67:235-235(2000).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschuler S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshynski S., Carninci P., Prange C.,  
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,  
RA Bobak S., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley R.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalleg D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.;

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RT      "Generation and initial analysis of more than 15,000 full-length
RT      human and mouse cDNA sequences."
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [5]
RP      SEQUENCE OF 135-224 FROM N.A.
RX      MEDLINE=90046832; PubMed=2570364;
RA      Shen W.-F., Larygan C., Lowrey P., Corral J.C., Detmer K.,
RA      Hauser C.A., Simiontch T.A., Hack F.M., Lawrence H.J.;
RT      "lineage-restricted expression of homeobox-containing genes in human
RT      hematopoietic cell lines."
RL      Proc. Natl. Acad. Sci. U.S.A. 86:8536-8540(1989).
RN      [6]
RP      PRELIMINARY SEQUENCE OF 136-240 FROM N.A.
RX      MEDLINE=85024858; PubMed=6091895;
RA      Levine M., Rubin G.M., Tjian R.;
RT      "Human DNA sequences homologous to a protein coding region conserved
RT      between homeotic genes of Drosophila."
RL      Cell 38:667-673(1984).
CC      -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC      A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC      SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC      -1- SUBCELLULAR LOCATION: Nuclear.
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=1;
CC      IsoId=p17509-1; Sequence=Displayed;
CC      Name=2; Synonyms=Homeobox-less;
CC      IsoId=p17509-2; Sequence=VSP_002389;
CC      -1- SIMILARITY: BELONGS TO THE ANTF HOMEOBOX FAMILY.
-----
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DR      EMBL, X58431; CAA41335.1; -.
DR      EMBL, X58431; CAA41336.1; -.
DR      EMBL, AF270993; CAB65909.1; -.
DR      GO, GO:0008595; P:determination of anterior/posterior axis, e...; NAS.
DR      EMBL, BC014651; AAH14651.1; -.
DR      EMBL, M30597; AAA36004.1; -.
DR      EMBL, K02571; -, NOT_ANNOTATED_CDS.
DR      PIR, S26400; S26400.
DR      HSSP, P02833; IHOM.
DR      TRANSFAC, T01732; -.
DR      Genew; HGNC:5117; HOXB6.
MIM, 142961; .
DR      GO, GO:0005634; C:nucleus; NAS.
DR      GO, GO:0003700; F:transcription factor activity; NAS.
DR      GO, GO:0008595; P:determination of anterior/posterior axis, e...; NAS.
DR      InterPro, IPR001827; Antennapedia.
DR      InterPro, IPR001356; Homeobox.
DR      Pfam, PF00046; homeobox; 1.
DR      PRINTS, PR00025; ANTENNAPEEDIA.
DR      PRINTS, PR00024; HOMEBOX.
DR      ProDom, PD000010; Homeobox; 1.
DR      SMART, SMO0389; HOX; 1.
DR      PROSITE, PS00032; ANTENNAPEDIA; 1.
DR      PROSITE, PS00027; HOMEBOX_2; 1.
DR      PROSITE, PS50071; HOMEBOX_2; 1.
KW      Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW      Transcription regulation; Alternative splicing.
FT      SITE          127       132
FT      DNA_BIND     146       205    HOMEBOX.
FT      DOMAIN      216       220    POLY_GLU.
FT      VASNPPLIC   140       140
FT                                     S -> E (in isoform 2).
FT                                     /FTID=VSP_002389.
FT      VASNPPLIC   141       224
FT                                     Missing (in isoform 2).
FT                                     /FTID=VSP_002389.

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FT CONFLICT      24      25      HV -> OL (IN REF. 3 AND 4).
PT CONFLICT      60      60      P -> R (IN REF. 1).
FT CONFLICT      73      73      D -> A (IN REF. 1).
PT CONFLICT      149     150      GR -> A (IN REF. 1).
SQ SEQUENCE      224 AA; 25427 MW; D8F6AFAFC893D878 CRC64;

Query March
Best Local Similarity 69.64; Score 103; DB 1; Length 224;
Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Db          187 EROIKIWFONRBMKWKESKILSOLSAE 216
           :|||||:|||||:|||||:|||||:|||||:
QY         1 DRQIKWIFONRRMKKKXTA--LDASALQTE 28
           :|||||:|||||:|||||:|||||:|||||:
DB         187 EROIKIWFONRBMKWKESKILSOLSAE 216


RESULT 2
HXB6 MOUSE STANDARD; PRG; 224 AA.
ID HXB6_MOUSE PO9023;
AC 01-NOV-1988 (Rel. 09, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 26-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B6 (Hox-2.2) (MH-22A).
GN HOXB6 OR HOXB-6 OR Hox-2.2.
OS Mus musculus (Mouse).
OC Mammalia; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090; [1]
RN RP SEQUENCE FROM N.A.
RA MEDLINE=88289762; PubMed=2898993;
RA Schughart K., Utset M.F., Awgulewitsch A., Ruddie F.H.;
RT "Structure and expression of Hox-2.2, a murine homeobox-containing gene";
RL Proc. Natl. Acad. Sci. U.S.A. 85:5582-5586(1988).
[2]
RN RP SEQUENCE FROM N.A.
RA MEDLINE=91187672; PubMed=1672751;
RA Shen W.F., Detmer K., Simionitch-Eason T.A., Lawrence H.J.,
RA Laryman C.;
RT "Alternative splicing of the HOX 2.2 homeobox gene in human hematopoietic cells and murine embryonic and adult tissues.";
RL Nucleic Acids Res. 19:539-545(1991).
[3]
RN RP SEQUENCE OF 144-224 FROM N.A.
RA MEDLINE=88054465; PubMed=2890503;
RA Lonai P., Arman B., Czernsek H., Ruddie F.H., Blatt C.;
RT "New murine homeoboxes: structure, chromosomal assignment, and differential expression in adult erythropoiesis.";
RL DNA 6:409-418(1987).
[4]
RN RP SEQUENCE OF 140-224 FROM N.A.
RA MEDLINE=88085193; PubMed=2891608;
RA Hart C.P., Painoso A., Ruddie F.H.;
RT "Sequence analysis of the murine Hox-2.2, -2.3, and -2.4 homeo boxes: evolutionary and structural comparisons.";
RL Genomics 1:182-195(1987).
CC CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC CC -1- SUBCELLULAR LOCATION: Nuclear.
CC CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/announcements or send an email to license@ebi.ac.uk).
DR EMBL; M18166; AAA37844.1; -.

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DR EMBL; X56459; CAA39834.1; ALT-SEQ.  
 DR EMBL; M18401; AAC27130.1; ALT-SEQ.  
 DR EMBL; J03782; AAA37843.1; ALT-SEQ.  
 DR PIR; A31324; A31324.  
 DR HSSP; P02833; IHOM.  
 DR TRANSFAC; T01733; -.  
 DR MGD; MGI:96187; Hoxb6.  
 DR InterPro; IPR001827; Antennapedia.  
 DR InterPro; IPR00156; Homeobox.  
 DR Pfam; PF00046; Homeobox.1.  
 DR PRINTS; PR00025; ANTENNAPEDIA.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR ProDom; PD00010; Homeobox.1.  
 DR SMART; SM00389; HOX.1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.  
 DR PROSITE; PS50071; HOMEBOX\_2; 1.  
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 KW Transcription regulation.  
 FT SITE 127 132 ANT-PTYPE HEXAPEPTIDE.  
 FT DNA\_BIND 146 205 HOMEBOX.  
 FT DOMAIN 216 220 POLY-GLU.  
 FT CONFLICT 186 186 T -> P (IN REF. 3).  
 SQ SEQUENCE 224 AA; 25310 MW; B8FC0BDEB57F5C3D CRC64;

Query Match 69.6%; Score 103; DB 1; Length 224;  
 Best Local Similarity 70.0%; Pred. No. 1.2e-08;  
 Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

OY 1 DROIKIFQNRNRMKKTALDASALQTE 28  
 DB 187 ERQIKIFQNRNRMKKTSLASQLSAE 216

RESULT 3  
 HXAT RAT STANDARD; PRT; 105 AA.  
 ID HXAT RAT  
 AC P09634;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Homeobox protein Hox-A7 (Hox-1.1) (R5) (Fragment).  
 GN HOXA7 OR HOXA-7.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=87277429; PubMed=2886401;  
 RA Falzon M., Sanderson N., Chung S.Y.;  
 RT "Cloning and expression of rat homeo-box-containing sequences";  
 RL Gene 54:23-32(1987).  
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
 A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
 SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.  
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 CC -----  
 CC EMBL; M16807; -, NOT\_ANNOTATED\_CDS.  
 DR PIR; A27471; A27471.  
 DR HSSP; P02833; NANT.  
 DR TRANSFAC; T01707; -.  
 DR InterPro; IPR001827; Antennapedia.

DR InterPro; IPR001356; Homeobox.  
 DR Pfam; PF00046; Homeobox.1.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR ProDom; PD00010; Homeobox.1.  
 DR SMART; SM00389; HOX.1.  
 DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS50071; HOMEBOX\_2; 1.  
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 KW Transcription regulation.  
 FT NON\_TER 1 1  
 FT DNA\_BIND 5 64 HOMEBOX.  
 FT DOMAIN 91 105 GLU-RICH (ACIDIC).  
 SQ SEQUENCE 105 AA; 12552 MW; 106C1DF93BF2864B CRC64;

Query Match 67.6%; Score 100; DB 1; Length 105;  
 Best Local Similarity 70.4%; Pred. No. 1.5e-08;  
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 DROIKIFQNRNRMKKTALDASALQTE 27  
 DB 46 ERQIKIFQNRNRMKKTSLASQLSAE 72

RESULT 4  
 HXAT MOUSE STANDARD; PRT; 229 AA.  
 ID HXAT MOUSE  
 AC P02830;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Homeobox protein Hox-A7 (Hox-1.1) (M6-12) (M6).  
 GN HOXA7 OR HOXA-7 OR HOX-1.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=87260976; PubMed=2885847;  
 RA Kessel M., Schulze F., Fibi M., Gruss P.;  
 RT "Primary structure and nuclear localization of a murine homeodomain  
 RT protein";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5306-5310(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=95197009; PubMed=7890170;  
 RA Parikh H., Shah S., Hilt D., Peterkofsky A.;  
 RT "Organization, sequence and regulation of expression of the murine  
 RT Hoxa-7 gene";  
 RL Gene 154:237-242(1995).  
 RN [3]  
 RP SEQUENCE OF 126-229 FROM N.A.  
 RC MEDLINE=85188311; PubMed=2986010;  
 RA Colberg-Poley A.M., Voss S.D., Chowdhury K., Gruss P.;  
 RT "Structural analysis of murine genes containing homeo box sequences  
 RT and their expression in embryonal carcinoma cells";  
 RL Nature 314:713-718(1985).  
 RN [4]  
 RP SEQUENCE OF 129-197 FROM N.A.  
 RC MEDLINE=87053860; PubMed=2877873;  
 RA Brieler G., Bucan M., Francke U., Colberg-Poley A.M., Gruss P.;  
 RT "Sequential expression of murine homeo box genes during F9 EC cell  
 RT differentiation";  
 RL EMBO J. 5:2209-2215(1986).  
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
 A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
 SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.  
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DR EMBL; M17192; AAA37833.1; -  
 DR PIR; A03314; AAC52160.1; -  
 DR PIR; A28329; A28329.  
 DR HSSP; P02833; 9ANT.  
 DR TRANSFAC; T01278; -  
 DR MGD; MGI:96179; Hoxa7.  
 DR InterPro; IPR001827; Antennapedia.  
 DR InterPro; IPR001356; Homeobox.  
 DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR00025; ANTENNAPEDIA.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR ProDom; PD00010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.  
 DR PROSITE; PS00027; HOMEBOX 1; 1.  
 DR PROSITE; PS00071; HOMEBOX 2; 1.  
 KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 KW transcription regulation.  
 FT SITE 118 123 ANTP-TYPE HEXAPEPTIDE.  
 FT DNA\_BIND 129 188 HOMEBOX.  
 FT DOMAIN 156 159 POLY-ARG.  
 FT DOMAIN 211 229 ASP/GLU-RICH (HIGHLY ACIDIC).  
 FT DOMAIN 215 229 POLY-GLU.  
 FT CONFLICT 43 45 GAG -> APA (IN REF. 1).  
 SQ SEQUENCE 229 AA; 25682 MW; D36E6BD61D8D5C6F CRC64;

Query Match 67.6%; Score 100; DB 1; Length 229;  
 Best Local Similarity 70.4%; Pred. No. 3.5e-08;  
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DROIKIWPQNRKMKKKTALDASALQT 27  
 Db 170 EROIKIWPQNRKMKKKTALDASALQT 196

RESULT 5  
 HNSA\_SALSA STANDARD; PRT; 75 AA.

AC P03636;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Homeobox protein S12-A (Fragment).  
 OS Salmo salar (Atlantic salmon).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostomi;  
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
 OC NCBI\_TaxID=8030;  
 RN NCBI\_TaxID=8030;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88226009; PubMed=2897318;  
 RA Fjose A., Mjølven A., Eiken H.G.;  
 RT "Molecular cloning and characterization of homeo-box-containing genes  
 RT from Atlantic salmon."  
 RL Gene 62:141-152(1988).  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).  
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.  
 CC -----  
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CC -----  
 DR EMBL; M18903; AAA49559.1; -  
 DR PIR; I51341; I51341.  
 DR HSSP; P02833; 9ANT.  
 DR InterPro; IPR001356; Homeobox.  
 DR Pfam; PF00046; homeobox; 1.  
 DR ProDom; PD00010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX 1; 1.  
 DR PROSITE; PS00071; HOMEBOX 2; 1.  
 KM Homeobox; DNA-binding; Developmental protein; Nuclear protein.  
 FT NON\_TER 1 1  
 FT DNA\_BIND 1 60 HOMEBOX.  
 FT NON\_TER 75 75  
 SQ SEQUENCE 75 AA; 9330 MW; FC02C3672F35475D CRC64;

Query Match 66.9%; Score 99; DB 1; Length 75;  
 Best Local Similarity 75.0%; Pred. No. 1.5e-08;  
 Matches 18; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DROIKIWPQNRKMKKKTALDASA 24  
 Db 42 EROIKIWPQNRKMKKKTALDASA 65

RESULT 6  
 HXB6 CHICK STANDARD; PRT; 84 AA.

AC P14839;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Homeobox protein Hox-B6 (HOX-2.2) (Fragment).  
 GN HOXB6 OR HOX-2.2.  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 CC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN NCBI\_TaxID=9031;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Erythrocyte;  
 RX MEDLINE=90126373; PubMed=2575515;  
 RA Wedden S.E., Pang K., Sichele G.;  
 RT "Expression pattern of homeobox-containing genes during chick  
 RT embryogenesis."  
 RL Development 105:639-650(1989).  
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.  
 CC -----  
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AC P02832;  
 DT 21-JUN-1986 (Rel. 01, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Homeobox protein Hox-C6 (XlHbox-1) (AC1).  
 GN HOXC6 OR XlHBOX1.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodidae; Xenopus.  
 NCBI\_TaxID=8355;  
 RX MEDLINE=88157707; PubMed=2894634;  
 RA Fritze A., de Robertis E.M.; Gehring W.J., de Robertis E.M.;  
 RT "Xenopus homeobox-containing cDNAs expressed in early development.";  
 RN Nucleic Acids Res. 16:1453-1469(1988).  
 RP MEDLINE=84205675; PubMed=6327066;  
 RX Carrascano A.E., McGinnis W., Gehring W.J., de Robertis E.M.;  
 RT "Cloning of an X. laevis gene expressed during early embryogenesis  
 RT coding for a peptide region homologous to Drosophila homeotic  
 RT genes.";  
 RN Cell 37:409-414(1984).  
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED EXCLUSIVELY IN EARLY XENOPUS  
 CC EMBRYOS.  
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.  
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 CC -----  
 DR EMBL: X12499; CAA31020.1; ALT\_INIT.  
 DR EMBL: X12500; CAA31021.1; -.  
 DR EMBL: K01943; AAA49743.1; -.  
 DR EMBL: X07101; CAA30122.1; -.  
 DR PIR: S00992; S00992.  
 DR HSP: P02833; 9ANT.  
 DR TRANSFAC: T01746; -.  
 DR InterPro: IPR001827; Antennapedia.  
 DR InterPro: IPR001356; Homeobox.  
 DR Pfam: PF00046; homeobox.1.  
 DR PRINTS: PR00025; ANTENNAPEIDIA.  
 DR PRINTS: PR00024; HOMEOBOX.  
 DR ProDom: PD000010; Homeobox.1.  
 DR SMART: SM00389; HOX.1.  
 DR PROSITE: PS00027; HOMEOBOX\_1; 1.  
 DR PROSITE: PS00032; ANTENNAPEIDIA; 1.  
 DR PROSITE: PS50071; HOMEOBOX\_2; 1.  
 DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 DR Transcription regulation.  
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 KM Transcription regulation.  
 FT CHAIN 1 234 HOMEOBOX PROTEIN HOX-C6 PRII.  
 FT SITE 83 234 HOMEOBOX PROTEIN HOX-C6 PRI.  
 FT SITE 122 127 ANTP-TYPE HEXAPEPTIDE.

FT DNA\_BIND 141 200 HOMEOBOX.  
 FT VARIANT 139 139 T -> S.  
 SQ SEQUENCE 234 AA; 26689 MW; 4C371CC5252D2C58 CRC64;  
 Query Match 64.9%; Score 96; DB 1; Length 234;  
 Best Local Similarity 72.0%; Pred. No. 1.5e-07;  
 Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 DRQIKWFONRMRKMKKTALDASAL 25  
 Db 182 ERQIKWFONRMRKMKKESNLSTL 206  
 RESULT 10  
 HXC6 SHEEP  
 ID HXC6 SHEEP STANDARD; PRT; 153 AA.  
 AC P49925;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Homeobox protein Hox-C6.  
 GN HOXC6.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Cooby N.C., Hernandez-Ledezma J., Mathialagan N., Roberts R.;  
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.  
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 CC -----  
 DR EMBL: U33049; AAA75473.1; -.  
 DR HSP: P02833; 9ANT.  
 DR InterPro: IPR001827; Antennapedia.  
 DR InterPro: IPR001356; Homeobox.  
 DR Pfam: PF00046; homeobox.1.  
 DR PRINTS: PR00025; ANTENNAPEIDIA.  
 DR PRINTS: PR00024; HOMEOBOX.  
 DR ProDom: PD000010; Homeobox.1.  
 DR SMART: SM00389; HOX.1.  
 DR PROSITE: PS00027; HOMEOBOX\_1; 1.  
 DR PROSITE: PS00032; ANTENNAPEIDIA; 1.  
 DR PROSITE: PS50071; HOMEOBOX\_2; 1.  
 DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 DR Transcription regulation.  
 KW Transcription regulation.  
 FT SITE 40 45 ANTP-TYPE HEXAPEPTIDE.  
 FT DNA\_BIND 59 118 HOMEOBOX.  
 FT DOMAIN 86 89 POLY-ARG.  
 FT DOMAIN 126 130 POLY-GLY.  
 FT DOMAIN 139 153 GLU/LYS-RICH.  
 SQ SEQUENCE 153 AA; 17804 MW; 291E24399159621E CRC64;  
 Query Match 64.2%; Score 95; DB 1; Length 153;  
 Best Local Similarity 72.0%; Pred. No. 1.3e-07;  
 Matches 16; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 Qy 1 DRQIKWFONRMRKMKKTALDASAL 25  
 Db 100 ERQIKWFONRMRKMKKESNLSTL 124

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RESULT 11
ID HXAX7 HUMAN STANDARD; PRT: 230 AA.
AC P1258: O43368; O43486; O95655; O9NSC8; Q9UDM1;
DT 01-JUN-1993 (Rel. 26, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A7 (Hox-1A) (Hox 1.1).
GN HOXA7 OR HOXA1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RL MEDLINE=99023755; PubMed=9804983;
RA Milhieton M.A., Brenner P.S., McMullin M.F., Maxwell A.P.,
RA Winter P.C., Lappin T.R.,
RT "Sequence characterisation and expression of homeobox HOX A7 in the
RT multi-potential erythrocytic cell line TF-1."
RL Biochim. Biophys. Acta 1442:329-333(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Bradshaw H., Hinde K., Keppler D.,
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RL MEDLINE=20369265; PubMed=10911612;
RA Kim M.H., Jin H., Seol E.Y., Yoo M., Park H.W.;
RT "Sequence analysis and tissue specific expression of human HOXA7."
RL Mol. Biotechnol. 14:19-24(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC Tissue=Placenta;
RA Albrecht R., Wewer U.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 1-91 FROM N.A.
RA Cho M., Kim M.H., Hwang C.Y., Min W.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 130-195 FROM N.A.
RL MEDLINE=90215255; PubMed=2576652;
RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,
RA Gaudino G., Stornaiuolo A., Cafiero M., Falletta A., Simeone A.;
RT "Organization of human class I homeobox genes."
RL Genome 31:745-756(1989).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC -----
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CC -----
CC EMBL; AF026397; AAB94604.1; -
CC EMBL; AJ005814; CA006713.1; -
CC EMBL; AC004080; -; NOT ANNOTATED_CDS.
CC EMBL; AF032095; AAD01939.2; -
CC EMBL; U92543; AAD00727.1; -
CC EMBL; X84803; CA59270.1; -

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DR EMBL; X84804; CA59270.1; JOINED.
DR PIR; S15536; S15536.
DR HSSP; P02833; NANT.
DR TRANSFAC; T01705; -.
DR Genew; HGNC:5108; HOXA7.
DR MIM; 142950; -.
DR GO; GO:0003700; F:transcription factor activity, TAS.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEOBOX.
DR ProDom; PD00010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00027; HOMEOBOX 1; 1.
DR PROSITE; PS50071; HOMEOBOX 2; 1.
KW Homeobox, DNA-binding, Developmental protein, Nuclear protein;
KW Transcription regulation.
FT SITE 119 124 ANTP-TYPE HEXAPEPTIDE.
FT DNA BIND 130 189 HOMEOBOX.
FT DOMAIN 157 160 POLY-ARG.
FT DOMAIN 196 199 POLY-ALA.
FT DOMAIN 214 230 ASP/GLU-RICH (HIGHLY ACIDIC).
FT DOMAIN 223 230 POLY-GLU.
FT CONFLICT 18 18 T -> A (IN REF. 3).
FT CONFLICT 75 76 DA -> RR (IN REF. 6).
FT CONFLICT 78 78 MISSING (IN REF. 5).
FT CONFLICT 174 174 I -> V (IN REF. 4).
FT CONFLICT 194 195 FT -> RL (IN REF. 5).
FT CONFLICT 195 195 T -> I (IN REF. 7).
FT CONFLICT 222 222 D -> Y (IN REF. 5).
SQ SEQUENCE 230 AA; 25385 MW; 6E2F1991F1BBED21 CRC64;

Query Match 64.2%; Score 95; DB 1; Length 230;
Best Local Similarity 81.0%; Pred. No. 2.1e-07;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DRQIKWPNRRMKWKCTALD 21
Db 171 ERQIKWPNRRMKWKCKEHD 191

RESULT 12
ID HXBS XENLA STANDARD; PRT: 230 AA.
AC P09019;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B5 (Xlhb-4) (Hox-1B) (Fragment).
GN HOXB5 OR XLHBX4.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RL MEDLINE=88157707; PubMed=2894634;
RA Fritz A., de Robertis E.M.;
RT "Xenopus homeobox-containing cDNAs expressed in early development."
RL Nucleic Acids Res. 16:1453-1469(1988).
RN [2]
RP SEQUENCE OF 155-214 FROM N.A.
RL MEDLINE=86274626; PubMed=3015593;
RA Harvey R.P., Tabin C.J., Melton D.A.;
RT "Embryonic expression and nuclear localization of Xenopus homeobox
RT (Xho) gene products."
RL EMBO J. 5:1237-1244(1986).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.

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CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DEVELOPMENTAL STAGE: EMBRYO.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
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DR EMBL; X07104; CA30125.1; -.
DR EMBL; M26883; AAA49755.1; -.
DR PIR; S00592; S00592.
DR HSSP; P02833; 1SAN.
DR TRANSPAC; T03764; -.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEOBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEOBOX_1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS50071; HOMEOBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON TER 1 1 ANTP-TYPE HEXAPEPTIDE.
FT SITE 137 142
FT DNA_BIND 155 214 HOMEOBOX.
SQ SEQUENCE 230 AA; 25276 MW; AD040C030F85532B CRC64;

Query Match 64.2%; Score 95; DB 1; Length 230;
Best Local Similarity 58.8%; Pred. No. 2.1e-07;
Matches 20; Conservative 2; Mismatches 4; Indels 8; Gaps 1;

Qy 1 DROIKIWFQNRMRMKWKK-----TALDASALQ 26
Db 196 ERQIKIWFQNRMRMKWKKDKSLKSMELATGSSAFQ 229

RESULT 13
HXCG NOTVI STANDARD; PRT; 234 AA.
AC P14858; P14857;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C6 (NvHox-1) (FH-2).
GN HOXC6 OR NVHox1.
OS Homophthalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroides; Salamandridae;
OC Notophthalmus.
OX NCBI_TaxID=8136;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89210814; PubMed=2907476;
RA Gavaud P., Gates P.B., Brookes J.P.;
RT "Position dependent expression of a homeobox gene transcript in
RT relation to amphibian limb regeneration.";
RL EMBO J. 7:4275-4282(1988).
RN [2]
RP SEQUENCE OF 131-234 FROM N.A.
RX MEDLINE=90091821; PubMed=2574663;
RA Tabin C.J.;
RT "Isolation of potential vertebrate limb-identity genes.";
RT Development 105:813-820(1989).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.

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CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
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DR EMBL; X13957; CA32139.1; -.
DR EMBL; X16848; CA34745.1; -.
DR PIR; S02014; S02014.
DR HSSP; P02833; 9ANT.
DR TRANSPAC; T01747; -.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PRINTS; PR00024; HOMEOBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEOBOX_1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS50071; HOMEOBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT SITE 122 127 ANTP-TYPE HEXAPEPTIDE.
FT DNA_BIND 141 200 HOMEOBOX.
SQ SEQUENCE 234 AA; 26901 MW; EA15EBD91ED294B0 CRC64;

Query Match 64.2%; Score 95; DB 1; Length 234;
Best Local Similarity 72.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DROIKIWFQNRMRMKWKKTALDASAL 25
Db 182 ERQIKIWFQNRMRMKKESNLTSTL 206

RESULT 14
HXCG HUMAN STANDARD; PRT; 235 AA.
AC P09630;
DT 01-MAR-1989 (Rel. 10, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C6 (Hox-3C) (HHO.C8) (CP25).
GN HOXC6 OR HOX3C.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=87260899; PubMed=2885844;
RA Simeone A., Mavilio F., Acampora D., Giampaolo A., Faiella A.;
RA Zappavigna V., D'Esposito M., Panese M., Russo G., Boncinelli E.,
RA Peschle C.;
RT "Two human homeobox genes, c1 and c8: structure analysis and
RT expression in embryonic development.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4914-4918(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=88262550; PubMed=2898768;
RA Simeone A., Panese M., Acampora D., D'Esposito M., Boncinelli E.;
RT "At least three human homeoboxes on chromosome 12 belong to the same
RT transcription unit.";
RL Nucleic Acids Res. 16:5379-5390(1988).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=97024425; PubMed=8870653;

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RA Charlot A., Castronovo V., Le P., Gillet C., Sobel M.E., Gtellen J.;  
 RT "Cloning and expression of a new HOXC6 transcript encoding a  
 RT repressing protein.";  
 RL Blochem. J. 319:91-97(1996).  
 RN (4)  
 RN SEQUENCE OF 141-206 FROM N.A.  
 RX MEDLINE=90215256; PubMed=2576652;  
 RA Bocciaelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,  
 RA Gaudino G., Stornaiuolo A., Cafiero M., Falella A., Simone A.;  
 RT "Organization of human class I homeobox genes.";  
 RL Genome 31:745-756(1989).  
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=P09630-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=P09630-2; Sequence=VSP\_002392;  
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.  
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 CC -----  
 DR EMBL; S82986; AAB46892.1; -;  
 DR EMBL; M16938; AAA36007.1; -;  
 DR PIR; B28030; W0H33C.  
 DR HSSP; P02833; 9ANT.  
 DR TRANSPAC; T01742; -;  
 DR GeneW; HGNC:5128; HOXC6.  
 DR MIM; 142972; -;  
 DR GO; GO:0003714; P:transcription co-repressor activity; TAS.  
 DR GO; GO:0007275; P:development; TAS.  
 DR GO; GO:0006357; P:regulation of transcription from Pol II pro. .; TAS.  
 DR InterPro; IPR001827; Antennapedia.  
 DR Pfam; PF00046; Homeobox; 1.  
 DR PRINTS; PR00025; ANTENNAPEDIA.  
 DR PRODOM; PD00010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX 1; 1.  
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.  
 DR PROSITE; PS00071; HOMEBOX 2; 1.  
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 KW Transcription regulation; Alternative splicing.  
 FT SITE 122 127 ANTP-TYPE HEXAPEPTIDE.  
 FT DNA\_BIND 141 200 HOMEBOX.  
 FT DOMAIN 168 171 POLY-ARG.  
 FT DOMAIN 208 212 POLY-GLY.  
 FT DOMAIN 221 235 GLU/LYS-RICH.  
 FT VASAPLIC 1 82 Missing (in isoform 2).  
 FT CONFLICT 218 218 M -> L (in REF. 3).  
 SQ SEQUENCE 235 AA; 26933 MW; BD68870347CB71C0 CRC64;  
 Query March 64.2%; Score 95; DB 1; Length 235;  
 Best Local Similarity 72.0%; Pred. No. 2.1e-07;  
 Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

HCX6\_MOUSE  
 ID HCX6\_MOUSE STANDARD; PRT; 235 AA.  
 AC P10629; 061683;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 21-JUL-1993 (Rel. 26, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Homeobox protein Hox-C6 (Hox-3.3) (Hox-6.1).  
 GN HCX6 OR HOXC-6 OR HOX-3.3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94131843; PubMed=7905473;  
 RA Shmied S.M., Gaunt S.J., Coletta P.L., Gaeda A.M., Sharpe P.T.;  
 RT "Spatial localisation of transcripts of the Hox-C6 gene.";  
 RL J. Anat. 183:515-523(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92102952; PubMed=1684715;  
 RA Coletta P.L., Shmied S.M., Chaudhuri C., Mueller U., Clarke J.P.,  
 RA Sharpe P.T.;  
 RT "Characterisation of the murine Hox-3.3 gene and its promoter.";  
 RL Mech. Dev. 35:129-142(1991).  
 RN [3]  
 RP SEQUENCE OF 15-235 FROM N.A.  
 RC TISSUE=Bone marrow, and Spleen;  
 RX MEDLINE=88329001; PubMed=2901346;  
 RA Kongswan K., Webb E., Housteaux P., Adams J.M.;  
 RT "Expression of multiple homeobox genes within diverse mammalian  
 RT hemopoietic lineages.";  
 RL EMBO J. 7:2131-2138(1988).  
 RN [4]  
 RP SEQUENCE OF 131-235 FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=88328811; PubMed=2458223;  
 RA Sharpe P.T., Miller J.R., Evans E.P., Burenshaw M.D., Gaunt S.J.;  
 RT "Isolation and expression of a new mouse homeobox gene.";  
 RL Development 102:397-407(1988).  
 RN [5]  
 RP SEQUENCE OF 133-235 FROM N.A.  
 RX MEDLINE=89357988; PubMed=2570032;  
 RA Shupliarsky K., Pravecheva D., Newman M.S., Hunihan L.W., Jiang Z.,  
 RA Ruddle P.H.;  
 RT "Isolation and regional localization of the murine  
 RT homeobox-containing gene Hox-3.3 to mouse chromosome region 15B.";  
 RL Genomics 5:76-83(1989).  
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=PR1;  
 CC Name=PR1;  
 CC IsoId=P10629-1; Sequence=Displayed;  
 CC Name=PR1;  
 CC IsoId=P10629-2; Sequence=VSP\_002393;  
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; J03074; AAA37837.1; -;  
 DR EMBL; M35986; AAA37854.1; -;  
 DR EMBL; X16511; CAA34518.1; -;  
 DR EMBL; X16510; CAA34517.1; -;  
 DR EMBL; S74185; AAB30717.1; -;

DR EMBL: X12504; CAA31022.1; -;  
 DR EMBL: X12504; CAA31023.1; -;  
 DR EMBL: X16838; CAA34737.1; -;  
 DR PIR: A32167; A32167.  
 DR PIR: A56568; A56568.  
 DR PIR: S00987; WJMSX6.  
 DR HSSP: P02833; 9ANT.  
 DR TRANSPAC: T01743; -.  
 DR TRANSPAC: T01744; -.  
 DR MGD; MGI:96197; Hoxc6.  
 DR InterPro; IPR001827; Antennapedia.  
 DR InterPro; IPR001356; Homeobox.  
 DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR00025; ANTENNAPEDIA.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX 1; 1.  
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.  
 DR PROSITE; PS50071; HOMEBOX 2; 1.  
 DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 KW transcription regulation; Alternative splicing.  
 FT SITE 122 127 ANTP-TYPE HEXAPEPTIDE.  
 FT DNA BIND 141 200 HOMEBOX.  
 FT DOMAIN 221 235 GLU/LYS-RICH.  
 FT VARSPLIC 1 82 Missing (in isoform PRI).  
 FT CONFLICT 15 18 AGGQ -> QGRP (IN REF. 3).  
 FT CONFLICT 131 131 S -> N (IN REF. 4).  
 FT CONFLICT 192 192 R -> A (IN REF. 4).  
 FT CONFLICT 228 229 TE -> OK (IN REF. 1 AND 2).  
 SQ SEQUENCE 235 AA; 26915 MW; BD695C7347CB71C0 CRC64;

Query Match 64.2%; Score 95; DB 1; Length 235;  
 Best Local Similarity 72.0%; Pred. No. 2.1e-07;  
 Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Cy 1 DROIKWPNRRMKKKTALDASL 25  
 DB 182 ERQIKWPNRRMKKESNLTSTL 206

Search completed: February 18, 2004, 14:28:15  
 Job time : 17.5789 secs

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# OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 81.0526 Seconds  
(without alignments)  
89.145 Million cell updates/sec

Title: US-09-643-260-19

Perfect score: 148

Sequence: 1 DRQIKWFRNRKMKKTALDASALQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL.23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110.5	74.7	274	5	Q9XYT7
2	101.5	68.6	627	5	Q95YH8
3	100	67.6	108	11	Q8JZM2
4	98	66.2	93	5	Q9U9Z5
5	97	65.5	60	5	Q26375
6	97	65.5	90	5	Q817C9
7	97	65.5	181	5	Q26611
8	97	65.5	194	5	Q26478
9	97	65.5	435	5	Q817C8
10	96.5	65.2	231	13	Q9PMM4
11	96	64.9	101	13	Q9PBD5
12	95.5	64.5	82	13	Q9PVS0
13	95	64.2	219	13	Q9U9Z9
14	94.5	63.9	43	13	Q57359
15	94.5	63.9	80	5	Q05008
16	94.5	63.9	230	11	Q9CZV0

17	94.5	63.9	275	13	Q8AWY7	Q8AWY7 brachydanio
18	94.5	63.9	276	13	Q8JH53	Q8JH53 brachydanio
19	94.5	63.9	276	13	Q9PMM0	Q9PMM0 brachydanio
20	94.5	63.9	348	5	Q8WRG6	Q8WRG6 artemia san
21	94	63.5	39	13	Q57368	Q57368 brachydanio
22	94	63.5	46	13	Q9PVR9	Q9PVR9 oryzias lat
23	94	63.5	51	5	Q27413	Q27413 ctenodrilus
24	94	63.5	51	5	Q23743	Q23743 ctenodrilus
25	94	63.5	51	5	Q26407	Q26407 ctenodrilus
26	94	63.5	57	13	Q9PVR8	Q9PVR8 oryzias lat
27	94	63.5	58	5	Q9Y188	Q9Y188 brachydanio
28	94	63.5	58	5	Q25208	Q25208 junonia coe
29	94	63.5	58	13	Q57362	Q57362 brachydanio
30	94	63.5	59	5	Q8WRM9	Q8WRM9 lithobius a
31	94	63.5	59	5	Q9NB42	Q9NB42 anopheles g
32	94	63.5	59	13	Q9PVR5	Q9PVR5 oryzias lat
33	94	63.5	60	5	Q77143	Q77143 archeogozete
34	94	63.5	60	5	Q77139	Q77139 archeogozete
35	94	63.5	60	13	Q8QGL5	Q8QGL5 petromyzon
36	94	63.5	60	13	Q8QGL3	Q8QGL3 petromyzon
37	94	63.5	60	13	Q8QGL6	Q8QGL6 petromyzon
38	94	63.5	60	13	Q8QGL2	Q8QGL2 petromyzon
39	94	63.5	60	13	Q8QGL8	Q8QGL8 petromyzon
40	94	63.5	60	13	Q8QGL7	Q8QGL7 petromyzon
41	94	63.5	61	5	Q27910	Q27910 polyandroca
42	94	63.5	63	5	Q77138	Q77138 archeogozete
43	94	63.5	63	5	Q8MXB2	Q8MXB2 holopneuste
44	94	63.5	66	13	Q57356	Q57356 brachydanio
45	94	63.5	69	5	Q9U9T4	Q9U9T4 nectris viro

## ALIGNMENTS

RESULT 1  
Q9XYT7 PRELIMINARY, PRT, 274 AA.  
AC Q9XYT7;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Scx-3 homeodomain protein (Fragment).  
GN SCX-3.  
OS Caesiopea xamachana.  
OC Eukaryota; Metazoa; Chordata; Scyphozoa; Rhizostomaeae; Caesiopelidae;  
OC Caesiopea.  
OX NCBI\_Taxid=12993;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kuhn K., Streit B., Schlerwater B.;  
RT "Isolation of Hox genes from the scyphozoan *Caesiopea xamachana*:  
RT implications for the early evolution of Hox genes.";  
RT J. Exp. Zool. 0:0-0(1999).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
DR EMBL: AF124593; ADJ32577.1; -.  
DR HSSP: P02833; GANT.  
DR InterPro: IPR001356; Homeobox.  
DR Pfam: PF00046; homeobox.1.  
DR PRINTS: PR00031; HTHREPRESSR.  
DR PRINTS: PR00024; HOMEBOX.  
DR ProDom: PD000010; Homeobox.1.  
DR SMART: SM00389; Hox.1.  
DR PROSITE: PS00027; HOMEBOX 1; 1.  
DR PROSITE: PS00071; HOMEBOX 2; 1.  
KW DNA-binding; Homeobox; Nuclear protein.  
FT NON\_TER  
SQ SEQUENCE 274 AA; 31041 MW; 588E91F6E540C3A9 CRC64;  
Query Match 74.7%; Score 110.5; DB 5; Length 274;  
Best local similarity 67.7%; Pred. No. 1.7e-08;  
Matches 21; Conservative 5; Mismatches 2; Indels 3; Gaps 1;

QY 1 DROIKIWFQNRKMKK---TALDASALQTE 28  
 DB 182 EROIKIWFQNRKMKKGGTTSIDANLEERE 212

## RESULT 2

ID Q95YH8 PRELIMINARY; PRT; 627 AA.  
 AC Q95YH8; 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 OS Homeotic protein.  
 OS Daphnia magna.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Diplostetraca;  
 OC Cladocera; Anomopoda; Daphniidae; Daphnia.  
 NCBI\_TaxID=35525;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shiga Y., Yasumoto R., Hayaashi S., Yamagata H.;  
 RT "Functional diversification of homeotic protein Antennapedia in  
 RT arthropod evolution."  
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL; AB069680; BAB64346.1; -  
 DR InterPro; IPR001827; Antennapedia.  
 DR InterPro; IPR001356; Homeobox.  
 DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR00025; ANTENNAPEDIA.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.  
 DR PROSITE; PS00027; HOMEBOX 1; 1.  
 DR PROSITE; PS50071; HOMEBOX 2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 SQ SEQUENCE 627 AA; 69425 MW; A5A7962761C85D10 CRC64;

Query Match 68.6%; Score 101.5; DB 5; Length 627;  
 Best Local Similarity 69.0%; Pred. No. 9.2e-07;  
 Matches 20; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY 1 DROIKIWFQNRKMKK---KTALDASALQ 26  
 DB 587 EROIKIWFQNRKMKKKNKAKDAGCLB 615

## RESULT 3

ID Q8UZW2 PRELIMINARY; PRT; 108 AA.  
 AC Q8UZW2; 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 OS Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Colon;  
 RA Straubberg R.;  
 RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC036986; AAH36986.1; -  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR000047; HTH\_Lamdrepressr.  
 DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR PRINTS; PR00031; HTHREPRESSR.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX 1; 1.

DR PROSITE; PS50071; HOMEBOX 2; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 108 AA; 13070 MW; 123A78CDD0E7D90 CRC64;

Query Match 67.6%; Score 100; DB 11; Length 108;  
 Best Local Similarity 70.4%; Pred. No. 2.5e-07;  
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRKMKKKTALDASALQ 27  
 DB 49 EROIKIWFQNRKMKKKEKHDSQAPT 75

## RESULT 4

ID Q9U9Z5 PRELIMINARY; PRT; 93 AA.  
 AC Q9U9Z5; 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 OS Sex combs reduced homeodomain protein (Fragment).  
 OS Lingula unguis.  
 OC Eukaryota; Metazoa; Brachiopoda; Linguliformes; Lingulata; Lingulida;  
 OC Linguloidae; Lingulidae; Lingula.  
 NCBI\_TaxID=7574;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 99318125; PubMed; 10391241;  
 RA de Rosa R., Grenier J.K., Andreeva T., Cook C.E., Adourte A., Akam M.,  
 RA Carroll S.B., Balavoine G.;  
 RT "Hox genes in brachiopods and priapulids and protostome evolution."  
 RL Nature 399:772-776 (1999).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL; AF144674; MAD45589.1; -  
 DR HSSP; P02833; ISAN.  
 DR TRANSFAC; T03872; -  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR00047; HTH\_Lamdrepressr.  
 DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR00031; HTHREPRESSR.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX 1; 1.  
 DR PROSITE; PS50071; HOMEBOX 2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON TER 1  
 SQ SEQUENCE 93 AA; 11224 MW; 5DC0379A30DF0137 CRC64;

Query Match 66.2%; Score 98; DB 5; Length 93;  
 Best Local Similarity 67.9%; Pred. No. 4.3e-07;  
 Matches 19; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRKMKKKTALDASALQTE 28  
 DB 48 EROIKIWFQNRKMKKKEKHDLTKTE 75

## RESULT 5

ID Q26375 PRELIMINARY; PRT; 60 AA.  
 AC Q26375; 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 OS DNA binding protein Ahox2 (Fragment).  
 GN AH0X2.  
 OS Styela clava (Sea squirt).  
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
 OC Stolidobranchia; Styelidae; Styela.  
 NCBI\_TaxID=7725;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=95011617; PubMed=7926803;  
RA Ge T., Lee H., Tomlinson C.R.;  
RT "Identification of an antenapedia-like homeobox gene in the ascidians  
Styela clava and S. plicata.";  
RL Gene 147:219-223 (1994).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
DR EMBL: S73920; AAB33061.2; -.  
DR HSSP: P02833; 9ANT.  
DR InterPro: IPR001356; Homeobox.  
DR InterPro: IPR000047; HTH\_lambdarepressr.  
DR Pfam: PF00046; homeobox\_1.  
DR PRINTS: PR00024; HOMEBOX.  
DR PRINTS: PR00031; HTHREPRESSR.  
DR ProDom: PD000010; Homeobox; 1.  
DR SMART: SM00389; HOX; 1.  
DR PROSITE: PS00027; HOMEBOX\_1; 1.  
DR PROSITE: PS50071; HOMEBOX\_2; 1.  
KW DNA-binding; Homeobox; Nuclear protein.  
FT NON\_TER 1  
FT SEQUENCE 60 AA; 7630 MW; F506301E9679BA25 CRC64;  
SQ  
Query Match 65.5%; Score 97; DB 5; Length 60;  
Best Local Similarity 94.1%; Pred. No. 3.9e-07;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRQIKWIFQNRMKMKK 17  
DB 42 DRQVKKWIFQNRMKMKK 58  
|||:|||||  
ID Q817C9 PRELIMINARY; PRT; 90 AA.  
AC Q817C9;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Putative homeobox protein Hox6/7 (Fragment).  
GN Hox6/7.  
OS Clona intestinalis.  
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
OC Phlebobranchia; Cloniidae; Clona.  
OX NCBI\_Taxid=7719;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Spagnuolo A., Ristoreatore F., Di Gregorio A., Antello F., Branno M.,  
RT Di Lauro R.;  
RT "Unusual number and genomic organization of Hox genes in the tunicate  
Clona intestinalis.";  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ535674; CAD59670.1; -.  
KW Homeobox; DNA-binding; Nuclear protein.  
FT NON\_TER 1  
FT SEQUENCE 90 AA; 11352 MW; CAAADGB261FE908E CRC64;  
SQ  
Query Match 65.5%; Score 97; DB 5; Length 90;  
Best Local Similarity 64.3%; Pred. No. 5.9e-07;  
Matches 18; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
QY 1 DRQIKWIFQNRMKMKKTDALDAALQTE 28  
DB 57 EROIKWIFQNRMKMKKENDIASNNB 84  
:|||||  
ID Q26611 PRELIMINARY; PRT; 181 AA.  
AC Q26611;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Homeobox protein (Fragment).  
SQ

OS Styela plicata (Sea squirt).  
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
OC Scolidobranchia; Styelidae; Styela.  
OX NCBI\_Taxid=7725;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ge T., Lee H., Tomlinson C.R.;  
RT "Identification of an Antenapedia-like Homeobox Gene in the Ascidians  
Styela clava and plicata.";  
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
DR EMBL: U05600; AAL16288.1; -.  
DR HSSP: P02833; 9ANT.  
DR InterPro: IPR001356; Homeobox.  
DR InterPro: IPR000047; HTH\_lambdarepressr.  
DR Pfam: PF00046; homeobox\_1.  
DR PRINTS: PR00024; HOMEBOX.  
DR PRINTS: PR00031; HTHREPRESSR.  
DR ProDom: PD000010; Homeobox; 1.  
DR SMART: SM00389; HOX; 1.  
DR PROSITE: PS00027; HOMEBOX\_1; 1.  
DR PROSITE: PS50071; HOMEBOX\_2; 1.  
KW DNA-binding; Homeobox; Nuclear protein.  
FT NON\_TER 1  
FT SEQUENCE 181 AA; 20873 MW; AF39911408F06672 CRC64;  
SQ  
Query Match 65.5%; Score 97; DB 5; Length 181;  
Best Local Similarity 94.1%; Pred. No. 1.2e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRQIKWIFQNRMKMKK 17  
DB 80 DRQVKKWIFQNRMKMKK 96  
|||:|||||  
ID Q26478 PRELIMINARY; PRT; 194 AA.  
AC Q26478;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Homeobox protein (fragment).  
GN Styela clava (Sea squirt).  
OS Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
OC Scolidobranchia; Styelidae; Styela.  
OX NCBI\_Taxid=7725;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ge T., Lee H., Tomlinson C.R.;  
RT "Identification of an Antenapedia-like Homeobox Gene in the Ascidians  
Styela clava and plicata.";  
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
DR EMBL: U05571; AAL16226.1; -.  
DR HSSP: P02833; 9ANT.  
DR InterPro: IPR001356; Homeobox.  
DR InterPro: IPR000047; HTH\_lambdarepressr.  
DR Pfam: PF00046; homeobox\_1.  
DR PRINTS: PR00024; HOMEBOX.  
DR PRINTS: PR00031; HTHREPRESSR.  
DR ProDom: PD000010; Homeobox; 1.  
DR SMART: SM00389; HOX; 1.  
DR PROSITE: PS00027; HOMEBOX\_1; 1.  
DR PROSITE: PS50071; HOMEBOX\_2; 1.  
KW DNA-binding; Homeobox; Nuclear protein.  
FT NON\_TER 1  
FT SEQUENCE 194 AA; 21866 MW; 8AD1B15B3R4800BC CRC64;  
SQ  
Query Match 65.5%; Score 97; DB 5; Length 194;



Best Local Similarity 94.1%; Pred. No. 1.3e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DROIKIWFQNRMMKK 17  
|||:|||||:|||||:|  
DB 52 DROVXKWFQNRMMKK 68

## RESULT 9

0817C8 PRELIMINARY; PRT; 435 AA.  
ID 0817C8  
AC 0817C8  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
GN HOX10.  
OS Clona intestinalis.  
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
OC Phlebobranchia; Clonidae; Clona.  
OX NCBI\_TaxID=7719;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Spagnuolo A., Ristocratore F., Di Gregorio A., Aniello F., Bramo M.,  
Di Lauro R.;  
RT "Unusual number and genomic organization of Hox genes in the tunicate  
Clona intestinalis."  
RL Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AJ535675; CAD59671.1; -.  
KW Homeobox; DNA-binding; Nuclear protein.  
SQ SEQUENCE 435 AA; 48739 MW; DBD0F579C02BC9E2 CRC64;

Query Match 65.5%; Score 97; DB 5; Length 435;  
Best Local Similarity 94.1%; Pred. No. 3e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DROIKIWFQNRMMKK 17  
|||:|||||:|||||:|  
DB 295 DROVXKWFQNRMMKK 311

## RESULT 10

09PMM4 PRELIMINARY; PRT; 231 AA.  
ID 09PMM4  
AC 09PMM4  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
GN Homeobox protein.  
DE HOXC6A.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99051425; PubMed=9831563;  
RA Amores A., Force A., Yan Y.-L., Wang Y.-L., Fritz A., Prince V.,  
Ho R., Amemiya C., Langeland J., Westerfield M., Ekker M.,  
Postlethwait J.;  
RT "Zebrafish hox clusters and vertebrate genome evolution."  
RL Science 282:1711-1714 (1998).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
DR EMBL; AF071265; AAD15958.1; -.  
DR HSSP; P02833; 9ANT.  
DR TRANSFAC; T03667;  
DR ZFIN; ZDB-GENE-990415-113; hox6a.  
DR InterPro; IPR001827; Antennapedia.  
DR Pfam; PF00046; homeobox; 1.  
DR PRINTS; PR00025; ANTENNAPEDIA.  
DR PRINTS; PR00024; HOMEOBOX.

DR ProDom; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00032; ANTENNAPEDIA; 1.  
DR PROSITE; PS00027; HOMEOBOX\_1; 1.  
DR PROSITE; PS50071; HOMEOBOX\_2; 1.  
KW DNA-binding; Homeobox; Nuclear protein.  
SQ SEQUENCE 231 AA; 26733 MW; 65164A13541D78BA CRC64;

Query Match 65.2%; Score 96.5; DB 13; Length 231;  
Best Local Similarity 69.0%; Pred. No. 1.8e-06;  
Matches 20; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

OY 1 DROIKIWFQNRMMKK-TLADNSALQTE 28  
:|||||:|||||:|||||:|  
DB 183 EROIKIWFQNRMMKKETLSTVPGTE 211

## RESULT 11

09PSDS PRELIMINARY; PRT; 101 AA.  
ID 09PSDS  
AC 09PSDS  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
GN HOXC-6.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=95151548; PubMed=7848839;  
RA Gaunt S.J.;  
RT "Conservation in the Hox code during morphological evolution."  
RL Int. J. Dev. Biol. 38:549-552 (1994).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
DR EMBL; X80114; CAB94151.1; -.  
DR HSSP; P02833; 9ANT.  
DR InterPro; IPR001356; Homeobox.  
DR Pfam; PF00046; homeobox; 1.  
DR PRINTS; PR00024; HOMEOBOX.  
DR ProDom; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00027; HOMEOBOX\_1; 1.  
DR PROSITE; PS50071; HOMEOBOX\_2; 1.  
KW DNA-binding; Homeobox; Nuclear protein.  
SQ SEQUENCE 101 AA; 11592 MW; 9637DB0AAB85546D CRC64;

Query Match 64.9%; Score 96; DB 13; Length 101;  
Best Local Similarity 72.0%; Pred. No. 9.4e-07;  
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 DROIKIWFQNRMMKKTALDASAL 25  
:|||||:|||||:|||||:|  
DB 49 EROIKIWFQNRMMKKESNLSTYL 73

## RESULT 12

09PVS0 PRELIMINARY; PRT; 82 AA.  
ID 09PVS0  
AC 09PVS0  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
GN HOXB5A (Fragment).  
OS Oryzias latipes (Medaka fish) (Japanese ricefish).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

OC Belontiiformes; Adriantichthyidae; Oryziinae; Oryzias.  
 OX NCBI\_TaxID=8090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kondo S., Naruse K., Shima A.;  
 RT "Hox genes of the medaka fish *Oryzias latipes*."  
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL; AB026959; BAA6242.1; -.  
 DR HSP; P02833; 9ANT.  
 DR InterPro; IPR01356; Homeobox.  
 DR Pfam; PF00046; homeobox; 1.  
 DR ProDom; PD00010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS50071; HOMEBOX\_2; 1.  
 KM DNA-binding; Homeobox; Nuclear protein.  
 FT NON TER 1 1  
 SQ SEQUENCE 82 AA; 9939 MW; 6B6828D280511888 CRC64;  
 Query Match 64.5%; Score 95.5; DB 13; Length 82;  
 Best Local Similarity 60.0%; Pred. No. 9e-07;  
 Matches 21; Conservative 1; Mismatches 4; Indels 9; Gaps 1;  
 Qy 1 DROIKIFQNRMRMKKK-----TALDASALQ 26  
 Db 47 EROIKIFQNRMRMKKKDKNKMSLTTPGASHQ 81  
 RESULT 13  
 Q09VZ9 PRELIMINARY; PRT; 219 AA.  
 ID Q09VZ9;  
 AC Q09VZ9;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hoxa-7 protein (Homeodomain transcription factor Hoxa-7).  
 GN Hoxa-7.  
 OS Gallus gallus (chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2125551; PubMed=11357191;  
 RA Gaunt S.C.;  
 RT "Gradients and forward spreading of vertebrate Hox gene expression  
 RL detected using a Hox1ac2 transgene."  
 RL Dev. Dyn. 221:26-36(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Oberig K.C., Eichele G.;  
 RT "Hox gene expression and regulation in the presumptive wing region of  
 RL the chick lateral plate mesoderm (Abstract # 286)."  
 RL Dev. Biol. 210:228-228(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Oberig K.C., Piza C.U., Creamer D.H., Revelle J.-P., Eichele G.;  
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL; AJ291729; CAC37629.1; -.  
 DR EMBL; AF408695; AL01899.1; -.  
 DR InterPro; IPR001827; Antennapedia.  
 DR InterPro; IPR001356; Homeobox.  
 DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR00025; ANTENNAPEDIA.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR ProDom; PD00010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS50071; HOMEBOX\_2; 1.

KM DNA-binding; Homeobox; Nuclear protein.  
 SQ SEQUENCE 219 AA; 24952 MW; 4BA89046D52C0705 CRC64;  
 Query Match 64.2%; Score 95; DB 13; Length 219;  
 Best Local Similarity 70.8%; Pred. No. 2.9e-06;  
 Matches 17; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 DROIKIFQNRMRMKKKKTALDASA 24  
 Db 170 EROIKIFQNRMRMKKKKKHKESS 193  
 RESULT 14  
 ID 057359 PRELIMINARY; PRT; 43 AA.  
 AC 057359;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Hoxa5 protein (Fragment).  
 GN HoxB5 OR HOXA5.  
 OS Brachydanio rerio (zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Prince V.E., Joly L., Ekker M., Ho R.K.;  
 RT "Zebrafish hox genes: genomic organization and modified collinear  
 RL expression patterns in the trunk."  
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL; Y14526; CAAY4861.1; -.  
 DR ZFIN; ZDB-GENE-000823-6; hoxb5b.  
 DR InterPro; IPR001356; Homeobox.  
 DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR ProDom; PD00010; Homeobox; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS50071; HOMEBOX\_2; 1.  
 KM DNA-binding; Homeobox; Nuclear protein.  
 FT NON TER 1 1  
 SQ SEQUENCE 43 AA; 5050 MW; 53034C37F3DFA596 CRC64;  
 Query Match 63.9%; Score 94.5; DB 13; Length 43;  
 Best Local Similarity 67.9%; Pred. No. 6.5e-07;  
 Matches 19; Conservative 3; Mismatches 5; Indels 1; Gaps 1;  
 Qy 1 DROIKIFQNRMRMKKKKTALDASALQ 27  
 Db 9 EROIKIFQNRMRMKKKDKNKMSLTAT 36  
 RESULT 15  
 ID 005008 PRELIMINARY; PRT; 80 AA.  
 AC 005008;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Antp protein (Fragment).  
 GN ANTP.  
 OS Artemia salina (brine shrimp) (Artemia franciscana).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;  
 OC Artemiidae; Artemia.  
 OX NCBI\_TaxID=6661;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=North arm of Great Salt Lake;  
 RA Averof M., Akam M.;  
 RT "Hox/Hox genes in a crustacean: implication for the origin of insect  
 and crustacean body plans.";

```

RL  Curr. Biol. 3:73-78(1993).
CC  -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR  EMBL; X70077; CAA49682.1; -.
DR  HSSP; P02833; 9ANT.
DR  InterPro; IPR001356; Homeobox.
DR  Pfam; PF00046; homeobox; 1.
DR  PRINTS; PR00024; HOMEBOX.
DR  ProDom; PD000010; Homeobox; 1.
DR  SMART; SM00389; HOX; 1.
DR  PROSITE; PS00027; HOMEBOX_1; 1.
DR  PROSITE; PS00071; HOMEBOX_2; 1.
KW  DNA-binding; Homeobox; Nuclear protein.
FT  NON_TER
SQ  SEQUENCE      1 9878 MM; 48472705CEDFCE7 CRC64;

Query Match      63.9%; Score 94.5; DB 5; Length 80;
Best Local Similarity 64.3%; Pred. No. 1.2e-06;
Matches 18; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

Qy      1 DROIKIFQNRMRKWK--KTALDASAL 25
      :|||||:|||||:|||||:|:|:|
Db      42 ERQIKIWFONRMRKWKENKSKVDGCL 69

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Search completed: February 18, 2004, 14:36:01  
 Job time : 81.0526 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 (Search time 30.7632 Seconds  
(without alignments)  
87.531 Million cell updates/sec)

Title: US-09-643-260-19

Perfect score: 148  
Sequence: 1 DRQIKWFGNRBMKMKKTALDASALQTE 28

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR.76:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	69.6	81	2	B29585
2	103	69.6	96	2	A05266
3	103	69.6	97	2	C27176
4	103	69.6	224	2	S26400
5	103	69.6	224	2	A31324
6	100	67.6	105	2	A27471
7	100	67.6	119	2	A03314
8	100	67.6	229	2	A28329
9	99	66.9	75	2	I51341
10	98	66.2	86	2	S08303
11	97	65.5	60	2	PC2399
12	97	65.5	60	2	PC2400
13	96.5	65.2	96	2	S08639
14	96	64.9	234	1	S00992
15	95	64.2	66	2	S15536
16	95	64.2	103	2	A32167
17	95	64.2	153	1	WJHUC
18	95	64.2	153	1	WJMSX6
19	95	64.2	230	2	S00592
20	95	64.2	234	1	S02014
21	95	64.2	235	2	A56568
22	95	64.2	235	2	S72429
23	95	64.2	242	1	A39164
24	94.5	63.9	118	2	A24777
25	94.5	63.9	118	2	UT0273
26	94.5	63.9	118	2	B24777
27	94.5	63.9	269	1	A43551
28	94.5	63.9	269	1	A45578
29	94.5	63.9	275	1	WJZFX2

30	94	63.5	33	2	S57235	antennapedia prote
31	94	63.5	42	2	I65241	homeotic protein H
32	94	63.5	45	2	PC1216	homeotic protein D
33	94	63.5	48	2	I51439	homeobox protein -
34	94	63.5	66	2	S15538	homeotic protein H
35	94	63.5	71	2	JC1161	homeotic protein 3
36	94	63.5	71	2	A60084	homeotic protein H
37	94	63.5	74	2	D34510	homeotic protein H
38	94	63.5	75	2	S58852	homeotic protein H
39	94	63.5	76	2	C43559	homeotic protein S
40	94	63.5	78	2	I51342	homeotic protein R
41	94	63.5	81	2	S47605	homeo box protein
42	94	63.5	82	2	S08302	homeotic protein H
43	94	63.5	83	2	S47603	homeotic protein H
44	94	63.5	83	2	S50066	homeotic protein H
45	94	63.5	86	2	A34510	homeotic protein H

## ALIGNMENTS

## RESULT 1

B29585

homeotic protein Hox 2.2 precursor - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 15-Dec-1988 #sequence\_revision 30-Sep-1991 #text\_change 17-Oct-1997

C/Accession: B29585

R:Lonai, P.; Arman, E.; Czornik, H.; Ruddle, F.H.; Blatt, C.

DNA 6, 409-418, 1987

A>Title: New murine homeoboxes: structure, chromosomal assignment, and differential ex

A:Reference number: A29585; MUID:88054465; PMID:2850503

A/Accession: B29585

A/Molecule type: DNA

A/Residues: 1-81 <LON>

A/Cross-references: GB:M18167

A/Note: the authors translated the codon CAG for residue 69 as Glu

C:Superfamily: unassigned homeobox proteins; homeobox homology

C/Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:4-60/Domain: homeobox homology <Hox>

Query Match 69.6%; Score 103; DB 2; Length 81;  
Best Local Similarity 70.0%; Pred. No. 4.5e-08;  
Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 DRQIKWFGNRBMKMKKTALDASALQTE 28

DB 44 EROIKWFGNRBMKMKKESITLSASQISAE 73

## RESULT 2

A05266

homeotic protein Hox B6 - human (fragment)

N/Alternate names: homeotic protein Hox 2B; homeotic protein Hu2

C:Species: Homo sapiens (man)

C>Date: 05-Jun-1987 #sequence\_revision 30-Sep-1991 #text\_change 17-Oct-1997

C/Accession: A05266; S15537

R:Levine, M.; Rudin, G.M.; Tjian, R.

Cell 38, 667-673, 1984

A>Title: Human DNA sequences homologous to a protein coding region conserved between h

A/Reference number: A05265; MUID:85024858; PMID:6091895

A/Accession: A05266

A/Molecule type: DNA

A/Residues: 1-96 <LEV>

A/Cross-references: EMBL:K02571

A/Note: this reading frame extends between two stop codons and does not begin with a s

R:Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; S

Genome 31, 745-756, 1989

A>Title: Organization of human class I homeobox genes

A/Reference number: S15036; MUID:90215256; PMID:257652

A/Accession: S15537

A/Molecule type: DNA

A/Residues: 18-19, 'R', 21-83 <BON>

C/Genetics:

A:Gene: GDB:H0XB6  
 A:Cross-references: GDB:120659; OMIM:142961  
 A:Map position: 17q21.3-17q21.3  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:19-75/Domain: homeobox homology <HOX>

Query Match 69.6%; Score 103; DB 2; Length 96;  
 Best Local Similarity 70.0%; Pred. No. 5.3e-08;  
 Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 1 DROIKIFQNRMRMKKTKTA--LDASALQTE 28  
 :|||||  
 Db 59 ERQIKIFQNRMRMKKTKLSASQLSAE 88

## RESULT 3

C27176 homeotic protein Hox 2.2 - mouse

C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 24-Sep-1999  
 C:Accession: C27176

R:Hart, C.P.; Painhod, A.; Ruddle, F.H.

A:Title: Sequence analysis of the murine Hox-2.2, -2.3, and -2.4 homeo boxes: evolutionary

A:Reference number: A27176; PMID:88085193; PMID:2891608

A:Accession: C27176

A:Molecule type: DNA

A:Residues: 1-97 <HAR>

A:Cross-references: GB:M18401; NID:g193936; PIDN:AACT730.1; PID:g3335322

C:Gene: Hox-2.2

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:20-76/Domain: homeobox homology <HOX>

Query Match 69.6%; Score 103; DB 2; Length 97;  
 Best Local Similarity 70.0%; Pred. No. 5.4e-08;  
 Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 1 DROIKIFQNRMRMKKTKTA--LDASALQTE 28  
 :|||||  
 Db 60 ERQIKIFQNRMRMKKTKLSASQLSAE 89

RESULT 4  
 S26400 homeotic protein Hox 2.2 (variant 1) - human

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 17-Nov-2000

C:Accession: S26400; S26401

R:Shen, W.; Derner, K.; Simionitch-Eason, T.A.; Lawrence, H.J.; Largman, C.

Nucleic Acids Res. 19, 539-545, 1991

A:Title: Alternative splicing of the Hox 2.2 homeobox gene in human hematopoietic cells

A:Reference number: S26400; PMID:91187672; PMID:1672751

A:Accession: S26400

A:Molecule type: DNA

A:Residues: 1-224 <SHE>

A:Cross-references: EMBL:X58431; NID:g32369; PIDN:CAA41335.1; PID:g32370

A:Experimental source: tissue-type placenta

A>Note: the authors translated the codon ACT for residue 55 as Tyr, CGC for residue 60 as

A>Note: the authors did not translate the codons for residues 139, and 140

C:Gene: Hox-2.2

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulation

F:147-203/Domain: homeobox homology <HOX>

Query Match 69.6%; Score 103; DB 2; Length 224;  
 Best Local Similarity 70.0%; Pred. No. 1.3e-07;  
 Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 1 DROIKIFQNRMRMKKTKTA--LDASALQTE 28  
 :|||||  
 Db 187 ERQIKIFQNRMRMKKTKLSASQLSAE 216

## RESULT 5

A31324 homeotic protein Hox 2.2 - mouse

C:Species: Mus musculus (house mouse)  
 C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 24-Sep-1999  
 C:Accession: A31324

R:Schughart, K.; Utset, M.P.; Awgulewitsch, A.; Ruddle, F.H.

Proc. Natl. Acad. Sci. U.S.A. 85, 5582-5586, 1988

A:Title: Structure and expression of Hox-2.2, a murine homeobox-containing gene.

A:Reference number: A31324; PMID:88289762; PMID:2899893

A:Accession: A31324

A:Molecule type: mRNA

A:Residues: 1-224 <SCH>

A:Cross-references: GB:J03782; NID:g193929; PIDN:AAA37843.1; PID:g387203

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:147-203/Domain: homeobox homology <HOX>

Query Match 69.6%; Score 103; DB 2; Length 224;  
 Best Local Similarity 70.0%; Pred. No. 1.3e-07;  
 Matches 21; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 1 DROIKIFQNRMRMKKTKTA--LDASALQTE 28  
 :|||||  
 Db 187 ERQIKIFQNRMRMKKTKLSASQLSAE 216

RESULT 6  
 A27471 homeotic protein R5 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 23-May-1997

C:Accession: A27471

R:Palzon, M.; Sanderson, N.; Chung, S.Y.

Gene 54, 23-32, 1987

A:Title: Cloning and expression of rat homeo-box-containing sequences.

A:Reference number: A91576; PMID:87277429; PMID:2886401

A:Accession: A27471

A:Molecule type: DNA

A:Residues: 1-105 <PAL>

C:Superfamily: unassigned homeobox proteins; homeobox homology

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:6-62/Domain: homeobox homology <HOX>

Query Match 67.6%; Score 100; DB 2; Length 105;  
 Best Local Similarity 70.4%; Pred. No. 1.6e-07;  
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DROIKIFQNRMRMKKTKTALDASALQTE 27  
 :|||||  
 Db 46 ERQIKIFQNRMRMKKTKENHDESGAPT 72

RESULT 7  
 A03314 homeotic protein m6 - mouse (fragment)

C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 24-Jul-1997  
 C:Accession: A03314; S14043  
 R:Colberg-Poley, A.M.; Voss, S.D.; Chowdhury, K.; Gruss, P.  
 Nature 314, 713-718, 1985  
 A:Title: Structural analysis of murine genes containing homeo box sequences and their

A:Reference number: A03314; PMID:95188311; PMID:2986010

A/Accession: A03314  
A/Molecule type: DNA  
A/Residues: 1-119 <COL>  
R/Beiler, G.; Bucan, M.; Francke, U.; Colberg-Poley, A.M.; Gruss, P.  
EMBO J. 5, 2209-2215, 1986  
A/Title: Sequential expression of murine homeo box genes during F9 EC cell differentiation  
A/Reference number: S13785; MUID:8705860; PMID:2877873  
A/Accession: S14063  
A/Molecule type: DNA  
A/Residues: 19-48; 'R', 51-87 <BRE>  
C/Genetics:  
A/Gene: m6  
C/Superfamily: unassigned homeobox proteins; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F/20-76/Domain: homeobox homology <HOX>

Query Match 67.6%; Score 100; DB 2; Length 119;  
Best Local Similarity 70.4%; Pred. No. 1.8e-07;  
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWPNRRMKWKKTALDASALQT 27  
:|||||  
Db 60 ERQIKWPNRRMKWKKTALDASALQT 86

RESULT 8  
A28329  
homeotic protein Hox A7 - mouse  
N/Alternate names: homeotic protein Hox 1.1; m6 homeotic protein  
C/Species: Mus musculus (house mouse)  
C/Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 20-Aug-1999  
C/Accession: A28329; I49131  
R/Kessel, M.; Schulze, F.; Fild, M.; Gruss, P.  
Proc. Natl. Acad. Sci. U.S.A. 84, 5306-5310, 1987  
A/Title: Primary structure and nuclear localization of a murine homeodomain protein.  
A/Reference number: A28329; MUID:87260976; PMID:2885847  
A/Accession: A28329  
A/Molecule type: mRNA  
A/Residues: 1-229 <RES>  
A/Cross-references: GB:M17192; NID:g193906; PIDN:AAA37833.1; PID:g309313  
R/Parikh, H.; Shah, S.; Hilt, D.; Peterkofsky, A.  
Gene 154, 237-242, 1995  
A/Title: Organization, sequence and regulation of expression of the murine Hoxa-7 gene.  
A/Reference number: I49131; MUID:95197009; PMID:7890170  
A/Accession: I49131  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-42; 'GAG', 46-229 <RES>  
A/Cross-references: EMBL:U15972; NID:g664757; PIDN:AAC52160.1; PID:g664758  
C/Genetics:  
A/Gene: Hoxa7  
A/Intons: 126/1  
C/Superfamily: homeotic protein Hox A7; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F/130-186/Domain: homeobox homology <HOX>

Query Match 67.6%; Score 100; DB 2; Length 229;  
Best Local Similarity 70.4%; Pred. No. 3.6e-07;  
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRQIKWPNRRMKWKKTALDASALQT 27  
:|||||  
Db 170 ERQIKWPNRRMKWKKTALDASALQT 196

RESULT 9  
I51341  
homeo box protein - Atlantic salmon (fragment)  
C/Species: Salmo salar (Atlantic salmon)  
C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 24-Sep-1999  
C/Accession: I51341  
R/Fjose, A.; Molven, A.; Eiken, H.G.  
Gene 62, 141-152, 1988

A/Title: Molecular cloning and characterization of homeobox-containing genes from Acta  
A/Reference number: I51341; MUID:88226009; PMID:2897318  
A/Accession: I51341  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-75 <FO>  
A/Cross-references: GB:M18903; NID:g213797; PIDN:AAA49559.1; PID:g213798  
C/Superfamily: unassigned homeobox proteins; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F/2-58/Domain: homeobox homology <HOX>

Query Match 66.9%; Score 99; DB 2; Length 75;  
Best Local Similarity 75.0%; Pred. No. 1.6e-07;  
Matches 18; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRQIKWPNRRMKWKKTALDASA 24  
:|||||  
Db 42 ERQIKWPNRRMKWKKTALDASA 65

RESULT 10  
S08303  
homeotic protein Hox 2.2 - chicken (fragment)  
C/Species: Gallus gallus (chicken)  
C/Date: 02-Dec-1993 #sequence\_revision 03-Aug-1995 #text\_change 17-Oct-1997  
C/Accession: S08303  
R/Wedden, S.E.; Pang, K.; Eichele, G.  
Development 105, 639-650, 1989  
A/Title: Expression pattern of homeobox-containing genes during chick embryogenesis.  
A/Reference number: S08302; MUID:90126373; PMID:2575515  
A/Accession: S08303  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-86 <WED>  
A/Cross-references: EMBL:X16847  
C/Superfamily: unassigned homeobox proteins; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F/10-66/Domain: homeobox homology <HOX>

Query Match 66.2%; Score 98; DB 2; Length 86;  
Best Local Similarity 66.7%; Pred. No. 2.6e-07;  
Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DRQIKWPNRRMKWKKTALDASALQTE 28  
:|||||  
Db 50 ERQIKWPNRRMKWKKTALDASALQTE 79

RESULT 11  
PC2399  
antennapedia-like homeotic protein Ahox 2 - sea equit (Styela clava) (fragment)  
C/Species: Styela clava  
C/Date: 13-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 21-Jul-2000  
C/Accession: PC2399  
R/Ge, T.; Lee, H.; Tomlinson, C.R.  
Gene 147, 219-222, 1994  
A/Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela  
A/Reference number: PC2399; MUID:95011617; PMID:7926803  
A/Accession: PC2399  
A/Molecule type: DNA  
A/Residues: 1-60 <GRT>  
A/Cross-references: GB:S73920; NID:g693714; PIDN:AAA33061.2; PID:g7387472  
A/Note: The authors translated the codon ATT for residue 47 as Glu  
C/Superfamily: unassigned homeobox proteins; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F/2-58/Domain: homeobox homology <HOX>

Query Match 65.5%; Score 97; DB 2; Length 60;  
Best Local Similarity 94.1%; Pred. No. 2.5e-07;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWPNRRMKWK 17  
:|||||

Db 42 DROVKIMFQNRMMKMKK 58

RESULT 12

PC2400

antennapedia-like homeotic protein Ahox 3 - sea squirt (Styela plicata) (fragment)

C/Species: Styela plicata

C/Date: 26-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 17-Oct-1997

C/Accession: PC2400

R/Gene: T.; Lee, H.; Tomlinson, C.R.

Gene 147, 219-222, 1994

A/Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela cl

A/Reference number: PC2399; MUID:95011617; PMID:7926803

A/Accession: PC2400

A/Molecule type: DNA

A/Residues: 1-60 <CET>

A/Note: The authors translated the codon ATA for residue 47 as Glu

C/Superfamily: unassigned homeobox proteins; homeobox homology

C/Keywords: DNA binding; homeobox; nucleus; transcription regulation

F/2-58/Domain: homeobox homology <HOX>

Query Match 65.5%; Score 97; DB 2; Length 60;

Best Local Similarity 94.1%; Pred. No. 2.5e-07;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DROIKIMFQNRMMKMKK 17

Db 42 DROVKIMFQNRMMKMKK 58

RESULT 13

S08639

homeotic protein zf-61 - zebra fish

C/Species: Brachydanio rerio (zebra fish)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-Sep-1999

C/Accession: S08639

R/NJ01etad, P.R.; Molven, A.; Apold, J.; Fjose, A.

EMBO J. 9, 515-524, 1990

A/Title: The zebrafish homeobox gene hox-2.2: transcription unit, potential regulatory

A/Reference number: S08639; MUID:90151628; PMID:1968004

A/Accession: S08639

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-96 <NCO>

A/Cross-references: EMBL:X17266; NID:962538; PIDN:CAA35170.1; PID:el6657; PID:91334622

C/Superfamily: unassigned homeobox proteins; homeobox homology

C/Keywords: DNA binding; homeobox; nucleus; transcription regulation

F/8-66/Domain: homeobox homology <HOX>

Query Match 65.2%; Score 96.5; DB 2; Length 96;

Best Local Similarity 69.0%; Pred. No. 4.8e-07;

Matches 20; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 1 DROIKIMFQNRMMKMKK-TALDASALQTE 28

Db 48 ERQIKIMFQNRMMKMKKETLSTVPGTE 76

RESULT 14

S00992

homeotic protein Hox 1 - African clawed frog

N/Alternate names: development-controlling protein; homeotic protein AC1; homeotic prote

C/Species: Xenopus laevis (African clawed frog)

C/Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 11-Jan-2002

C/Accession: S00992; S00993; A03116; S00590; T0106

R/Cho, K.W.Y.; Goetz, J.; Wright, C.V.E.; Fritz, A.; Hardwicke, J.; de Robertis, E.M.

EMBO J. 7, 2139-2149, 1988

A/Title: Differential utilization of the same reading frame in a Xenopus homeobox gene

A/Reference number: S00991; MUID:88329002; PMID:2901347

A/Accession: S00992

A/Molecule type: DNA

A/Residues: 1-234 <CHO>

A/Cross-references: EMBL:X12500; NID:964743; PIDN:CAA31021.1; PID:964744

A/Note: 216-Ser and 225-Gln were also found and are interpreted as minor allelic diffe

A/Accession: S00993

A/Molecule type: DNA

A/Residues: 83-215, 'S', 217-224, 'Q', 226-234 <CHW>

A/Cross-references: EMBL:X12499; NID:964740; PIDN:CAA1020.1; PID:964742

R/Carrasco, A.E.; McGinnis, W.; Gehring, W.J.; De Robertis, E.M.

Cell 37, 409-414, 1984

A/Title: Cloning of a Xenopus laevis gene expressed during early embryogenesis coding

A/Reference number: A03116; MUID:84205675; PMID:6327066

A/Accession: A03116

A/Molecule type: DNA

A/Residues: 134-138, 'S', 140-200 <CAR>

A/Cross-references: GB:K01943; NID:9214242; PIDN:AAA9743.1; PID:9214243

A/Note: The authors translated the codon AGC for residue 200 as Arg

R/Fritz, A.; de Robertis, E.M.

Nucleic Acids Res. 16, 1453-1469, 1988

A/Title: Xenopus homeobox-containing cDNAs expressed in early development.

A/Reference number: S00590; MUID:88157707; PMID:2894634

A/Accession: S00590

A/Molecule type: mRNA

A/Residues: 121-215, 'S', 217-224, 'Q', 226-234 <PRI>

A/Cross-references: EMBL:X07101; NID:964738; PIDN:CAA30122.1; PID:91334649

C/Genetics:

A/Gene: AC1

C/Superfamily: unassigned homeobox proteins; homeobox homology

C/Keywords: DNA binding; homeobox; nucleus; transcription regulation

F/1-234/Product: homeotic protein Hbox1, allelic version PRI #status predicted <MAT>

F/83-215/Product: homeotic protein Hbox1, allelic version PRI #status predicted <MAT>

F/142-198/Domain: homeobox homology <HOX>

Query Match 64.9%; Score 96; DB 2; Length 234;

Best Local Similarity 72.0%; Pred. No. 1.4e-06;

Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DROIKIMFQNRMMKMKKTALDASAL 25

Db 182 ERQIKIMFQNRMMKMKKESNLSSTL 206

RESULT 15

S15536

homeotic protein Hox A7 - human (fragment)

N/Alternate names: homeotic protein Hox 1A

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 29-Aug-1997

C/Accession: S15536

R/Boncinelli, E.; Acampora, D.; Pannese, M.; d'Episcopo, M.; Somma, R.; Gaudino, G.; S

Genome 31, 745-756, 1989

A/Title: Organization of human class I homeobox genes.

A/Reference number: S15036; MUID:90215256; PMID:2576652

A/Accession: S15536

A/Status: not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1-66 <BON>

C/Genetics:

A/Gene: GDB:H0XA7

A/Cross-references: GDB:120647; OMIM:142950

A/Map position: 7p15.3-7p15.3

C/Superfamily: unassigned homeobox proteins; homeobox homology

C/Keywords: DNA binding; homeobox; nucleus; transcription regulation

F/2-58/Domain: homeobox homology <HOX>

Query Match 64.2%; Score 95; DB 2; Length 66;

Best Local Similarity 81.0%; Pred. No. 5.4e-07;

Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DROIKIMFQNRMMKMKKTALD 21

Db 42 ERQIKIMFQNRMMKMKKSHKD 62

Search completed: February 18, 2004, 14:38:53

Job time : 30.7632 secs





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## OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 32.9737 Seconds  
(without alignments)  
35.929 Million cell updates/sec

Title: US-09-643-260-19

Perfect score: 148

Sequence: 1 DRQIKWFOQRNKKKTLADASALQTE 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	64.2	24	4 US-09-419-826-34	Sequence 34, Appl
2	95	64.2	27	4 US-09-040-725A-2	Sequence 2, Appl
3	94	63.5	34	4 US-09-347-504-79	Sequence 79, Appl
4	94	63.5	61	2 US-08-202-044-3	Sequence 3, Appl
5	94	63.5	61	3 US-08-751-348-3	Sequence 3, Appl
6	94	63.5	61	3 US-08-751-348-6	Sequence 6, Appl
7	94	63.5	61	3 US-08-751-348-9	Sequence 9, Appl
8	93	62.8	22	4 US-09-057-363C-50	Sequence 50, Appl
9	93	62.8	27	3 US-09-051-934-51	Sequence 51, Appl
10	93	62.8	27	3 US-09-051-934-52	Sequence 52, Appl
11	93	62.8	61	3 US-08-751-348-7	Sequence 7, Appl
12	92	62.2	16	2 US-08-928-958-7	Sequence 7, Appl
13	92	62.2	16	2 US-08-810-540-3	Sequence 3, Appl
14	92	62.2	16	2 US-08-810-540-6	Sequence 6, Appl
15	92	62.2	16	2 US-09-072-429-7	Sequence 7, Appl
16	92	62.2	16	2 US-08-964-302A-6	Sequence 6, Appl
17	92	62.2	16	3 US-09-116-294-4	Sequence 4, Appl
18	92	62.2	16	3 US-08-964-614A-4	Sequence 4, Appl
19	92	62.2	16	3 US-08-849-486-1	Sequence 1, Appl
20	92	62.2	16	3 US-08-849-486-4	Sequence 4, Appl
21	92	62.2	16	3 US-09-208-966-54	Sequence 54, Appl
22	92	62.2	16	3 US-09-308-935-8	Sequence 8, Appl
23	92	62.2	16	3 US-09-441-416A-6	Sequence 6, Appl
24	92	62.2	16	4 US-09-296-089-33	Sequence 33, Appl
25	92	62.2	16	4 US-09-419-826-35	Sequence 35, Appl
26	92	62.2	16	4 US-09-302-305C-10	Sequence 10, Appl
27	92	62.2	16	4 US-09-346-847-1	Sequence 1, Appl

28	92	62.2	16	4 US-09-346-847-25	Sequence 25, Appl
29	92	62.2	16	4 US-09-057-363C-47	Sequence 47, Appl
30	92	62.2	16	4 US-09-043-560B-3	Sequence 3, Appl
31	92	62.2	17	4 US-09-346-847-17	Sequence 17, Appl
32	92	62.2	17	4 US-09-346-847-20	Sequence 20, Appl
33	92	62.2	17	4 US-09-346-847-22	Sequence 22, Appl
34	92	62.2	17	4 US-09-346-847-27	Sequence 27, Appl
35	92	62.2	18	3 US-08-838-545-20	Sequence 20, Appl
36	92	62.2	18	3 US-09-349-532-20	Sequence 20, Appl
37	92	62.2	19	4 US-09-346-847-23	Sequence 23, Appl
38	92	62.2	19	4 US-09-658-517C-7	Sequence 7, Appl
39	92	62.2	20	4 US-09-466-772-3	Sequence 3, Appl
40	92	62.2	20	4 US-09-346-847-16	Sequence 16, Appl
41	92	62.2	20	4 US-09-346-847-18	Sequence 18, Appl
42	92	62.2	20	4 US-09-346-847-30	Sequence 30, Appl
43	92	62.2	20	4 US-09-658-517C-8	Sequence 8, Appl
44	92	62.2	22	4 US-09-466-847-28	Sequence 28, Appl
45	89	60.1	42	3 US-08-751-344B-4	Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-09-419-826-34  
Sequence 34, Application US/09419826  
Patent No. 6306832  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: PEPTIDE ANTINEOGEN COMPOSITIONS AND METHODS FOR TREATING BREAST CANCER  
NUMBER OF SEQUENCES: 39  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/419,826  
FILING DATE: 14-OCT-1999  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US98/07711  
FILING DATE: 14-APR-1998  
APPLICATION NUMBER: US 60/043,545  
FILING DATE: 14-APR-1997  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 19  
OTHER INFORMATION: /note= "X = Phosphotyrosine"  
US-09-419-826-34  
Query Match 64.2%; Score 95; DB 4; Length 24;  
Best Local Similarity 85.0%; Pred. No. 1.1e-07;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 RQIKWFOQRNKKKTLAD 21  
DB 1 RQIKWFOQRNKKKTLAD 20  
RESULT 2  
US-09-040-725A-2  
Sequence 2, Application US/09040725A  
Patent No. 6399584  
GENERAL INFORMATION:  
APPLICANT: Institut Curie  
APPLICANT: CNRS

APPLICANT: Arpin, Monique  
APPLICANT: Crepaldi, Tiziana  
APPLICANT: Gautreau, Alexis  
APPLICANT: Louvard, Daniel  
TITLE OF INVENTION: Pharmaceutical composition containing ezrin mutated  
TITLE OF INVENTION: on tyrosine 353  
FILE REFERENCE: 39108200100  
CURRENT APPLICATION NUMBER: US/09/040,725A  
CURRENT FILING DATE: 1998-03-18  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 27  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: variation  
LOCATION: (22)  
OTHER INFORMATION: Xaa = tyrosine or a phosphorylated tyrosine  
US-09-040-725A-2

Query Match 64.2%; Score 95; DB 4; Length 27;  
Best Local Similarity 66.7%; Pred. No. 1.2e-07;  
Matches 18; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 2 ROIKIWFQNRMRKMKKTALDASALQTE 28  
Db 1 ROIKIWFQNRMRKMKKRLQDXEERTK 27

RESULT 3  
US-09-347-504-79  
Sequence 79, Application US/09347504  
Patent No. 6399075  
GENERAL INFORMATION:  
APPLICANT: Howley, Peter M.  
APPLICANT: Benson, John  
APPLICANT: Kasukawa, Hiroaki  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING  
TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS  
FILE REFERENCE: HMV-041.01  
CURRENT APPLICATION NUMBER: US/09/347,504  
CURRENT FILING DATE: 1999-07-02  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 79  
LENGTH: 34  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-347-504-79

Query Match 63.5%; Score 94; DB 4; Length 34;  
Best Local Similarity 94.1%; Pred. No. 2.3e-07;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DROIKIWFQNRMRKMKK 17  
Db 1 EROIKIWFQNRMRKMKK 17

RESULT 4  
US-08-202-044-3  
Sequence 3, Application US/08202044  
Patent No. 5858973  
GENERAL INFORMATION:  
APPLICANT: Habener M.D., Joel F.  
APPLICANT: Miller Ph.D., Christopher P.  
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes  
STREET: Ten Post Office Square

CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,044  
FILING DATE: 23-FEB-1994  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Ph.D., Kathleen A.  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: MGH-124XX  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-2290  
TELEFAX: (617) 451-0313  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
US-08-202-044-3

Query Match 63.5%; Score 94; DB 2; Length 61;  
Best Local Similarity 94.1%; Pred. No. 4.3e-07;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DROIKIWFQNRMRKMKK 17  
Db 43 EROIKIWFQNRMRKMKK 59

RESULT 5  
US-08-751-344B-3  
Sequence 3, Application US/08751344B  
Patent No. 6210960  
GENERAL INFORMATION:  
APPLICANT: Habener M.D., Joel F.  
APPLICANT: Miller Ph.D., Christopher P.  
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Wilcoff, Ltd.  
STREET: One Financial Center  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/751,344B  
FILING DATE: 19-NOV-6210960-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/202,044  
FILING DATE: 23-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Ph.D., Kathleen M.  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 345-9100  
TELEFAX: (617) 345-9111  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
US-08-751-344B-3

Query Match 63.5%; Score 94; DB 3; Length 61;  
Best Local Similarity 94.1%; Pred. No. 4.3e-07;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRKMKKK 17  
:|||||

Db 43 ERQIKIWFQNRKMKKK 59

RESULT 6  
US-08-751-344B-6  
Sequence 6, Application US/08751344B  
Patent No. 6210960  
GENERAL INFORMATION:  
APPLICANT: Habener M.D., Joel F.  
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES  
TITLE OF INVENTION: THEREFOR  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Ltd.  
STREET: One Financial Center  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/751,344B  
FILING DATE: 19-No. 6210960-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/202,044  
FILING DATE: 23-Feb-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Ph.D., Kathleen M.  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 345-9100  
TELEFAX: (617) 345-9111  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
US-08-751-344B-6

Query Match 63.5%; Score 94; DB 3; Length 61;  
Best Local Similarity 94.1%; Pred. No. 4.3e-07;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRKMKKK 17

Db 43 ERQIKIWFQNRKMKKK 59  
:|||||

RESULT 7  
US-08-751-344B-9  
Sequence 9, Application US/08751344B  
Patent No. 6210960  
GENERAL INFORMATION:  
APPLICANT: Habener M.D., Joel F.  
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES  
TITLE OF INVENTION: THEREFOR  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff, Ltd.  
STREET: One Financial Center  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/751,344B  
FILING DATE: 19-No. 6210960-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/202,044  
FILING DATE: 23-Feb-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Ph.D., Kathleen M.  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 345-9100  
TELEFAX: (617) 345-9111  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
US-08-751-344B-9

Query Match 63.5%; Score 94; DB 3; Length 61;  
Best Local Similarity 94.1%; Pred. No. 4.3e-07;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRKMKKK 17  
:|||||

Db 43 ERQIKIWFQNRKMKKK 59

RESULT 8  
US-09-057-363C-50  
Sequence 50, Application US/09057363C  
Patent No. 6551994  
GENERAL INFORMATION:  
APPLICANT: Blaschuk, Orest W.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE  
INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed Intellectual Property Law Group  
STREET: 701 Fifth Avenue, Suite 6300  
CITY: Seattle

STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/057,363C  
FILING DATE: 08-Apr-1998  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Christensen, William T.  
REGISTRATION NUMBER: 44,614  
REFERENCE/DOCKET NUMBER: 100086.406  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 50:  
US-09-057-363C-50

Query Match 62.8%; Score 93; DB 4; Length 22;  
Best Local Similarity 94.1%; Pred. No. 2e-07;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DROIKWFORRMKMKK 17  
:|||||  
Db 6 NROIKWFORRMKMKK 22

RESULT 9  
US-09-051-934-51  
Sequence 51, Application US/09051934C  
Patent No. 6028053  
GENERAL INFORMATION:  
APPLICANT: Van der Geer  
TITLE OF INVENTION: Peptide Inhibitors of a Phosphotyrosine-Binding Domain  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/051,934C  
CURRENT FILING DATE: 1998-04-22  
EARLIER APPLICATION NUMBER: 60/011,799  
EARLIER FILING DATE: 1996-02-20  
EARLIER APPLICATION NUMBER: 60/010,384  
EARLIER FILING DATE: 1996-01-22  
EARLIER APPLICATION NUMBER: 60/005,944  
EARLIER FILING DATE: 1995-10-27  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 51  
LENGTH: 27  
TYPE: PRT  
ORGANISM: phosphotyrosine binding domain  
US-09-051-934-51

Query Match 62.8%; Score 93; DB 3; Length 27;  
Best Local Similarity 80.0%; Pred. No. 2.5e-07;  
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 ROIKWFORRMKMKKKTALD 21  
:|||||  
Db 1 ROIKWFORRMKMKKKTALD 20

RESULT 10  
US-09-051-934-52

Sequence 52, Application US/09051934C  
Patent No. 6028053  
GENERAL INFORMATION:  
APPLICANT: Van der Geer  
TITLE OF INVENTION: Peptide Inhibitors of a Phosphotyrosine-Binding Domain  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/051,934C  
CURRENT FILING DATE: 1998-04-22  
EARLIER APPLICATION NUMBER: 60/011,799  
EARLIER FILING DATE: 1996-02-20  
EARLIER APPLICATION NUMBER: 60/010,384  
EARLIER FILING DATE: 1996-01-22  
EARLIER APPLICATION NUMBER: 60/005,944  
EARLIER FILING DATE: 1995-10-27  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 52  
LENGTH: 27  
TYPE: PRT  
ORGANISM: phosphotyrosine binding domain  
FEATURE:  
NAME/KEY: MOD RES  
LOCATION: (24)  
OTHER INFORMATION: Phosphorylated at Tyr  
US-09-051-934-52

Query Match 62.8%; Score 93; DB 3; Length 27;  
Best Local Similarity 80.0%; Pred. No. 2.5e-07;  
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 ROIKWFORRMKMKKKTALD 21  
:|||||  
Db 1 ROIKWFORRMKMKKKTALD 20

RESULT 11  
US-08-751-344B-7  
Sequence 7, Application US/08751344B  
Patent No. 6210960  
GENERAL INFORMATION:  
APPLICANT: Habener M.D., Joel F.  
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES  
TITLE OF INVENTION: THEREFOR  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Wilcoff, Ltd.  
STREET: One Financial Center  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/751,344B  
FILING DATE: 19-NO. 6210960-1996  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER: 08/202,044  
FILING DATE: 23-Feb-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Ph.D., Kathleen M.  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 345-9111  
TELEFAX: (617) 345-9111  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
US-08-751-344B-7

Query Match 62.2%; Score 93; DB 3; Length 61;  
Best Local Similarity 88.2%; Pred. No. 6e-07;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKIWFQNRRMKWKK 17  
DB 43 ERQVKIWFQNRRMKWKK 59

RESULT 12  
US-08-928-958-7  
Sequence 7, Application US/08928958  
Patent No. 5877282  
GENERAL INFORMATION:  
APPLICANT: NADLER, STEVEN G.  
APPLICANT: CLEAVELAND, JEFFREY S.  
APPLICANT: BLAKE, JAMES  
APPLICANT: HAFER, OMAR K.  
TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN  
TITLE OF INVENTION: TRANSLLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROBINS & ASSOCIATES  
STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
CITY: MENLO PARK  
STATE: CA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/928,958  
FILING DATE: 12-SEP-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026978  
ATTORNEY/AGENT INFORMATION:  
FILING DATE: 20-SEP-1996  
NAME: ROBINS, ROBERTA L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5998-0019  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 325-7812  
TELEFAX: (650) 325-7823  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-928-958-7

Query Match 62.2%; Score 92; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RQIKIWFQNRRMKWKK 17  
DB 1 RQIKIWFQNRRMKWKK 16

RESULT 13  
US-08-810-540-3  
Sequence 3, Application US/08810540  
Patent No. 5929042  
GENERAL INFORMATION:  
APPLICANT: TROY, CAROL M.  
APPLICANT: SHELANAKI, MICHAEL L.  
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL  
TITLE OF INVENTION: DEATH AND USES THEREOF  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham, LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/810,540  
FILING DATE: 03-MAR-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq., John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/51247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0526  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-810-540-3

Query Match 62.2%; Score 92; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RQIKIWFQNRRMKWKK 17  
DB 1 RQIKIWFQNRRMKWKK 16

RESULT 14  
US-08-810-540-6  
Sequence 6, Application US/08810540  
Patent No. 5929042  
GENERAL INFORMATION:  
APPLICANT: TROY, CAROL M.  
APPLICANT: SHELANAKI, MICHAEL L.  
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL  
TITLE OF INVENTION: DEATH AND USES THEREOF  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham, LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/810,540  
FILING DATE: 03-MAR-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq., John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/51247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0526  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-810-540-6

Query Match 62.2%; Score 92; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ROIKIWFONRMRMKKK 17  
DB 1 ROIKIWFONRMRMKKK 16

RESULT 15  
US-09-072-429-7  
Sequence 7, Application US/09072429  
Patent No. 5962415  
GENERAL INFORMATION:  
APPLICANT: Nadler, Steven G.  
TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE  
TITLE OF INVENTION: INHIBITOR OF NUCLEAR PROTEIN TRANSLLOCATION AND AN  
TITLE OF INVENTION: IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bristol-Myers Squibb Company  
STREET: P.O. Box 4000  
CITY: Princeton  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 08543-4000  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/072,429  
FILING DATE: 04-MAY-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Klein, Christopher A.  
REGISTRATION NUMBER: 34,363  
REFERENCE/DOCKET NUMBER: ON0141b  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 252-3714  
TELEFAX: (609) 252-4526  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-072-429-7

Query Match 62.2%; Score 92; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 ROIKIWFONRMRMKKK 17  
DB 1 ROIKIWFONRMRMKKK 16

Search completed: February 18, 2004, 14:41:52  
Job time : 32.9737 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: February 18, 2004, 14:09:39 ; Search time 81.0526 Seconds  
(without alignments)  
89.145 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162

Sequence: 1 DRQIKIWFQNRRMKWKKALDMSWLGTE 28

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL\_23:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mmc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriophage:\*

17: sp\_archaeop:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101.5	62.7	274	5	Q9XYT7
2	97	59.9	108	5	Q26375
3	97	59.9	108	11	Q8UZW2
4	97	59.9	181	5	Q26611
5	97	59.9	194	5	Q26478
6	97	59.9	435	5	Q817C8
7	95.5	59.0	90	5	Q817C9
8	94	58.0	39	13	Q57368
9	94	58.0	43	13	Q57359
10	94	58.0	46	13	Q9PVR9
11	94	58.0	51	5	Q27413
12	94	58.0	51	5	Q23743
13	94	58.0	51	5	Q26407
14	94	58.0	57	13	Q9PVR8
15	94	58.0	57	13	Q9Y188
16	94	58.0	58	5	Q25208

17	94	58.0	58	13	Q57362	057362 brachydanio
18	94	58.0	59	5	Q8WRM9	Q8WRM9 lithobius a
19	94	58.0	59	5	Q9NB42	Q9NB42 anopheles g
20	94	58.0	59	13	Q9PVR5	Q9PVR5 oryzias lat
21	94	58.0	60	5	Q77143	Q77143 archegozete
22	94	58.0	60	5	Q77139	Q77139 archegozete
23	94	58.0	60	13	Q8QGL5	Q8QGL5 petromyzon
24	94	58.0	60	13	Q8QGL3	Q8QGL3 petromyzon
25	94	58.0	60	13	Q8QGL6	Q8QGL6 petromyzon
26	94	58.0	60	13	Q8QGL2	Q8QGL2 petromyzon
27	94	58.0	60	13	Q8QGL8	Q8QGL8 petromyzon
28	94	58.0	60	13	Q8QGL7	Q8QGL7 petromyzon
29	94	58.0	61	5	Q27910	Q27910 polyandroca
30	94	58.0	63	5	Q77138	Q77138 archegozete
31	94	58.0	63	5	Q8KMB2	Q8KMB2 holopneuste
32	94	58.0	66	13	Q57356	Q57356 brachydanio
33	94	58.0	69	5	Q9U9T4	Q9U9T4 nerela vires
34	94	58.0	69	5	Q9BMF7	Q9BMF7 halloctis ar
35	94	58.0	70	5	Q967W5	Q967W5 folisoma ca
36	94	58.0	71	13	Q9PVS3	Q9PVS3 oryzias lat
37	94	58.0	71	13	Q9PVS1	Q9PVS1 oryzias lat
38	94	58.0	73	5	Q9Y186	Q9Y186 priapulid c
39	94	58.0	74	13	Q57367	Q57367 brachydanio
40	94	58.0	75	5	Q25209	Q25209 junonia coe
41	94	58.0	75	13	Q9PVR6	Q9PVR6 oryzias lat
42	94	58.0	76	5	Q44257	Q44257 ethmostigm
43	94	58.0	77	5	Q44260	Q44260 ethmostigm
44	94	58.0	77	5	Q9Y187	Q9Y187 priapulid c
45	94	58.0	77	5	Q9U9Z4	Q9U9Z4 lingula ung

## ALIGNMENTS

### RESULT 1

Q9XYT7 PRELIMINARY; PRT; 274 AA.

AC Q9XYT7

DT 01-NOV-1999 (TRMBLrel. 12, Created)

DT 01-NOV-1999 (TRMBLrel. 12, Last sequence update)

DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)

DE SCOX-3 homeodomain protein (Fragment).

GN SCOX-3.

OS Casatlopea xamachana.

OC Eukaryota; Metazoa; Chordata; Scyphozoa; Rhizostomaeae; Casatlopeidae;

OC Casatlopea.

OX NCBI\_TaxID=12993;

RN [1]

RP SEQUENCE FROM N.A.

RA Kuhn K., Streit B., Schlierwater B.,

RT "Isolation of Hox genes from the scyphozoan Casatlopea xamachana:

RT Implications for the early evolution of Hox genes."

RL J. Exp. Zool. 0:0-0(1999).

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

DR EMBL; AF124593; AAD32577.1; -.

DR HSSP; P02833; 9ANT.

DR InterPro; IPR001356; Homeobox.

DR InterPro; IPR000047; HTH\_lambdarepressor.

DR Pfam; PF00046; homeobox\_1.

DR PRINTS; PR00024; HOMEBOX.

DR PRINTS; PR00031; HTHREPRESSR.

DR ProDom; PD000010; Homeobox; 1.

DR SMART; SM00389; HOK; 1.

DR PROSITE; PS00027; HOMEBOX\_1; 1.

DR PROSITE; PS00071; HOMEBOX\_2; 1.

KW DNA-binding; Homeobox; Nuclear protein.

FT NON\_TER

SQ

Query Match 62.7%; Score 101.5; DB 5; Length 274;

Best local similarity 64.5%; Pred. No. 7e-06;

Matches 20; Conservative 5; Mismatches 3; Indels 3; Gaps 1;

Qy 1 DROIKIFONRRMKKK--TALDMSWLOT 28  
 Db 182 EROIKIFONRRMKKKGGTTSIDANELEEE 212

## RESULT 2

ID Q26375 PRELIMINARY; PRT; 60 AA.  
 AC Q26375;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE DNA binding protein AHOX2 (Fragment).  
 GN AHOX2.  
 OS Styela clava (Sea squirt).  
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
 OC Stolidobranchia; Styelidae; Styela.  
 OX NCBI\_TaxId=7725;

RM [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95011617; PubMed=7926803;  
 RA Ge T., Lee H., Tomlinson C.R.;  
 RT "Identification of an antennapedia-like homeobox gene in the ascidians  
 RL Styela clava and S. plicata."  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL; S73920; AAB33061.2; -  
 DR HSSP; P02833; 9ANT.  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR000047; HTH\_lambdarepressr.  
 DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR PRODOM; PD00010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS50071; HOMEBOX\_2; 1.  
 DR DNA-binding; Homeobox; Nuclear protein.  
 FT NON\_TER 1  
 FT NON\_TER 60  
 SQ SEQUENCE 60 AA; 7630 MW; F506301E979BA25 CRC64;

Query Match 59.9%; Score 97; DB 5; Length 60;  
 Best Local Similarity 94.1%; Pred. No. 6.3e-06;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DROIKIFONRRMKKK 17  
 Db 42 DROIKIFONRRMKKK 58

## RESULT 3

ID Q8JZW2 PRELIMINARY; PRT; 108 AA.  
 AC Q8JZW2;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon;  
 RA Strusberg R.;  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC036986; AAH36986.1; -  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR000047; HTH\_lambdarepressr.  
 DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR00024; HOMEBOX.

DR PRINTS; PR00031; HTHREPRESSR.  
 DR Prodom; PD00010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS50071; HOMEBOX\_2; 1.  
 KM Hypothetical protein.  
 SQ SEQUENCE 108 AA; 13070 MW; 123A78FCDD0E7D90 CRC64;

Query Match 59.9%; Score 97; DB 11; Length 108;  
 Best Local Similarity 70.4%; Pred. No. 1.1e-05;  
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DROIKIFONRRMKKKTALDMSWLOT 27  
 Db 49 EROIKIFONRRMKKKHDESOAPT 75

## RESULT 4

ID Q26611 PRELIMINARY; PRT; 181 AA.  
 AC Q26611;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Homeobox protein (Fragment).  
 OS Styela plicata (Sea squirt).  
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
 OC Stolidobranchia; Styelidae; Styela.  
 OX NCBI\_TaxId=7726;

RM [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ascidian;  
 RA Ge T., Lee H., Tomlinson C.R.;  
 RT "Identification of an Antennapedia-like Homeobox Gene in the Ascidians  
 RL Styela clava and plicata."  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL; U05600; AAA16288.1; -  
 DR HSSP; P02833; 9ANT.  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR000047; HTH\_lambdarepressr.  
 DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR PRODOM; PD00010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS50071; HOMEBOX\_2; 1.  
 DR DNA-binding; Homeobox; Nuclear protein.  
 FT NON\_TER 1  
 FT NON\_TER 181  
 SQ SEQUENCE 181 AA; 20873 MW; AF39911408F06672 CRC64;

Query Match 59.9%; Score 97; DB 5; Length 181;  
 Best Local Similarity 94.1%; Pred. No. 1.9e-05;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DROIKIFONRRMKKK 17  
 Db 80 DROIKIFONRRMKKK 96

## RESULT 5

ID Q26478 PRELIMINARY; PRT; 194 AA.  
 AC Q26478;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Homeobox protein (Fragment).  
 OS Styela clava (Sea squirt).  
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
 OC Stolidobranchia; Styelidae; Styela.



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OX NCB1_TaxID=7725;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Ascidian;
RA Ge T., Lee H., Tomlinson C.R.;
RT "Identification of an Antennapedia-like Homeobox Gene in the Ascidians
  Styela clava and Plicata."
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; U05571; AA16226.1; -.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_LambdaRepressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR PRODOM; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KM DNA-binding; Homeobox; Nuclear protein.
FT NON_TER
SQ SEQUENCE 194 AA; 2186 MW; 8AD1B15B3E4800BC CRC64;

Query Match 59.9%; Score 97; DB 5; Length 194;
Best Local Similarity 94.1%; Pred. No. 2e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFGNRKMKKK 17
DB 52 DRQVKIWFQNRKMKKK 68

RESULT 6
ID Q817C8 PRELIMINARY; PRT; 435 AA.
AC Q817C8;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Putative homeobox protein Hox10.
GN HOX10.
OS Clona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Clona.
OX NCB1_TaxID=7719;
RN RN
RP SEQUENCE FROM N.A.
RA Spagnuolo A., Ristoreatore F., Di Gregorio A., Anello F., Branno M.,
  Di Lauro R.;
RT "Unusual number and genomic organization of Hox genes in the tunicate
  Clona intestinalis."
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ535675; CAD59670.1; -.
DR Homeobox; DNA-binding; Nuclear protein.
SQ SEQUENCE 435 AA; 48739 MW; D8D0F579C02BC9E2 CRC64;

Query Match 59.9%; Score 97; DB 5; Length 435;
Best Local Similarity 94.1%; Pred. No. 4.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFGNRKMKKK 17
DB 295 DRQVKIWFQNRKMKKK 311

RESULT 7
ID Q817C9 PRELIMINARY; PRT; 90 AA.
AC Q817C9;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

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DE Putative homeobox protein Hox6/7 (Fragment).
GN HOX6/7.
OS Clona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Clona.
OX NCB1_TaxID=7719;
RN RN
RP SEQUENCE FROM N.A.
RA Spagnuolo A., Ristoreatore F., Di Gregorio A., Anello F., Branno M.,
  Di Lauro R.;
RT "Unusual number and genomic organization of Hox genes in the tunicate
  Clona intestinalis."
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ535674; CAD59670.1; -.
KM Homeobox; DNA-binding; Nuclear protein.
FT NON_TER
SQ SEQUENCE 90 AA; 11352 MW; CAAD6B261FE908E CRC64;

Query Match 59.0%; Score 95.5; DB 5; Length 90;
Best Local Similarity 57.6%; Pred. No. 1.5e-05;
Matches 19; Conservative 3; Mismatches 6; Indels 5; Gaps 1;

QY 1 DRQIKWFGNRKMKKTALDWS----WLTQE 28
DB 57 ERQIKWFGNRKMKKKENDIAESNNWECRE 89

RESULT 8
ID Q57368 PRELIMINARY; PRT; 39 AA.
AC Q57368;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hoxc5 protein (Fragment).
GN HOC5A OR HOC5.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCB1_TaxID=7955;
RN RN
RP SEQUENCE FROM N.A.
RA Prince V.E., Joly L., Ekker M., Ho R.K.;
RT "Zebrafish hox genes: genomic organization and modified colinear
  expression patterns in the trunk."
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; Y14539; CAAT4874.1; -.
DR ZFIN; ZDB-GENE-980526-533; hoxc5a.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_LambdaRepressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR PRODOM; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KM DNA-binding; Homeobox; Nuclear protein.
FT NON_TER
SQ SEQUENCE 39 AA; 4827 MW; 592A0FEC12B58860 CRC64;

Query Match 58.0%; Score 94; DB 13; Length 39;
Best Local Similarity 94.1%; Pred. No. 1e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRQIKWFGNRKMKKK 17
DB 13 BRQIKWFGNRKMKKK 29

RESULT 9

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057359          PRELIMINARY;      PRT;      43 AA.
ID 057359
AC 057359
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE Hoxa5 protein (Fragment).
GN Hoxb5b OR Hoxa5.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
OX
RN
RP SEQUENCE FROM N.A.
RA Prince V.E., Joly L., Ekker M., Ho R.K.;
RT "Zebrafish hox genes: genomic organization and modified colinear
RT expression patterns in the trunk."
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; Y14526; CAAT4861.1; -.
DR ZFIN; ZDB-GENE-000823-6; hoxb5b.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KM DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 43 AA; 5050 MW; 53034C37F3DFA596 CRC64;

Query Match      58.0%; Score 94; DB 13; Length 43;
Best Local Similarity 94.1%; Pred. No. 1.1e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIFQNRMMKKK 17
   :|||||
Db 9 EROIKIFQNRMMKKK 25

RESULT 10
Q9PVR9          PRELIMINARY;      PRT;      46 AA.
ID Q9PVR9
AC Q9PVR9
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE HoxC5A (Fragment).
GN HoxC5A.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adiantichthyidae; Oryziinae; Oryzias.
OC NCBI_TaxID=8090;
OX
RN
RP SEQUENCE FROM N.A.
RA Kondo S., Naruse K., Shima A.;
RT "Hox genes of the medaka fish Oryzias latipes."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AB026960; BAA86243.1; -.
DR HSSP; P02833; IHOM.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KM DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 46 AA; 5955 MW; 60399999ED4294D3 CRC64;

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Query Match      58.0%; Score 94; DB 13; Length 46;
Best Local Similarity 94.1%; Pred. No. 1.2e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIFQNRMMKKK 17
   :|||||
Db 22 EROIKIFQNRMMKKK 38

RESULT 11
Q27413          PRELIMINARY;      PRT;      51 AA.
ID Q27413
AC Q27413
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE LOX5 ORTHOLOG homeobox (Fragment).
GN CTS-LOX5.
OS Ctenodrilus serratus.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
OC Terebellida; Ctenodrilidae; Ctenodrilus.
OC NCBI_TaxID=40316;
OX
RN
RP SEQUENCE FROM N.A.
RA Dick M.H., Bues L.W.;
RX MEDLINE=94356262; PubMed=7915607;
RA Dick M.H., Bues L.W.;
RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus
RT (Annelida: Polychaeta)."
RL Mol. Phylogenet. Evol. 3:146-158(1994).
RN
RP SEQUENCE FROM N.A.
RA Dick M.H., Bues L.W.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; U26629; AAC46851.1; -.
DR EMBL; S76226; AAB31777.1; -.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambdarepress.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KM DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
SQ SEQUENCE 51 AA; 6278 MW; 88C8F65161E94A22 CRC64;

Query Match      58.0%; Score 94; DB 5; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.4e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIFQNRMMKKK 17
   :|||||
Db 22 EROIKIFQNRMMKKK 38

RESULT 12
Q23743          PRELIMINARY;      PRT;      51 AA.
ID Q23743
AC Q23743
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Deformed ortholog homeobox (Fragment).
GN CTS-DFD.
OS Ctenodrilus serratus.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
OC Terebellida; Ctenodrilidae; Ctenodrilus.

```

OX NCBI\_TaxID=40316;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94356262; PubMed=7915607;  
 RA "A PCR-based survey of homeobox genes in Ctenodrilus serratus  
 RT (Annelida: Polychaeta)."  
 RL Mol. Phylogenet. Evol. 3:146-158(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Dick M.H., Bues L.W.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL; U02833; AAC46849.1; -.  
 DR HSSP; P02833; 9ANT.  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR000047; HTH\_lambdarepressr.  
 DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR PRINTS; PR00031; HTHREPRESSR.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS50071; HOMEBOX\_2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON\_TER 1 1  
 FT SEQUENCE 51 AA; 6533 MW; 9EDB50C927FBCBD5 CRC64;  
 SQ  
 Query Match 58.0%; Score 94; DB 5; Length 51;  
 Best Local Similarity 94.1%; Pred. No. 1.4e-05;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIFQNRMKKK 17  
 DB 22 EROIKIFQNRMKKK 38

RESULT 13  
 Q26407  
 ID Q26407 PRELIMINARY; PRT; 51 AA.  
 AC Q26407;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Cts-Did protein (fragment).  
 GN CTS-DPD.  
 OS Ctenodrilus serratus.  
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;  
 OC Terebellida; Ctenodrilidae; Ctenodrilus.  
 OC NCBI\_TaxID=40316;  
 OX [1]  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94356262; PubMed=7915607;  
 RA Dick M.H., Bues L.W.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL; S76416; AAB31775.1; -.  
 DR HSSP; P02833; 9ANT.  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR000047; HTH\_lambdarepressr.  
 DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR PRINTS; PR00031; HTHREPRESSR.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR SMART; SM00389; HOK; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS50071; HOMEBOX\_2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON\_TER 1 1  
 FT SEQUENCE 51 AA; 6533 MW; 9EDB50C927FBCBD5 CRC64;  
 SQ

Query Match 58.0%; Score 94; DB 5; Length 51;  
 Best Local Similarity 94.1%; Pred. No. 1.4e-05;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIFQNRMKKK 17  
 DB 22 EROIKIFQNRMKKK 38

RESULT 14  
 Q9PVR8  
 ID Q9PVR8 PRELIMINARY; PRT; 57 AA.  
 AC Q9PVR8;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE HOXA5A (Fragment).  
 GN HOXA5A.  
 OS Oryzias latipes (Medaka fish) (Japanese ricefish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorphia; Acanthopterygii; Percomorpha; Atherinomorphia;  
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.  
 OX NCBI\_TaxID=8090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kondo S., Naruse K., Shima A.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL; AB026961; BA06244.1; -.  
 DR HSSP; P02833; 1HOM.  
 DR InterPro; IPR001356; Homeobox.  
 DR Pfam; PF00046; homeobox; 1.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR SMART; SM00389; HOK; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS50071; HOMEBOX\_2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON\_TER 1 1  
 FT SEQUENCE 57 AA; 6891 MW; 5A6430320F68C04 CRC64;  
 SQ  
 Query Match 58.0%; Score 94; DB 13; Length 57;  
 Best Local Similarity 94.1%; Pred. No. 1.5e-05;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIFQNRMKKK 17  
 DB 22 EROIKIFQNRMKKK 38

RESULT 15  
 Q9Y188  
 ID Q9Y188 PRELIMINARY; PRT; 58 AA.  
 AC Q9Y188;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Hbl homeodomain protein (fragment).  
 GN Hbl.  
 OS Priapulus caudatus.  
 OC Eukaryota; Metazoa; Priapulida; Priapulidae; Priapulins.  
 OC NCBI\_TaxID=37621;  
 OX [1]  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99318125; PubMed=10391241;  
 RA de Rosa R., Grenier J.K., Andreeva T., Cook C.E., Adoutte A., Akam M.,  
 RA Carroll S.B., Balavoine G.;  
 RL "Hox genes in brachiopods and priapulids and protostome evolution."  
 RL Nature 399:772-776(1999).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL; AF144888; AAD40644.1; -.  
 DR HSSP; P02833; 9ANT.  
 SQ

DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR000047; HTR\_Lambdarepressr.  
DR Pfam; PF00046; Homeobox; 1.  
DR PRINTS; PR00024; HOMEBOX.  
DR PRINTS; PR00031; HTRREPRESSR.  
DR ProDom; PD00010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00027; HOMEBOX\_1; 1.  
DR PROSITE; PS00721; HOMEBOX\_2; 1.  
DR DNA-binding; Homeobox; Nuclear protein.  
KW NON\_TER 1  
SQ SEQUENCE 58 AA; 7323 MW; 572F30DA57C9A613 CRC64;

Query Match 58.0%; Score 94; DB 5; Length 58;  
Best Local Similarity 94.1%; Pred. No. 1.5e-05;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DROIKIFQNRMRMKKK 17  
:|||||  
Db 23 EROIKIFQNRMRMKKK 39

Search completed: February 18, 2004, 14:36:01  
Job time : 83.0526 secs

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OM protein - protein search, using SW model

Run on: February 18, 2004, 13:39:39 ; Search time 16.5789 Seconds  
(without alignments)  
79.423 Million cell updates/sec

Title: US-09-643-260-18

Perfect score: 162  
Sequence: 1 DRQIKWIFQNRMRKMKKTALDMSWLQTE 28

Scoring table: BLASTSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	59.9	105	1 HXA7_RAT	P09634 ratnus norv
2	97	59.9	229	1 HXA7_MOUSE	P02830 mus musculu
3	96	59.3	75	1 HXA7_SALSA	P09636 salmo salar
4	95	58.6	224	1 HXB6_HUMAN	P17509 homo sapien
5	95	58.6	224	1 HXB6_MOUSE	P09023 mus musculu
6	95	58.6	230	1 HXA7_HUMAN	P31568 homo sapien
7	94	58.0	48	1 HXB6_XENLA	P31565 xenopus lae
8	94	58.0	49	1 HXA5_SHEEP	P02859 ovis aries
9	94	58.0	71	1 HXA7_SHEEP	P02860 ovis aries
10	94	58.0	71	1 HXC5_NOTVI	P31562 notophthalm
11	94	58.0	74	1 HX90_APIME	P15860 apis mellif
12	94	58.0	76	1 HXC4_RAT	P15865 ratnus norv
13	94	58.0	78	1 HXA5_SALSA	P09637 salmo salar
14	94	58.0	80	1 HXA4_LINSA	P81192 linus gang
15	94	58.0	81	1 HXB5_BRARE	P09013 brachydantio
16	94	58.0	82	1 HXB5_CHICK	P14838 gallus gall
17	94	58.0	84	1 HXB6_CHICK	P14839 gallus gall
18	94	58.0	86	1 SCR_APIME	P15869 apis mellif
19	94	58.0	87	1 HXC5_XENLA	P09020 xenopus lae
20	94	58.0	93	1 HXB6_PIG	P09078 sus scrofa
21	94	58.0	96	1 HXC6_BRARE	P15862 brachydantio
22	94	58.0	105	1 HXB4_BRARE	P22574 brachydantio
23	94	58.0	112	1 HXB7_RAT	P18864 ratnus norv
24	94	58.0	148	1 HXA5_AMBMB	P50208 ambystoma m
25	94	58.0	153	1 HXC6_SHEEP	P49925 ovis aries
26	94	58.0	209	1 HXA7_HETFR	P09071 xenopus lae
27	94	58.0	209	1 HXA7_XENLA	P09070 xenopus lae
28	94	58.0	217	1 HXB7_BOVIN	P09078 bos taurus
29	94	58.0	217	1 HXB7_HUMAN	P09024 mus musculu
30	94	58.0	217	1 HXB7_MOUSE	P09024 mus musculu
31	94	58.0	220	1 HXB7_XENLA	P04476 xenopus lae
32	94	58.0	220	1 HXB7_XENLA	P04476 xenopus lae
33	94	58.0	222	1 HXC5_HUMAN	P00444 homo sapien

34	94	58.0	222	1 HXC5_MOUSE	P32043 mus musculu
35	94	58.0	225	1 HXA7_MORSA	P09644 morone saxa
36	94	58.0	228	1 HXB6_BRARE	P15861 brachydantio
37	94	58.0	229	1 HXA5_HETFR	P09019 xenopus lae
38	94	58.0	230	1 HXB5_XENLA	P09019 xenopus lae
39	94	58.0	232	1 HXA6_MOUSE	P09092 mus musculu
40	94	58.0	232	1 HXA4_XENLA	P09070 xenopus lae
41	94	58.0	232	1 HXC5_BRARE	P09074 brachydantio
42	94	58.0	233	1 HXA5_RAT	P52949 ratnus norv
43	94	58.0	233	1 HXA6_HUMAN	P31267 homo sapien
44	94	58.0	234	1 HXC6_NOTVI	P14858 notophthalm
45	94	58.0	234	1 HXC6_XENLA	P02832 xenopus lae

## ALIGNMENTS

RESULT 1  
HXA7\_RAT  
ID HXA7\_RAT  
AC P09634;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Homeobox protein Hox-A7 (Hox-1.1) (R3) (Fragment).  
GN HoxA7 OR HOXA-7.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OK NCBI\_Taxid=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=87277429; PubMed=2886401;  
RA Falzon M., Sanderson N., Chung S.Y.;  
RT "Cloning and expression of rat homeo-box-containing sequences."  
RL Gene 54:23-32(1987).  
CC  
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
CC  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC  
CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.  
CC  
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CC  
CC -----  
CC EMBL: M16807; -; NOT\_ANNOTATED\_CDS.  
CC PIR: A27471; A27471.  
CC  
CC DR HSSP: P02833; NANT.  
CC DR TRANSFAC: T01707; -;  
CC DR INTERPRO: IPR001827; Antennapedia.  
CC DR INTERPRO: IPR001356; Homeobox.  
CC Pfam: PF00046; homeobox; 1.  
CC DR PRINTS: PR00024; HOMEOBOX.  
CC DR PRODOM: PD000010; Homeobox; 1.  
CC DR SMART: SM00389; HOX; 1.  
CC DR PROSITE: PS00032; ANTENNAPEDIA; PARTIAL.  
CC DR PROSITE: PS00027; HOMEOBOX\_1; 1.  
CC DR PROSITE: PS00071; HOMEOBOX\_2; 1.  
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
CC Transcription regulation.  
CC KW NON\_TER  
CC FT DNA\_BIND 1  
CC FT DOMAIN 5 64  
CC FT SEQUENCE 105 AA; 12552 MW; 106C1DF938F2864B CRC64;  
Query Match  
Best Local Similarity 59.9%; Score 97; DB 1; Length 105;  
70.4%; Pred. No. 1.1e-06;

Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DROIKIWFQNRBMKKTALDMSWLOT 27  
 Db 46 EROIKIWFQNRBMKKTALDMSWLOT 72

RESULT 2  
 HXA7 MOUSE STANDARD; PRT; 229 AA.

AC P02830; 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Homeobox protein Hox-A7 (Hox-1.1) (M6-12) (M6).  
 GN HXA7 OR HXA7-7 OR HXA7-1.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87260976; PubMed=2885847;  
 RA Kessel M., Schultze F., Fidi M., Gruss P.;  
 RT "Primary structure and nuclear localization of a murine homeobox domain protein";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5306-5310(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=95197009; PubMed=7890170;  
 RA Parikh H., Shah S., Hilt D., Peterkofsky A.;  
 RT "Organization, sequence and regulation of expression of the murine Hoxa-7 gene";  
 RL Gene 154:237-242(1995).  
 RN [3]  
 RP SEQUENCE OF 126-229 FROM N.A.  
 RX MEDLINE=85188311; PubMed=2986010;  
 RA Colberg-Poley A.M., Voss S.D., Chowdhury K., Gruss P.;  
 RT "Structural analysis of murine genes containing homeo box sequences and their expression in embryonal carcinoma cells";  
 RL Nature 314:713-718(1985).  
 RN [4]  
 RP SEQUENCE OF 129-197 FROM N.A.  
 RX MEDLINE=87053860; PubMed=287873;  
 RA Breier G., Bucan M., Francke U., Colberg-Poley A.M., Gruss P.;  
 RT "Sequential expression of murine homeo box genes during F9 EC cell differentiation";  
 RL EMBO J. 5:2209-2215(1986).  
 RL -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; M17192; AAA37833.1; -;  
 DR EMBL; U15972; AAC52160.1; -;  
 DR PIR; A03314; A03314.  
 DR PIR; A28329; A28329.  
 DR HSSP; P02833; 9ANT.  
 DR TRASNFPAC; T01278; -;  
 DR MGD; MGI:96179; Hoxa7.  
 DR InterPro; IPR001827; Antennapedia.  
 DR InterPro; IPR001356; Homeobox.  
 DR Pfam; PF00046; homeobox; 1.

DR PRINTS; PR00025; ANTENNAPEIDIA.  
 DR PRINTS; PR00024; HOMEOBOX.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00032; ANTENNAPEIDIA; 1.  
 DR PROSITE; PS00027; HOMEOBOX\_1; 1.  
 DR PROSITE; PS00071; HOMEOBOX\_2; 1.  
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 KM Transcription regulation.  
 FT SITE 118 123 ANTP-TYPE HEXAPEPTIDE.  
 FT DNA\_BIND 129 188 HOMEOBOX.  
 FT DOMAIN 156 159 POLY-ARG.  
 FT DOMAIN 211 229 ASP/GLU-RICH (HIGHLY ACIDIC).  
 FT DOMAIN 215 229 POLY-GLU.  
 FT CONFLICT 43 45 GAG -> APA (IN REF. 1).  
 SQ SEQUENCE 229 AA; 25682 MW; D3E6BD61D8DC6F CRC64;

Query Match Score 97; DB 1; Length 229;  
 Best Local Similarity 70.4%; Fred. No. 2.4e-06;  
 Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DROIKIWFQNRBMKKTALDMSWLOT 27  
 Db 170 EROIKIWFQNRBMKKTALDMSWLOT 196

RESULT 3  
 HMSA SALSA STANDARD; PRT; 75 AA.

AC P09636; 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Homeobox protein S12-A (Fragment).  
 OS Salmo salar (Atlantic salmon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
 CX NCBI\_TaxId=8030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88226009; PubMed=2897318;  
 RA Fjose A., Mølven A., Eiken H.G.;  
 RT "Molecular cloning and characterization of homeo-box-containing genes from Atlantic salmon";  
 RL Gene 62:141-152(1988).  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).  
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; M18903; AAA49559.1; -;  
 DR PIR; I51341; I51341.  
 DR HSSP; P02833; 9ANT.  
 DR InterPro; IPR001356; Homeobox.  
 DR Pfam; PF00046; homeobox; 1.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEOBOX\_1; 1.  
 DR PROSITE; PS00071; HOMEOBOX\_2; 1.  
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.  
 FT NON\_TER 1 1  
 FT DNA\_BIND 1 60 HOMEOBOX.  
 FT NON\_TER 75 75  
 SQ SEQUENCE 75 AA; 9330 MW; FC02C3672F35475D CRC64;

Query Match Score 96; DB 1; Length 75;

Best Local Similarity 78.3%; Pred. No. 1e-06;  
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DROIKIWFONRMKMKKTALDWS 23  
Db 42 EROIKIWFONRMKMKKHDEHS 64

RESULT 4  
HXB6 HUMAN STANDARD; PRT; 224 AA.  
AC P17509; P09068; Q9HB11; Q9UGH2;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Homeobox protein Hox-B6 (Hox-2.2) (HU-2).  
GN HOXB6 OR HOXB2.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RC TISSUE=Placenta;  
RX MEDLINE=91187672; PubMed=1672751;  
RA Shen W.-F., Delmer K., Simonitch-T.A., Lawrence H.J.,  
LA Largman C.;  
RT "Alternative splicing of the HOX 2.2 homeobox gene in human  
hematopoietic cells and murine embryonic and adult tissues";  
RL Nucleic Acids Res. 19:539-545(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Frezza D., D'Esposito M., Migliaccio E., Santini S.M., Frasca A.;  
RT "Expression of HOX genes in T lymphocytes and hairy leukemia cell  
lines";  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Kidd K.K., Buoygina V., Demille M.M.C., Speed W.C., Ruggeri V.,  
RT "Overall linkage disequilibrium in 33 populations for highly  
informative multiallelic haplotypes spanning the HOXB gene cluster";  
RL Am. J. Hum. Genet. 67:235-235(2000).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein M.J., Udell T.B., Toohyuk S., Cantucci P., Prange C.,  
RA Raba S.S., Loguelfino N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalobos S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
RA Phelan J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP SEQUENCE OF 135-224 FROM N.A.  
RX MEDLINE=90046832; PubMed=2573064;  
RA Shen W.-F., Largman C., Lowney P., Corral J.C., Delmer K.,  
RA Hauser C.A., Simonitch T.A., Hack F.M., Lawrence H.J.;  
RT "Lineage-restricted expression of homeobox-containing genes in human

RT hematopoietic cell lines";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:8536-8540(1989).  
RN [6]  
RP PRELIMINARY SEQUENCE OF 136-240 FROM N.A.  
RX MEDLINE=85024858; PubMed=6091895;  
RA Levine M., Rubin G.M., Tjian R.;  
RT "Human DNA sequences homologous to a protein coding region conserved  
between homeotic genes of Drosophila";  
RL Cell 38:667-673(1984).  
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=P17509-1; Sequence=Displayed;  
CC Name=2; Synonym=Homeobox-1e68;  
CC IsoId=P17509-2; Sequence=VSP\_002389, VSP\_002389;  
CC -1- SIMILARITY: BELONGS TO THE ANTF HOMEOBOX FAMILY.  
CC -----  
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CC -----  
DR EMBL; X58431; CAA41335.1; -  
DR EMBL; X58431; CAA41336.1; -  
DR EMBL; AJ270993; CAB65909.1; -  
DR EMBL; AF287967; AAG31552.1; -  
DR EMBL; BC014651; AAH14651.1; -  
DR EMBL; M30597; AAA36004.1; -  
DR EMBL; X02571; -; NOT\_ANNOTATED\_CDS.  
DR PIR; S26400; S26400.  
DR HSSP; P02833; IHOM.  
DR TRANSFAC; T01732; -  
DR Genew; HGNC:5117; HOXB6.  
DR MIM; 142961; -  
DR GO; GO:0005634; C:nucleus; NAS.  
DR GO; GO:0003700; F:transcription factor activity; NAS.  
DR GO; GO:0008595; P:determination of anterior/posterior axis, e...; NAS.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.  
DR InterPro; IPR001827; Antennapedia.  
DR InterPro; IPR001356; Homeobox.  
DR Pfam; PF00046; homeobox; 1.  
DR PRINTS; PR00025; ANTENNAPEDIA.  
DR PRINTS; PR00024; HOMEBOX.  
DR ProDom; PD000010; HOMEBOX.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00032; ANTENNAPEDIA; 1.  
DR PROSITE; PS00027; HOMEBOX; 1.  
DR PROSITE; PS50071; HOMEBOX; 2; 1.  
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
KW Transcription regulation; Alternative splicing.  
KW SITE 127 132  
FT DNA BIND 146 205  
FT DOMAIN 216 220  
FT VARSPLIC 140 140  
FT FTID=VSP\_002389.  
FT VARSPLIC 141 224  
FT FTID=VSP\_002389.  
FT CONFLICT 24 25  
FT CONFLICT 33 33  
FT CONFLICT 60 60  
FT CONFLICT 73 73  
FT CONFLICT 149 150  
SQ SEQUENCE 224 AA; 25427 MW; D8P6FAAC93D878 CRC64;  
Query Match 58.6%; Score 95; DB 1; Length 224;  
Best Local Similarity 66.7%; Pred. No. 4.5e-06;

Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Oy 1 DROIKIFQNRBMKKKTA--LDMSWLQTE 28  
 Db 187 EROIKIFQNRBMKKKESKLSASQLSAE 216

RESULT 5  
 ID\_HXB6\_MOUSE STANDARD; PRT; 224 AA.

AC P09023; 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 10, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Homeobox protein Hox-B6 (Hox-2.2) (MH-22A).  
 GN HOXB6 OR HOXB-6 OR HOX-2.2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88289762; PubMed=2898993;  
 RA Schugart K., Utset M.F., Awgulewitsch A., Ruddle P.H.;  
 RT "Structure and expression of Hox-2.2, a murine homeobox-containing gene."  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:5582-5586(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91187672; PubMed=1672751;  
 RA Shen W.F., Detmer K., Simolitch-Eason T.A., Lawrence H.J.,  
 RA Largman C.;  
 RT "Alternative splicing of the HOX 2.2 homeobox gene in human hematopoietic cells and murine embryonic and adult tissues."  
 RL Nucleic Acids Res. 19:539-545(1991).  
 RN [3]  
 RP SEQUENCE OF 144-224 FROM N.A.  
 RX MEDLINE=88054465; PubMed=2890503;  
 RA Lonai P., Arman B., Czoenek H., Ruddle P.H., Blatt C.;  
 RT "New murine homeoboxes: structure, chromosomal assignment, and differential expression in adult erythropoiesis."  
 RL DNA 6:409-418(1987).  
 RN [4]  
 RP SEQUENCE OF 140-224 FROM N.A.  
 RX MEDLINE=88085193; PubMed=2891608;  
 RA Hart C.P., Fainrod A., Ruddle P.H.;  
 RT "Sequence analysis of the murine Hox-2.2, -2.3, and -2.4 homeo boxes: evolutionary and structural comparisons."  
 RL Genomics 1:182-195(1987).  
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL, M18166; AAA37844.1; -;  
 DR EMBL, X56459; CAA39834.1; -;  
 DR EMBL, M18401; AAC27130.1; ALT\_SEQ.  
 DR EMBL, J03782; AAA37843.1; -;  
 DR PIR, A31324; A31324.  
 DR HSSP, P02833; 1HOM.  
 DR TRNSPAC, T01733; -;  
 DR MGD, MGI:96187; Hoxb6.  
 DR InterPro, IPR001827; Antennapedia.  
 DR InterPro, IPR001356; Homeobox.

DR Pfam; PF00046; homeobox; 1.  
 DR PRINTS; PR00025; ANTENNAPEDIA.  
 DR PRINTS; PR00024; HOMEBOX.  
 DR Prodom; PD000010; Homeobox; 1.  
 DR SMART; SM00389; HOX; 1.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.  
 DR PROSITE; PS50071; HOMEBOX\_2; 1.  
 KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 KW Transcription regulation.  
 FT SITE 127 132 ANTP-TYPE HEXAPEPTIDE.  
 FT DOMAIN 146 205 HOMEBOX.  
 FT DOMAIN 216 220 POLY-GLU.  
 FT CONFLICT 186 186 T -> P (IN REF. 3).  
 SQ SEQUENCE 224 AA; 25310 MW; E8FC0DBE57F5C3D CRC64;

Query Match 58.6%; Score 95; DB 1; Length 224;  
 Best Local Similarity 66.7%; Pred. No. 4; Se-06;  
 Matches 20; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Oy 1 DROIKIFQNRBMKKKTA--LDMSWLQTE 28  
 Db 187 EROIKIFQNRBMKKKESKLSASQLSAE 216

RESULT 6  
 ID\_HXA7\_HUMAN STANDARD; PRT; 230 AA.

AC P1256; 043368; 043486; 095655; Q9NSC8; Q9UDM1;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Homeobox protein Hox-A7 (Hox-1A) (Hox 1.1).  
 GN HOXA7 OR HOX1A.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX POLAKOWSKA R., LACELLE P.T.;  
 RA Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99023755; PubMed=9804983;  
 RA McMillan M.A., Bremner P.S., McMullin M.F., Maxwell A.P.,  
 RA Winter P.C., Lappin T.R.;  
 RT "Sequence characterization and expression of homeobox HOX A7 in the multi-potential erythroleukemic cell line TF-1."  
 RL Biochim. Biophys. Acta 1442:329-333(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA BREDSHAW H., HINDS K., KEPPLER D.;  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20369265; PubMed=10911612;  
 RA Kim M.H., Jin H., Seol E.Y., Yoo M., Park H.W.;  
 RT "Sequence analysis and tissue specific expression of human HOXA7."  
 RL Mol. Biotechnol. 14:19-24(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RA Albrechtsen R., Wewer U.;  
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE OF 1-91 FROM N.A.  
 RA Cho M., Kim M.H., Hwang C.Y., Min W.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE OF 130-195 FROM N.A.  
 RX MEDLINE=90215256; PubMed=2576652;  
 RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,



RA Gaudio G., Stornaiuolo A., Cafiero M., Falella A., Simeone A.;  
 RT "Organization of human class I homeobox genes.";  
 RL Genome 31:745-756(1989).  
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.  
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 CC -----  
 DR EMBL, AF026397, AAB94604.1; -;  
 DR EMBL, AF005814, CAA06713.1; -;  
 DR EMBL, AC004080; -; NOT ANNOTATED\_CDS.  
 DR EMBL, AF032095, AAD01339.2; -;  
 DR EMBL, U92543, AAD00727.1; -;  
 DR EMBL, X64803, CAA59270.1; -;  
 DR EMBL, X64804, CAA59270.1; JOINED.  
 DR PIR, S1536, S1536.  
 DR HSSP, P02833, 9ANT.  
 DR TRANSFAC, T01705; -;  
 DR Genew, HGNC:5108; HOXA7.  
 DR MIM, 142950; -;  
 DR GO, GO:0003700, F:transcription factor activity, TAS.  
 DR InterPro, IPR001827, Antennapedia.  
 DR InterPro, IPR001356, Homeobox.  
 DR Pfam, PF00046, homeobox, 1.  
 DR PRINTS, PR00025, ANTENNAPEDIA.  
 DR PRINTS, PR00024, HOMEOBOX.  
 DR Prodom, PD000010, Homeobox, 1.  
 DR SMART, SM00389, HOX, 1.  
 DR PROSITE, PS00032, ANTENNAPEDIA, 1.  
 DR PROSITE, PS00027, HOMEOBOX 1, 1.  
 DR PROSITE, PS50071, HOMEOBOX 2, 1.  
 KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 KW Transcription regulation.  
 FT SITE 119 124 ANTP-TYPE HEXAPEPTIDE.  
 FT DNA\_BIND 130 189 HOMEOBOX.  
 FT DOMAIN 157 160 POLY-ARG.  
 FT DOMAIN 196 199 POLY-ALA.  
 FT DOMAIN 214 230 ASP/GLU-RICH (HIGHLY ACIDIC).  
 FT DOMAIN 223 230 POLY-GLU.  
 FT CONFLICT 18 18 T->A (IN REF. 3).  
 FT CONFLICT 75 76 DA->RR (IN REF. 6).  
 FT CONFLICT 78 78 MISSING (IN REF. 5).  
 FT CONFLICT 174 174 I->V (IN REF. 4).  
 FT CONFLICT 194 195 PT->RL (IN REF. 5).  
 FT CONFLICT 195 195 T->I (IN REF. 7).  
 FT CONFLICT 222 222 D->Y (IN REF. 5).  
 SQ SEQUENCE 230 AA; 25385 MW; 6E2F1991F1BBED21 CRC64;  
 Query Match 58.6%; Score 95; DB 1; Length 230;  
 Best Local Similarity 81.0%; Pred. No. 4.6e-06;  
 Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 DRQIKIWFQNRMRMKCKKTD 21  
 DB 171 ERQIKIWFQNRMRMKCKKTD 191  
 RESULT 7  
 ID HXB6\_XENLA STANDARD; PRT; 48 AA.  
 AC P31256;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Homeobox protein Hox-B6 (XlHox-2.2) (Fragment).  
 GN HOXB6 OR XLHOX-2.2.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 NCBI\_TaxID=8355;  
 RN [1]  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE=93043517; PubMed=1384809;  
 RA Leroy P., de Robertis E.M.;  
 RT "Effects of lithium chloride and retinoic acid on the expression of  
 RT genes from the Xenopus laevis Hox 2 complex.";  
 RL Dev. Dyn. 194:21-32(1992).  
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.  
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 CC -----  
 DR EMBL, M91587, AAA49750.1; -;  
 DR PIR, I51439, I51439.  
 DR InterPro, IPR001827, Antennapedia.  
 DR InterPro, IPR001356, Homeobox.  
 DR Pfam, PF00046, homeobox, 1.  
 DR PRINTS, PR00024, HOMEOBOX.  
 DR Prodom, PD000010, Homeobox, 1.  
 DR SMART, SM00389, HOX, 1.  
 DR PROSITE, PS00027, HOMEOBOX 1, 1.  
 DR PROSITE, PS00032, ANTENNAPEDIA, PARTIAL.  
 DR PROSITE, PS50071, HOMEOBOX 2, 1.  
 KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
 KW Transcription regulation.  
 FT NON\_TER 1 1  
 FT DNA\_BIND <1 26 HOMEOBOX.  
 SQ SEQUENCE 48 AA; 5716 MW; BC39E36822EDDD2A CRC64;  
 Query Match 58.0%; Score 94; DB 1; Length 48;  
 Best Local Similarity 94.1%; Pred. No. 1.2e-06;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRQIKIWFQNRMRMKCKK 17  
 DB 11 ERQIKIWFQNRMRMKCKK 27  
 RESULT 8  
 ID HXAS\_SHEEP STANDARD; PRT; 49 AA.  
 AC Q28559;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Homeobox protein Hox-A5 (Fragment).  
 GN HOXA5 OR HOXA-5.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 NCBI\_TaxID=9940;  
 OX [1]  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Roche P.J.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF

```

CC      A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC      SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC      ALSO BINDS TO ITS OWN PROMOTER. BINDS SPECIFICALLY TO THE MOTIF:
CC      5'-CYNATATATGTY-3'.
CC      -1- SUBCELLULAR LOCATION: Nuclear.
CC      -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC      -----
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CC      or send an email to license@ibt-sib.ch).
CC      -----
DR      EMBL; U61978; AAB04754.1; -.
DR      HSSP; P02833; IHOM.
DR      InterPro; IPR001356; Homeobox.
DR      Pfam; PF00046; homeobox; 1.
DR      ProDom; PD000010; Homeobox; 1.
DR      SMART; SM00389; HOX; 1.
DR      PROSITE; PS00027; HOMEOBOX_1; 1.
DR      PROSITE; PS50077; HOMEOBOX_2; 1.
KW      Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW      Transcription regulation.
FT      NON_TER      1      1
FT      DNA_BIND      <1      49
FT      NON_TER      49      49
SO      SEQUENCE      49 AA; 6331 MW; 1EE702315E7C099B CRC64;

Query Match      58.0%; Score 94; DB 1; Length 49;
Best Local Similarity 94.1%; Pred. No. 1.2e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DROTKIWFQNRMRMKKK 17
Db      31 ERQIKIWFQNRMRMKKK 47

RESULT 9
HXAT_SHEEP
ID      HXAT_SHEEP      STANDARD;      PRT;      71 AA.
AC      Q28600;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Homeobox protein Hox-A7 (Fragment).
GN      HOXA7 OR HOXA-7.
OS      Ovis aries (Sheep).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Caprinae; Ovis.
OX      NCBI_TaxId=9940;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Roche P.J.;
RL      Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC      A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC      SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC      -1- SUBCELLULAR LOCATION: Nuclear.
CC      -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
CC      -----
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CC      or send an email to license@ibt-sib.ch).
CC      -----
DR      EMBL; U61979; AAB04755.1; -.
DR      HSSP; P02833; GANT.

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DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR00047; HTH_lamdrepresser.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; Hox; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON TER 1 1 HOMEBOX.
FT DNA_BIND 4 63
FT NON TER 71 71
SQ SEQUENCE 71 AA: 8888 MW: 931049PACIBAACB7 CRC64;

Query Match 58.0%; Score 94; DB 1; Length 71;
Best Local Similarity 94.1%; Pred. No. 1.8e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DROIKIWFONRRMKKK 17
Db 45 ERQIKIWFONRRMKKK 61

RESULT 10
HCXS NOTVI STANDARD; PRT; 71 AA.
AC P31262;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C5 (NvHox-3.4) (Fragment).
OS Notochthalamus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
OC Notochthalamus.
OX NCBI_TaxID=8316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92290273; PubMed=1351019;
RA Belleville S., Beauchemin M., Tremblay M., Noiseux N., Savard P.;
RT "Homeobox-containing genes in the newt are organized in clusters
RT similar to other vertebrates.";
RL Gene 114:179-186(1992).
CC -! FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -! SUBCELLULAR LOCATION: Nuclear.
CC -! SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
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CC -----
CC EMBL; M84001; AAA49397.1; ALT_INIT.
CC PIR; JCI161; JCI161.
CC HSSP; P02833; ISAN.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; Homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; Hox; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00032; ANTENNAPEdia; PARTIAL.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON TER 1 1

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FT  DNA_BIND 4 63 HOMEBOX.
FT  NON_TER 71
SQ  SEQUENCE 71 AA; 8979 MW; 079999FDE8995B42 CRC64;

Query Match 58.0%; Score 94; DB 1; Length 71;
Best Local Similarity 94.1%; Pred. No. 1.8e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMMKKK 17
:|||||
Db 45 EROIKIWFQNRMMKKK 61

RESULT 11
HM90_APIME STANDARD; PRT; 74 AA.
ID HM90_APIME
AC P15860;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein H90 (Fragment).
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apoidea; Apis.
NC NCBI_TaxID=7460;
RX MEDLINE=9009384; PubMed=2574865;
RA Walldorf U., Fleig R., Gehring W.J.;
RT "Comparison of homeobox-containing genes of the honeybee and
RT Drosophila."
RL Proc. Natl. Acad. Sci. U.S.A. 86:9971-9975(1989).
CC CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
CC -----
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CC -----
CC EMBL; M29493; AAA27728.1; -.
DR PIR; D34510; D34510.
DR HSSP; P02833; IHOM.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS50071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT NON_TER 1 1
FT DNA_BIND 8 67 HOMEBOX.
FT NON_TER 74
SQ SEQUENCE 74 AA; 9263 MW; 5FC8F84F723D837 CRC64;

Query Match 58.0%; Score 94; DB 1; Length 74;
Best Local Similarity 94.1%; Pred. No. 1.9e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMMKKK 17
:|||||
Db 49 EROIKIWFQNRMMKKK 65

RESULT 12
HXCA_RAT STANDARD; PRT; 76 AA.
ID HXCA_RAT
AC P18865;
DT 01-NOV-1990 (Rel. 16, Created)

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DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C4 (R3) (Fragment).
GN HOXC4 OR HOXC-4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=8921502; PubMed=2907739;
RA Falzon M., Chung S.Y.;
RT "The expression of rat homeobox-containing genes is developmentally
RT regulated and tissue specific."
RL Development 103:601-610(1988).
CC CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY SPINAL CORD AND KIDNEY.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY.
CC "DEFORMED" SUBFAMILY.
CC -----
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CC -----
CC EMBL; M37567; AAA41343.1; -.
DR PIR; C43559; C43559.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_Lambdaressar.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS50071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 11 70 HOMEBOX.
FT SEQUENCE 76 AA; 9293 MW; 5235F65C0672385 CRC64;

Query Match 58.0%; Score 94; DB 1; Length 76;
Best Local Similarity 94.1%; Pred. No. 1.9e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DROIKIWFQNRMMKKK 17
:|||||
Db 52 EROIKIWFQNRMMKKK 68

RESULT 13
HXAS_SALSA STANDARD; PRT; 78 AA.
ID HXAS_SALSA
AC P09637;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A5 (S12-B) (Fragment).
GN HOXA5.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.

```

CC NCBI\_TaxID=8030;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88226009; PubMed=2897318;  
RA Fjose A., Molven A., Eiken H.G.;  
RT "Molecular cloning and characterization of homeo-box-containing genes  
from Atlantic salmon";  
RL Gene 62:141-152(1988).  
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.  
CC -----  
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CC -----  
DR EMBL; M18904; AAA49560.1; -  
DR PIR; I51342; I51342.  
DR HSSP; P02833; 9ANT.  
DR InterPro; IPR001827; Antennapedia.  
DR InterPro; IPR001356; Homeobox.  
DR Pfam; PF00046; homeobox; 1.  
DR ProDom; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00027; HOMEOBOX\_1; 1.  
DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.  
DR PROSITE; PS50071; HOMEOBOX\_2; 1.  
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
KM Transcription regulation.  
FT NON\_TER 1 1  
FT DNA\_BIND 1 60 HOMEOBOX.  
SQ SEQUENCE 78 AA; 9489 MW; 82BDEBD78AC820 CRC64;  
Query Match 58.0%; Score 94; DB 1; Length 78;  
Best local similarity 94.1%; Pred. No. 2e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DROIKIWFQRRMKWK 17  
DB 42 EROIKIWFQRRMKWK 58  
RESULT 14  
HXLA\_LINSA STANDARD; PRT; 80 AA.  
ID HXLA\_LINSA  
AC P81192;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Homeobox protein Hox-A4 (Hox4) (Fragment).  
GN HOXA4.  
OS LIneus sanguineus (Ribon worm).  
OC Eukaryota; Metazoa; Nemertea; Anopla; Heteronemertea; Lineidae;  
OC LIneus.  
CC Lineus.  
OX NCBI\_TaxID=48190;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98169491; PubMed=9501210;  
RA Kmlita-Cunisse M., Looisli F., Blerne J., Gehring W.J.;  
RT "Homeobox genes in the ribonworm LIneus sanguineus: evolutionary  
implications";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:3030-3035(1998).  
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS (BY  
SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.  
CC "DEFORMED" SUBFAMILY.  
DR HSSP; P02833; 9ANT.  
DR InterPro; IPR001827; Antennapedia.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR000047; HTH\_Jamrepressr.  
DR Pfam; PF00046; homeobox; 1.  
DR PRINTS; PR00024; HOMEOBOX.  
DR PRINTS; PR00031; HTHREPRESSR.  
DR ProDom; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00027; HOMEOBOX\_1; 1.  
DR PROSITE; PS00071; HOMEOBOX\_2; 1.  
DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.  
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
KM Transcription regulation.  
FT NON\_TER 1 1  
FT DNA\_BIND 1 80 HOMEOBOX.  
SQ SEQUENCE 80 AA; 9860 MW; F2CE1B01CB8042F1 CRC64;  
Query Match 58.0%; Score 94; DB 1; Length 80;  
Best local similarity 94.1%; Pred. No. 2.1e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DROIKIWFQRRMKWK 17  
DB 52 EROIKIWFQRRMKWK 68  
RESULT 15  
HXSL\_BRARE STANDARD; PRT; 81 AA.  
ID HXSL\_BRARE  
AC P09013;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Homeobox protein Hox-B5 like (ZP-54) (Fragment).  
GN HOXB5 OR ZP54 OR ZP-54.  
OS Brachydanio rerio (Zebrafish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
CC NCBI\_TaxID=7955;  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89016617; PubMed=2902580;  
RA Njolstad P.R., Molven A., Hordvik I., Apold J., Fjose A.;  
RT "Primary structure, developmentally regulated expression and  
potential duplication of the zebrafish homeobox gene ZP-21";  
RL Nucleic Acids Res. 16:9097-9113(1988).  
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.  
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CC -----  
DR EMBL; X12803; CAA31291.1; -  
DR HSSP; P02833; 1SAN.  
DR ZFIN; ZDB-GENE-000823-6; hoxb5b.  
DR InterPro; IPR001356; Homeobox.  
DR Pfam; PF00046; homeobox; 1.  
DR PRINTS; PR00024; HOMEOBOX.  
DR ProDom; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.

DR PROSITE; PS00027; HOMEBOX\_1; 1.  
DR PROSITE; PS50071; HOMEBOX\_2; 1.  
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
KW Transcription regulation.  
FT NON\_TER 1 1  
FT DNA\_BIND 6 65 HOMEBOX.  
SQ SEQUENCE 81 AA; 9977 MW; B7698AFFFEB3C6B4 CRC64;

Query Match 58.0%; Score 94; DB 1; Length 81;  
Best Local Similarity 94.1%; Pred. No. 2.1e-06;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRQIKIWFQNRMRMKKK 17  
:|||||  
Db 47 ERQIKIWFQNRMRMKKK 63

Search completed: February 18, 2004, 14:28:14  
Job time : 16.5789 sec

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OM protein - protein search, using SW model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds  
(without alignments)  
89.145 Million cell updates/sec

Title: US-09-643-260-17  
Perfect score: 41  
Sequence: 1 LDMWML 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL 23: \*  
1: sp\_archaea: \*  
2: sp\_bacteria: \*  
3: sp\_fungi: \*  
4: sp\_human: \*  
5: sp\_invertebrate: \*  
6: sp\_mammal: \*  
7: sp\_mhc: \*  
8: sp\_organelle: \*  
9: sp\_phage: \*  
10: sp\_plant: \*  
11: sp\_rodent: \*  
12: sp\_virus: \*  
13: sp Vertebrate: \*  
14: sp\_unclassified: \*  
15: sp\_virus: \*  
16: sp\_bacteriap: \*  
17: sp\_archaeap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	95.1	513	2 Q8VPV8	Q8VPV8 synchococc
2	37	90.2	107	9 Q9FZX5	Q9FZX5 bacterioph
3	37	90.2	274	16 Q8DKO6	Q8DKO6 synchococc
4	37	90.2	282	16 Q8D354	Q8D354 wigleswort
5	37	90.2	288	2 Q8VTT4	Q8VTT4 pseudomon
6	37	90.2	308	2 Q8K2S2	Q8K2S2 acetobacter
7	37	90.2	311	5 Q94380	Q94380 caenorhabd
8	37	90.2	313	2 Q8VU06	Q8VU06 pseudomon
9	37	90.2	318	16 Q8ZC58	Q8ZC58 yersinia pe
10	37	90.2	329	16 Q8XVB4	Q8XVB4 ralsionia s
11	37	90.2	331	16 Q91427	Q91427 pseudomon
12	37	90.2	341	16 Q8G3A8	Q8G3A8 bruceella su
13	37	90.2	344	16 Q8YEH7	Q8YEH7 bruceella me
14	37	90.2	353	16 Q9A7F0	Q9A7F0 caulobacter
15	37	90.2	377	17 Q59445	Q59445 pyrococcus
16	37	90.2	378	17 Q8U022	Q8U022 pyrococcus

17	37	90.2	379	17 Q9V1M1	Q9V1M1 pyrococcus
18	37	90.2	386	16 Q92U27	Q92U27 rhizobium m
19	37	90.2	393	16 Q987Z1	Q987Z1 rhizobium 1
20	37	90.2	399	16 Q8PFO8	Q8PFO8 xanthomonas
21	37	90.2	404	17 Q57734	Q57734 pyrococcus
22	37	90.2	405	17 Q9UXV2	Q9UXV2 pyrococcus
23	37	90.2	1291	5 Q9VP46	Q9VP46 dirosophila
24	37	90.2	1449	5 Q8MNA4	Q8MNA4 dictyostell
25	37	90.2	1578	5 Q81BF7	Q81BF7 plasmodium
26	37	90.2	2283	5 Q8IC35	Q8IC35 plasmodium
27	36	87.8	82	17 Q26213	Q26213 methanobact
28	36	87.8	162	16 Q53756	Q53756 mycobacteri
29	36	87.8	313	16 Q8FU02	Q8FU02 corynebacte
30	36	87.8	322	16 Q8YGR7	Q8YGR7 bruceella me
31	36	87.8	347	16 Q98KR3	Q98KR3 rhizobium 1
32	36	87.8	347	16 Q92QP5	Q92QP5 rhizobium m
33	36	87.8	347	16 Q8G1B0	Q8G1B0 bruceella su
34	36	87.8	348	16 Q8UPX0	Q8UPX0 agrobacteri
35	36	87.8	414	16 Q9KL94	Q9KL94 vibrio chol
36	36	87.8	439	2 Q93Q61	Q93Q61 klebsiella
37	36	87.8	443	16 Q8ZDM7	Q8ZDM7 yersinia pe
38	36	87.8	451	16 Q8D0S7	Q8D0S7 yersinia pe
39	36	87.8	618	15 Q88284	Q88284 snakehead r
40	36	87.8	740	6 Q9SKV1	Q9SKV1 bos taurus
41	36	87.8	745	11 Q8CBT3	Q8CBT3 mus musculu
42	36	87.8	756	6 Q9SKV0	Q9SKV0 bos taurus
43	36	87.8	764	16 Q8U6N1	Q8U6N1 agrobacteri
44	36	87.8	1120	16 Q8ZRA5	Q8ZRA5 salmonella
45	36	87.8	1120	16 Q8ZRT6	Q8ZRT6 salmonella

## ALIGNMENTS

## RESULT 1

Q8VPV8 PRELIMINARY; PRT; 513 AA.  
AC Q8VPV8; Q8VPV8; 01-MAR-2002 (TRENBLREL. 20, Created)  
DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)  
DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)  
DE NADPH dehydrogenase subunit 4.  
GN NDH3.  
OS Synchococcus sp. (strain PCC 7942) (Anacystis nidulans R2).  
OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.  
OX NCBI\_Taxid=1140;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PCC 7942;  
RA Maeda S., Badger M.R., Price G.D.;  
RT "Identification of Cpx and Cpy, catalyzing light-dependent CO2  
hydrogenation involved in CO2 uptake in Cyanobacteria.";  
RT Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY029338; AAK37764.1; -  
DR InterPro; IPR003918; NADHb\_oxred4.  
DR InterPro; IPR001750; Oxidored\_q1.  
DR Pfam; PF00361; oxidored\_q1.  
DR PRINTS; PR01437; NUOXDRDTASB4.  
DR NAD; Oxidoreductase; Plastocyanine.  
SQ SEQUENCE 513 AA; 54237 MW; 2732576B55224AB CRC64;

Query Match 95.1%; Score 39; DB 2; Length 513;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMWML 6  
Db 59 IDWML 64

RESULT 2  
Q9FZX5 PRELIMINARY; PRT; 107 AA.

AC Q9FZK5;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical 12.6 kDa protein.  
 OS Bacteriophage GA-1.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
 OC phi-29-like viruses.  
 OC NCBI\_TaxID=12345;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97094855; PubMed=8940089;  
 RA Freire R., Serrano M., Salas M., Hermoso J.;  
 RT "Activation of replication origins in phi29-related phages requires  
 RT the recognition of initiation proteins to specific nucleoprotein  
 RT complexes.";  
 RL J. Biol. Chem. 271:31000-31007 (1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97123975; PubMed=8969297;  
 RA Iliana B., Blanco L., Salas M.;  
 RT "Functional characterization of the genes coding for the terminal  
 RT protein and DNA polymerase from bacteriophage GA-1. Evidence for a  
 RT sliding-back mechanism during protein-primed GA-1 DNA replication.";  
 RL J. Mol. Biol. 264:453-464 (1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99370049; PubMed=10438592;  
 RA Horcajadas J.A., Monsalve M., Rojo F., Salas M.;  
 RT "The switch from early to late transcription in phage GA-1:  
 RT characterization of the regulatory protein p4G.";  
 RL J. Mol. Biol. 290:917-928 (1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20280072; PubMed=10773070;  
 RA Gascon I., Lazaro J.M., Salas M.;  
 RT "Differential functional behavior of viral phi29, NF and GA-1 SSB  
 RT proteins.";  
 RL Nucleic Acids Res. 28:2034-2042 (2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MedJel W.J.J., Horcajadas J.A., Salas M.;  
 RT "Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases."  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Horcajadas J.A., MedJel W.J.J., Rojo F., Salas M.;  
 RT "Transcriptional map of the Bacillus bacteriophage GA-1. Analysis of  
 RT the viral C2 promoter.";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X96987; CAC21518.1; -.  
 KM Hypothetical protein.  
 SQ SEQUENCE 107 AA; 12636 MW; ABEF24B68A255B02 CRC64;

Query Match 90.2%; Score 37; DB 9; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 87;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMEWL 6  
 DB 100 DMEWL 104

RESULT 3  
 Q8DK06 PRELIMINARY; PRT; 274 AA.  
 ID Q8DK06  
 AC Q8DK06;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Cbby family protein.  
 GN TR80803.  
 OS Synechococcus elongatus (Thermosynechococcus elongatus).

OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.  
 OX NCBI\_TaxID=32046;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BP-1;  
 RX MEDLINE=22225144; PubMed=12240834;  
 RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,  
 RA Watanabe A., Iriyuchi M., Kawashima K., Kimura T., Kishida Y.,  
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,  
 RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the thermophilic cyanobacterium  
 RT Thermosynechococcus elongatus BP-1.";  
 RL DNA Res. 9:123-130 (2002).  
 DR EMBL; AP005371; BAC08354.1; -.  
 KM Complete proteome.  
 SQ SEQUENCE 274 AA; 30329 MW; 021D35F51D8A77E CRC64;

Query Match 90.2%; Score 37; DB 16; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 2,2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMEW 5  
 DB 49 LDMEW 53

RESULT 4  
 Q8D354 PRELIMINARY; PRT; 282 AA.  
 ID Q8D354  
 AC Q8D354;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Cyoa protein.  
 GN CYOA.  
 OS Wigglesworthia brevipalpis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Wigglesworthia.  
 OX NCBI\_TaxID=164609;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22297718; PubMed=12219091;  
 RA Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,  
 RA Aksoy S.;  
 RT "Genome sequence of the endocellular obligate symbiont of tsetse  
 RT flies, Wigglesworthia glossinidia.";  
 RL Nat. Genet. 32:402-407 (2002).  
 DR EMBL; AB063521; BAC24293.1; -.  
 KM Complete proteome.  
 SQ SEQUENCE 282 AA; 32500 MW; 39CC286285F3B35 CRC64;

Query Match 90.2%; Score 37; DB 16; Length 282;  
 Best Local Similarity 83.3%; Pred. No. 2,3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMEW 6  
 DB 134 LDMEW 139

RESULT 5  
 Q8VT74 PRELIMINARY; PRT; 288 AA.  
 ID Q8VT74  
 AC Q8VT74;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Cytochrome o ubiquinol oxidase A (Fragment).  
 GN CYOA.  
 OS Pseudomonas putida.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=303;

RN [1]  
 SEQUENCE FROM N.A.  
 RC STRAIN=PM1;  
 RA Syn C.K.C., Liew C.F., Swarup S.;  
 RT "Pseudomonas putida cytochrome o ubiquinol oxidase A, B, C, and D  
 genes";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF321090; AAL57192.1;  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR006333; CytoA\_II.  
 DR ProDom; PD000131; Copper\_CuA; 1.  
 DR TIGRFAMs; TIGR01433; CytoA; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 288 AA; 31882 MW; 60E40B3A36516BFC CRC64;  
 Query Match 90.2%; Score 37; DB 2; Length 288;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEML 6  
 DB 108 LDWKMVL 113

## RESULT 6

Q8KZS2 PRELIMINARY; PRT; 308 AA.  
 AC Q8KZS2;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Ubiquinol oxidase subunit II.  
 OS Acetobacter pasteurianus (Acetobacter turbidans).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;  
 OC Acetobacteraceae; Acetobacter.  
 CX NCBI\_TaxID=438;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=NCI 1193;  
 RA Takakuwa N., Yamane K., Oda Y., Fukaya M., Tsukamoto Y., Ohnishi M.;  
 RT "Identification of the acetic acid bacterium NCI 1193 and nucleotide  
 RT sequences of the genes encoding enzymes related to acetic acid  
 RT production";  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB066015; BAB97173.1;  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR006333; CytoA\_II.  
 DR InterPro; IPR002429; Cyt\_Cox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CuA; 1.  
 DR TIGRFAMs; TIGR01433; CytoA; 1.  
 KW Oxidoreductase.  
 SQ SEQUENCE 308 AA; 33988 MW; F93006DBE528AD2C CRC64;

Query Match 90.2%; Score 37; DB 2; Length 308;  
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEML 6  
 DB 135 LDWKMVL 140

## RESULT 7

Q94380 PRELIMINARY; PRT; 311 AA.  
 AC Q94380;  
 DT 01-FEB-1997 (TREMBlrel. 02, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE ZC47.13 protein.  
 GN ZC47.13.

OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditicoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 CX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA McMurtry A.A.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851915;  
 RA none;  
 RT "Genome sequence of the nematode C. elegans: A platform for  
 RT investigating biology";  
 RL Science 282:2012-2018(1998).  
 DR EMBL; Z81141; CAB03488.2;  
 DR WormPep; ZC47.13; CE25668.  
 DR InterPro; IPR002900; DUF38.  
 DR InterPro; IPR001810; F-box.  
 DR Pfam; PF00646; F-box; 1.  
 DR Pfam; PF01827; FTH; 1.  
 SQ SEQUENCE 311 AA; 36603 MW; 92846420868C48B CRC64;

Query Match 90.2%; Score 37; DB 5; Length 311;  
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEML 6  
 DB 295 LDWEMVL 300

## RESULT 8

Q8VU06 PRELIMINARY; PRT; 313 AA.  
 AC Q8VU06;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Cytochrome o oxidase A.  
 GN CYOA.  
 OS Pseudomonas putida.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 CX NCBI\_TaxID=303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KT2442;  
 RA Fukumori F., Kishii M.;  
 RT "Characterization of the toluene-sensitive mutants of Pseudomonas  
 RT putida KT2442TOL";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB066295; BAB83593.1;  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR006333; CytoA\_II.  
 DR InterPro; IPR002429; Cyt\_Cox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR ProDom; PD000131; Copper\_CuA; 1.  
 DR TIGRFAMs; TIGR01433; CytoA; 1.  
 KW Oxidoreductase.  
 SQ SEQUENCE 313 AA; 34557 MW; 193B3F78EBDA42B CRC64;

Query Match 90.2%; Score 37; DB 2; Length 313;  
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEML 6  
 DB 133 LDWKMVL 138

## RESULT 9

Q8ZC58



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ID 082C58 PRELIMINARY; PRT; 318 AA.
AC 082C58;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Cytochrome o ubiquinol oxidase subunit II (EC 1.10.3.-).
GN CYOA OR YR03164 OR Y1021.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
CX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titchell R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Baaham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltham T., Hamlin N., Holtroyd S., Jagers K., Kariyeh A.V.,
RA Leather S., Moul S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.,
RA "Genome sequence of Yersinia pestis, the causative agent of plague.";
RT Nature 413:523-527(2001).
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=21242430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau D.J., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Staley S.C., McDonough K.A., Niles M.L., Mason J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
RN [3]
RP EMBL; AF141455; CAC92399.1; -
DR EMBL; AF141455; CAC92399.1; -
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006333; CyOA_II.
DR ProDom; PD000131; Copper_CuA; 1.
DR TIGRFAMs; TIGR01433; CyOA; 1.
DR Oxidoreductase; Complete proteome.
KW SEQUENCE 318 AA; 35049 MW; E2947941923016D3 CRC64;
SQ
Query Match 90.2%; Score 37; DB 16; Length 318;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Cy 1 LDWEMT 6
Db 133 LDWKWL 140

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RA Chandler M., Choiane N., Claudel-Renard C., Cumac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Siguler P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
RN EMBL; AL646072; CAD16624.1; -
DR EMBL; AL646072; CAD16624.1; -
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006333; CyOA_II.
DR InterPro; IPR002429; Cyt_cox_2.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00116; COX2; 1.
DR ProDom; PD000131; Copper_CuA; 1.
DR TIGRFAMs; TIGR01433; CyOA; 1.
DR PROSITE; PS00038; HLH_1; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 329 AA; 35781 MW; 08DA178C39A5964A CRC64;
Query Match 90.2%; Score 37; DB 16; Length 329;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Cy 1 LDWEMT 6
Db 133 LDWKWL 138

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RESULT 10
08XVB4 PRELIMINARY; PRT; 329 AA.
AC 08XVB4;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Probable transmembrane cytochrome O ubiquinol oxidase (Subunit II)
GN CYOA1 OR RSC2917 OR R500308.
OS Oxidoreductase protein (EC 1.10.3.-).
OC Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
CX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM1100;
RX MEDLINE=21681879; PubMed=11823852;
RA Salenouat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Broctier P., Camus J.C., Catolico L.,

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RA Chandler M., Choiane N., Claudel-Renard C., Cumac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Siguler P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
RN EMBL; AL646072; CAD16624.1; -
DR EMBL; AL646072; CAD16624.1; -
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006333; CyOA_II.
DR InterPro; IPR002429; Cyt_cox_2.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00116; COX2; 1.
DR ProDom; PD000131; Copper_CuA; 1.
DR TIGRFAMs; TIGR01433; CyOA; 1.
DR PROSITE; PS00038; HLH_1; 1.
KW Complete proteome.
SQ SEQUENCE 331 AA; 36623 MW; DC449ED0F0B66 CRC64;
Query Match 90.2%; Score 37; DB 16; Length 331;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Cy 1 LDWEMT 6
Db 133 LDWKWL 138

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RESULT 12  
Q8G3A8 PRELIMINARY; PRT; 341 AA.  
ID Q8G3A8  
AC Q8G3A8;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Ubiqinol oxidase, subunit II.  
GN CYOA OR BR0042.  
OS Brucella suis.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Brucellaceae; Brucella.  
OX NCBI\_TaxID=29451;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1330 / Biovar 1;  
RX MEDLINE=22247741; PubMed=12271122;  
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,  
RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,  
RA Daugherty S.C., Debroy R.T., Durkin A.S., Kolonay J.F., Madupu R.,  
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,  
RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,  
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;  
RT "The Brucella suis genome reveals fundamental similarities between  
RT animal and plant pathogens and symbionts."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).  
DR EMBL, AE014319; AN28999.1; -.  
DR TIGR, BR0042; -.  
KW Complete proteome.  
SQ SEQUENCE 341 AA; 38563 MW; 38856F075123F5D CRC64;  
Query Match 90.2%; Score 37; DB 16; Length 341;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDWMTL 6  
DB 138 LDMKWL 143  
RESULT 13  
Q8YEH7 PRELIMINARY; PRT; 344 AA.  
ID Q8YEH7  
AC Q8YEH7;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Cytochrome O ubiqlinol oxidase subunit II (BC 1.10.3.-).  
GN BME11901.  
OS Brucella melitensis.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Brucellaceae; Brucella.  
OX NCBI\_TaxID=29459;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=16M / ATCC 23456 / Biotype 1;  
RX MEDLINE=20020109; PubMed=1175668;  
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mufier C., Los T.,  
RA Ivanova N., Anderson I., Bhattacharya A., Lykakis A., Resnik G.,  
RA Jablonka L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,  
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,  
RA Haselkorn R., Kyriides N., Overbeek R.;  
RT "The genome sequence of the facultative intracellular pathogen  
RT Brucella melitensis."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).  
DR EMBL, AE009623; AL53082.1; -.  
DR InterPro, IPR001505; Copper\_Gua.  
DR InterPro, IPR006333; CyOA\_II.  
DR ProDom, PD000131; Copper\_Gua; 1.  
DR TIGRFAW, TIGR01433; CyOA; 1.  
KW Oxidoreductase; Complete proteome.

SQ SEQUENCE 344 AA; 38948 MW; B643C91321B600EC CRC64;  
Query Match 90.2%; Score 37; DB 16; Length 344;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDWMTL 6  
DB 141 LDMKWL 146  
RESULT 14  
Q9A7F0 PRELIMINARY; PRT; 353 AA.  
ID Q9A7F0  
AC Q9A7F0;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Ubiqinol oxidase subunit II.  
GN CC1773.  
OS Caulobacter crescentus.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;  
OC Caulobacteraceae; Caulobacter.  
OX NCBI\_TaxID=155892;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 19089 / CB15;  
RX MEDLINE=21173698; PubMed=11259647;  
RA Newman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,  
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,  
RA Debroy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,  
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,  
RA Uteback T., Tran K., Wolf A., Vamathavan J., Ermolaeva M., White O.,  
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
RT "Complete genome sequence of Caulobacter crescentus."  
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
DR EMBL, AE005851; AK23749.1; -.  
DR HSP, P18400; ICYW.  
DR TIGR, CC1773; -.  
DR InterPro, IPR001505; Copper\_Gua.  
DR InterPro, IPR006333; CyOA\_II.  
DR ProDom, PD000131; Copper\_Gua; 1.  
DR TIGRFAW, TIGR01433; CyOA; 1.  
KW Complete proteome.  
SQ SEQUENCE 353 AA; 38817 MW; 607AP178B2AD184D CRC64;  
Query Match 90.2%; Score 37; DB 16; Length 353;  
Best Local Similarity 83.3%; Pred. No. 2.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDWMTL 6  
DB 146 LDMKWL 151  
RESULT 15  
O59445 PRELIMINARY; PRT; 377 AA.  
ID O59445  
AC O59445;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE 377A long hypothetical sarcosine oxidase.  
GN PH1751.  
OS Pyrococcus horikoshii.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=53953;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=OT3;  
RX MEDLINE=98344137; PubMed=9679194;

RA Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,  
 RA Yamamoto S., Sekine M., Baba S.-I., Koguchi H., Hosoyama A., Nagai Y.,  
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,  
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,  
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb P.T., Horikoshi K.,  
 RA Masuchi Y., Shizuya H., Kikuchi H.,  
 RT "Complete sequence and gene organization of the genome of a hyper-  
 thermophilic archaeobacterium, *Pyrococcus horikoshii* OT3.";  
 RL DNA Res. 5:55-76 (1998).  
 DR EMBL: AP000007; BAA30865.1; -;  
 DR InterPro: IPR006076; IPR006076.  
 DR InterPro: IPR00205; NAD\_binding.  
 DR Pfam: PF01266; DAO; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 377 AA; 42421 MW; FA9B096528EA097 CRC64;

Query Match 90.2%; Score 37; DB 17; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEM 5  
 |||||  
 DB 354 LDWEM 358

Search completed: February 18, 2004, 14:35:59  
 Job time : 18.3684 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds  
(without alignments)  
79.423 Million cell updates/sec

Title: US-09-643-260-17

Perfect score: 41  
Sequence: 1 LDMEWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	95.1	501	1 YB06_YEAST	P38081 saccharomyc
2	37	90.2	210	1 KTHY_SCHPO	P36590 echizomacch
3	37	90.2	281	1 Y373_MYCPN	P75227 mycoplasma
4	37	90.2	296	1 CY0A_BUCAI	P57544 buchnera ap
5	37	90.2	307	1 QOX2_ACEAC	P50653 acetobacter
6	37	90.2	314	1 CY0A_PSEPU	P95971 pseudomonas
7	37	90.2	488	1 YK11_CABEL	P34312 caenorhabdi
8	37	90.2	1275	1 RPRC_MYXXA	P08664 myxococcu
9	36	87.8	289	1 Y250_CORGL	P42459 corynebacte
10	36	87.8	290	1 CY0A_BUCAP	P48393 buchnera ap
11	36	87.8	745	1 IKKA_HUMAN	P15111 h inhibitor
12	36	87.8	745	1 IKKA_MOUSE	P06680 m inhibitor
13	36	87.8	756	1 IKKE_HUMAN	P14920 homo sapien
14	36	87.8	757	1 IKKE_MOUSE	P08351 mus musculi
15	36	87.8	757	1 IKKE_RAT	P09478 rattus norv
16	35	85.4	385	1 YPSC_BACSU	P50840 bacillus su
17	34	82.9	191	1 GDIR_CABEL	P020496 caenorhabdi
18	34	82.9	470	1 NOS2_ONCMY	P50977 oncorhynch
19	34	82.9	473	1 LAGC_LACAC	P10730 lactobacill
20	34	82.9	844	1 AMPN_LACHE	P47386 mycoplasma
21	34	82.9	1113	1 Y140_MYCGE	P75033 mycoplasma
22	34	82.9	1113	1 Y140_MYCPN	P73358 escherichia
23	34	82.9	1120	1 KEPA_ECOLI	P53658 acetobacter
24	33	80.5	94	1 FIXX_AZCVI	P64253 mycobacteri
25	33	80.5	125	1 VG61_BPMD2	P08677 photorhabdu
26	33	80.5	156	1 RNH_PHOIU	P51768 pseudomonas
27	33	80.5	152	1 PHZE_PSEPU	P28094 strongyloce
28	33	80.5	223	1 WNT1_STRPU	P24218 escherichia
29	33	80.5	387	1 INTD_ECOLI	P09289 vibrio para
30	33	80.5	418	1 HLT_VIBPA	P09615 druseophila
31	33	80.5	468	1 WNTG_DROME	P08412 aspergillus
32	33	80.5	483	1 ENGA_BRUME	P09455 pyrococcus
33	33	80.5	547	1 SPAK_HUMAN	P09456 homo sapien

34	33	80.5	553	1 SPAK_RAT	O08506 rattus norv
35	33	80.5	556	1 SPAK_MOUSE	O921w9 mus musculu
36	33	80.5	725	1 AREA_PENCL	O01582 penicillium
37	33	80.5	807	1 PHK_RHILIO	O088v7 rhizobium 1
38	33	80.5	860	1 AREA_PENRO	O13508 penicillium
39	33	80.5	865	1 AREA_PENRO	O02269 penicillium
40	33	80.5	866	1 AREA_ASPOR	O13415 aspergillus
41	33	80.5	876	1 AREA_EMENT	P17429 emericella
42	33	80.5	878	1 SVY_METUA	O58413 methanococc
43	33	80.5	882	1 AREA_ASPNG	O13412 aspergillus
44	33	80.5	891	1 SVY_PYPAB	O9455 pyrococcus
45	33	80.5	891	1 SVY_PYPHO	O58052 pyrococcus

## ALIGNMENTS

RESULT 1  
YB06\_YEAST  
ID YB06\_YEAST STANDARD, PRT, 501 AA.  
AC P38081;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical 57.8 kDa protein in PRP6-MDM2 intergenic region.  
GN YBR056W OR YBR0510.  
OS Saccharomyces cerevisiae (Baker's Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycas.  
OX NCBI\_Taxid=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288C;  
RX MEDLINE=95321020; PubMed=7597852;  
RA Allinovic G., Pohl T.M.;  
RT "Sequence and analysis of 24 kb on chromosome II of Saccharomyces  
cerevisiae.";  
RL Yeast 11:475-479(1995).  
CC -1 SIMILARITY: BELONGS TO CELLULOSE FAMILY A (FAMILY 5 OF GLYCOSYL  
HYDROLASES).  
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CC  
CC EMBL; 235925; CA84999.1; -;  
DR EMBL; 246260; CA86399.1; -;  
DR PIR; S45914; S45914.  
DR SGD; S0000260; YBR056W.  
DR InterPro; IPR001547; Glyco\_hydro\_5.  
DR PROSITE; PS00659; GLYCOSYL\_HYDROL\_F5; FALSE\_NEG.  
KW Hypothetical protein; Hydrolase; Glycosidase.  
FT ACT\_SITE 236 236 PROTON DONOR (BY SIMILARITY).  
FT ACT\_SITE 333 333 NUCLEOPHILE (BY SIMILARITY).  
SQ SEQUENCE 501 AA; 57822 MW; 5133A161736ADD3 CRC64;  
Query Match 95.1%; Score 39; DB 1; Length 501;  
Best Local Similarity 83.3%; Pred. No. 28;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 LDMEWL 6  
DB 109 IDMEWL 114  
RESULT 2  
KTHY\_SCHPO STANDARD; PRT; 210 AA.  
AC P36590; O74528;

DT 01-JUN-1994 (Rel. 29, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Thymidylate kinase (EC 2.7.4.9) (dTMP kinase).  
 GN TNP OR SPCCT0.07C.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 CX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9300330; PubMed=1327149;  
 RA Adair L.T., Yeh Y.I., Jong A.Y.;  
 RT "Functional and structural conservation of Schizosaccharomyces pombe  
 RT dTMP kinase gene."  
 RL Biochim. Biophys. Acta 1132:222-224(1992).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=1848401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltyell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,  
 RA Jones P., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Mouton S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Voiclaert G., Aert R., Robben J., Grympos B.,  
 RA Welfens I., Vanstreels E., Rieger M., Schefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Leinisch H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
 RA Goffeau A., Cadiu E., Dreano S., Gloux S., Lelaire V., Mortier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Roche M., Galliard C., Tallada V.A., Garzon A., Rhode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,  
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nuree P.;  
 RT "The genome sequence of Schizosaccharomyces pombe."  
 RL Nature 415:871-880(2002).  
 CC -1- FUNCTION: Catalyzes the conversion of dTMP to dUMP.  
 CC -1- CATALYTIC ACTIVITY: ATP + thymidine 5'-phosphate = ADP + thymidine  
 CC 5'-diphosphate.  
 CC -1- PATHWAY: Biosynthesis of dTMP from dUMP.  
 CC -1- SIMILARITY: BELONGS TO THE THYMIDYLATE KINASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; X65868; CAA46698.1; -;  
 CC EMBL; AL023794; CAA1357.1; -;  
 CC PIR; T41553; T41553.  
 CC HSP; P00572; ITMK.  
 CC GeneDB Spombe; SPCCT0.07C;  
 CC InterPro; IPR000062; Thymidylate\_kin.  
 CC Pfam; PF02223; Thymidylate\_kin; 1.  
 CC TIGRfam; TIGR00041; dTMP\_kinase; 1.  
 CC PROSITE; PS01331; THYMIDYLATE\_KINASE; 1.  
 CC Transferrase; Kinase; Nucleotide biosynthesis; ATP-binding.  
 CC NP BIND 14 21 ATP (POTENTIAL).  
 CC CONFLICT 33 39 SGEKAE -> LMKRLK (IN REF. 1).

FT CONFLICT 59 59 K -> T (IN REF. 1).  
 FT CONFLICT 80 93 T T OYIYEQINKVT -> PSIIYRANQRCN (IN REF.  
 FT CONFLICT 125 125 P -> T (IN REF. 1).  
 FT CONFLICT 164 164 P -> L (IN REF. 1).  
 FT CONFLICT 186 186 S -> Y A (IN REF. 1).  
 FT CONFLICT 191 191 H -> D (IN REF. 1).  
 SQ SEQUENCE 210 AA; 24249 MW; 4266144ABAB6C0 CRC64;  
 Query Match 90.2%; Score 37; DB 1; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMEW 5  
 DB 112 LDMEW 116  
 RESULT 3  
 Y373 MYCPN STANDARD; PRT; 261 AA.  
 AC P75237;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Hypothetical protein MG373 homolog (G12\_07281).  
 GN MFN551 OR MP291.  
 OS Mycoplasma pneumoniae.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmatetaceae; Mycoplasma.  
 CX NCBI\_TaxID=2104;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 29342 / M129;  
 RX MEDLINE=97105885; PubMed=8948633;  
 RA Himmelfrich R., Hilbert H., Plagens H., Pirk E., Li B.-C.,  
 RA Herrmann R.;  
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma  
 RT pneumoniae."  
 RL Nucleic Acids Res. 24:4420-4449(1996).  
 CC -----  
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 CC -----  
 CC EMBL; AB000027; AAB95939.1; -;  
 CC PIR; S73617; S73617.  
 CC Hypothetical protein; Complete proteome.  
 CC KW SEQUENCE 281 AA; 32569 MW; FC70957510D7BEF3 CRC64;  
 Query Match 90.2%; Score 37; DB 1; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DMEWL 6  
 DB 271 DMEWL 275  
 RESULT 4  
 CYOA BUCAI STANDARD; PRT; 296 AA.  
 ID CYOA BUCAI  
 AC P57544;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Ubiquinol oxidase poly(ubiquitin) precursor (EC 1.10.3.-) (Cytochrome O  
 DE subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase  
 DE subunit 2).  
 GN CYOA OR BU472.

```

OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum)
OC Bacterioides bacterium)
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=118099;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-Tokyo 1998;
RA MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
CC OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
CC GROWN AT HIGH AERATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: SOME TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.
CC -----
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CC -----
DR EMBL; AP001119; BAB13169.1; -
DR HSSP; P18400; 1CYW.
DR InterPro; IPR001505; Copper_Cua.
DR InterPro; IPR006333; Cyto_c_ox_2.
DR InterPro; IPR002429; Cyt_c_ox_2.
DR InterPro; IPR000437; Prok_LipoProt.
DR Pfam; PF00116; COX2; 1.
DR ProDom; PD000131; Copper_Cua; 1.
DR TIGRfam; TIGR01433; Cyto_c_ox_2.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; FALSE NEG.
DR Oxioreductase; Respiratory chain; Electron transport; Transmembrane;
DR Signal; Lipoprotein; Complete proteome.
DR SIGNAL; 1 15
DR CHAIN 1 296
DR LIPID 16 296
DR DOMAIN 16 16
DR TRANSMEM 34 33
DR DOMAIN 55 54
DR TRANSMEM 79 78
DR DOMAIN 100 99
DR SIGNAL; 296
DR SEQUENCE 296 AA; 34180 MW; 1AB3B4F0408FBAC CRC64;

Query Match
Best Local Similarity 90.2%; Score 37; DB 1; Length 296;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWMTL 6
DB 125 LDMWTL 130

RESULT 5
ID COX2_ACEAC STANDARD; PRT; 307 AA.
AC P50653;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome
DE A1 subunit 2) (Oxidase BA(3) subunit 2).
GN CYAB.
OS Acetobacter aceti.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Acetobacter.

```

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OX NCBI_TaxID=435;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=1023;
RX MEDLINE=93322308; PubMed=8392509;
RA Fukaya M., Tayama K., Tamaki T., Ebisuya H., Okumura H.,
RA Kawamura Y., Horiouchi S., Beppu T.;
RT "Characterization of a cytochrome al that functions as a ubiquinol
RT oxidase in Acetobacter aceti.";
RL J. Bacteriol. 175:4307-4314(1993).
CC -1- PATHWAY: TERMINAL OXIDASE FOR ETHANOL OXIDATION.
CC -1- SUBUNIT: HETEROTETRAMER OF THE SUBUNITS 1, 2, 3 AND 4.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: SOME TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.
CC -----
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CC -----
DR EMBL; D13185; BAA02480.1; -
DR PIR; A36885; A36885.
DR HSSP; P18400; 1CYW.
DR InterPro; IPR001505; Copper_Cua.
DR InterPro; IPR006333; Cyto_c_ox_2.
DR InterPro; IPR002429; Cyt_c_ox_2.
DR Pfam; PF00116; COX2; 1.
DR PRINTS; PR01166; CYCOXIDASEII.
DR ProDom; PD000131; Copper_Cua; 1.
DR TIGRfam; TIGR01433; Cyto_c_ox_2.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
DR Oxioreductase; Transmembrane; Respiratory chain; Signal;
DR LipoProtein.
DR SIGNAL; 1 23
DR CHAIN 24 307
DR LIPID 24 24
DR TRANSMEM 46 66
DR TRANSMEM 87 107
DR SEQUENCE 307 AA; 33921 MW; B66734B84410996D CRC64;

Query Match
Best Local Similarity 83.3%; Score 37; DB 1; Length 307;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWMTL 6
DB 135 LDMWTL 140

RESULT 6
ID CYOA_PSEPU STANDARD; PRT; 314 AA.
AC Q9WWR1;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
DE subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase
DE subunit 2).
GN CYOA.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=IH-2000;
RX MEDLINE=99085656; PubMed=9868765;
RA Hirayama H., Takami H., Inoue A., Horikoshi K.;

```

RT "Isolation and characterization of toluene-sensitive mutants from  
 RL *Pseudomonas putida* IH-2000."  
 CC FEMS Microbiol. Lett. 169:219-225(1998).  
 CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT  
 CC OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE  
 CC GROWN AT HIGH AERATION (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.  
 CC BUT LACK HEME-BINDING DOMAIN.  
 CC  
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 CC  
 CC EMBL; AB016787; BAA76356.1; -.  
 CC  
 CC DR HSSP; P18400; 1CYM.  
 CC DR InterPro; IPR001505; Copper\_Gua.  
 CC DR InterPro; IPR006333; Cytochrome\_II.  
 CC DR InterPro; IPR002423; Cytochrome\_2.  
 CC DR Pfam; PF00116; COX2; 1.  
 CC DR ProDom; PD000131; Copper\_Gua; 1.  
 CC DR TIGRFAMs; TIGR01433; Cytochrome\_1.  
 CC DR PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.  
 CC KW Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;  
 CC Inner membrane; Signal; Lipoprotein.  
 CC FT SIGNAL 1 23  
 CC FT CHAIN 1 23  
 CC FT LIPID 24 314  
 CC FT LIPID 24 314  
 CC FT DOMAIN 24 42  
 CC FT TRANSSEM 43 63  
 CC FT DOMAIN 64 86  
 CC FT TRANSSEM 87 107  
 CC FT DOMAIN 108 314  
 CC FT DOMAIN 108 314  
 CC SQ SEQUENCE 314 AA; 34702 MW; 96EB04FC3AA77F07 CRC64;  
 CC  
 CC Query Match 90.2%; Score 37; DB 1; Length 314;  
 CC Best Local Similarity 83.3%; Pred. No. 37;  
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 LDWEML 6  
 CC DB 133 LDWEML 138  
 CC  
 CC RESULT 7  
 CC YKTL CABEL STANDARD; PRT; 488 AA.  
 CC ID YKTL CABEL  
 CC AC P34313;  
 CC DT 01-FEB-1994 (Rel. 28, Created)  
 CC DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 CC DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 CC DE Hypothetical protein C07A9.1 in chromosome III precursor.  
 CC GN C07A9.1.  
 CC OS *Caenorhabditis elegans*.  
 CC OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabdilitidae;  
 CC OC Rhabdilitidae; Pelodierinae; Caenorhabdilitis.  
 CC OX NCBI\_TaxID=6239;  
 CC OX NCBI\_TaxID=6239;  
 CC RN  
 CC RP SEQUENCE FROM N.A.  
 CC RC STRAIN=Br1501 N2;  
 CC RX MEDLINE=94150718; PubMed=7906398;  
 CC Wilson R., Ainscough R., Anderson K., Baynes C., Berts M.,  
 CC Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,  
 CC Craik M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,  
 CC Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,  
 CC Johnson L., Jones M., Kerhaw J., Kirsten J., Laisner N.,  
 CC Lacroix P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
 CC Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Snowken R.,

RA Sims M., Smailson N., Smith A., Smith M., Sonhammer E., Staden R.,  
 RA Suleston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,  
 RA Watson R., Watson A., Weinstock L., Wilkinson-Sproat J.,  
 RA Woldman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C.*  
 RT *elegans*."  
 RT Nature 368:32-38(1994).  
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; Z29094; CA82340.1; -.  
 CC  
 CC DR PIR; S40706; S40706.  
 CC DR HSSP; P23807; 1LXX.  
 CC DR WormRep; C07A9.1; CE00502.  
 CC DR InterPro; IPR002619; CX.  
 CC DR InterPro; IPR001304; Lectin\_C.  
 CC DR Pfam; PF00059; Lectin\_C; 1.  
 CC DR ProDom; PD006744; CX; 1.  
 CC DR SMART; SM00034; CLECT; 1.  
 CC DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE\_NEG.  
 CC DR PROSITE; PS50041; C-TYPE LECTIN 2; 1.  
 CC KW Hypothetical protein; Lectin; Signal.  
 CC FT SIGNAL 1 49  
 CC FT CHAIN 1 49  
 CC FT CHAIN 50 488  
 CC FT DOMAIN 224 341  
 CC FT CARBOHYD 187 341  
 CC FT CARBOHYD 237 341  
 CC FT CARBOHYD 409 488  
 CC FT CARBOHYD 409 488  
 CC SQ SEQUENCE 488 AA; 54717 MW; 9022691E47078814 CRC64;  
 CC  
 CC Query Match 90.2%; Score 37; DB 1; Length 488;  
 CC Best Local Similarity 100.0%; Pred. No. 56;  
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 2 DWEML 6  
 CC DB 287 DWEML 291  
 CC  
 CC RESULT 8  
 CC RFB\_C MYXA STANDARD; PRT; 1275 AA.  
 CC ID RFB\_C MYXA  
 CC AC O50864;  
 CC DT 01-NOV-1997 (Rel. 35, Created)  
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 CC DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 CC DE O-antigen biosynthesis protein rfbC.  
 CC GN RFB\_C.  
 CC OS *Myxococcus xanthus*.  
 CC OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;  
 CC OC Cytiobacteriinae; Myxococcaceae; Myxococcus.  
 CC OX NCBI\_TaxID=34;  
 CC OX NCBI\_TaxID=34;  
 CC RN  
 CC RP SEQUENCE FROM N.A.  
 CC RC STRAIN=DK6640;  
 CC RX MEDLINE=96198166; PubMed=8626291;  
 CC Guo D., Bowden M.G., Perhad R., Kaplan H.B.;  
 CC "The *Myxococcus xanthus* rfbC operon encodes an ATP-binding cassette  
 CC transporter homolog required for O-antigen biosynthesis and  
 CC multicellular development."  
 CC J. Bacteriol. 178:1631-1639(1996).  
 CC -1- FUNCTION: INVOLVED IN O-ANTIGEN BIOSYNTHESIS.  
 CC  
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Qy	Db	2 DWEVL 6	349 DWEVL 353	90.2%; Score 37; DB 1; Length 1275; Best Local Similarity 100.0%; Pred. No. 1,4e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 9				
ID	Y250	CORGL	STANDARD;	PRT; 289 AA.
AC	P42459;			
DT	01-NOV-1995	(Rel. 32, Created)		
DT	28-FEB-2003	(Rel. 41, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Hypothetical protein CG10250 (ORF).			
GN	CG10250.			
OS	Corynebacterium glutamicum (Brevibacterium flavum).			
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;			
OC	Corynebacteriineae; Corynebacteriaceae; Corynebacterium.			
OX	NCBI_TaxID=1718;			
RV	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;			
RC	MEDLINE=94161495; PubMed=8117072;			
RX	Patek M., Krumbach K., Eggeling L., Sahm H.;			
RA	"Leucine synthesis in corynebacterium glutamicum: enzyme activities,			
RT	structure of leuB, and effect of leuA inactivation on lysine			
RT	synthesis.";			
RT	Appl. Environ. Microbiol. 60:133-140(1994).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;			
RC	Nakagawa S.;			
RA	"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."			
RT	Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.			
RL	-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).			
CC	-1- CAUTION: Ref.1 sequence differs from that shown due to a			
CC	frameshift in position 59.			
CC	-----			
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	or send an email to <a href="mailto:license@1sb-sib.ch">license@1sb-sib.ch</a> ).			
CC	-----			
CC	EMBL; X70959; CA50297.1; ALT_FRAME.			
DR	EMBL; AP005274; BAB97642.1; -.			
KW	Hypothetical protein; Transmembrane, Complete proteome.			
FT	TRANSMEM 4 24			POTENTIAL.
FT	TRANSMEM 44 64			POTENTIAL.
FT	TRANSMEM 68 88			POTENTIAL.
FT	TRANSMEM 106 125			POTENTIAL.
FT	TRANSMEM 138 158			POTENTIAL.
FT	TRANSMEM 166 186			POTENTIAL.

FT	TRANSMEM	196	216	POTENTIAL.
FT	TRANSMEM	230	250	POTENTIAL.
FT	TRANSMEM	258	278	POTENTIAL.
SO	SEQUENCE	289 AA;	31381 MW;	5C7A38DCBFP078A CRC64;
Query Match				
Query	Local	Similarity	66.7%;	Score 36; DB 1; Length 289;
Matches	4;	Conservative	2;	Mismatches 0; Indels 0; Gaps 0;
OY	1	LDWEM1	6	
DB	256	VDWEM1	261	
RESULT 10				
ID	CYOA_BUCAP	STANDARD;	PRT;	290 AA.
AC	08K993;			
DT	28-FEB-2003	(Rel. 41, Created)		
DT	28-FEB-2003	(Rel. 41, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Ubiqunol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O			
DE	subunit 2) (Oxidase B0(3) subunit 2) (Cytochrome O ubiqunol oxidase			
GN	CYOA OR BUSG456.			
OS	Buchnera aphidicola (subsp. Schizaphis graminum).			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OX	NCBI_TaxID=98794;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22084549; PubMed=12089438;			
RA	Tamas I., Kleason L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,			
RT	Wernegren U.J.J., Sandstrom J.P., Moran N.A., Andersson S.G.E.;			
RL	"50 million years of genomic stasis in endosymbiotic bacteria.";			
CC	Science 296:2376-2379(2002).			
CC	-1- FUNCTION: Cytochrome O terminal oxidase complex is the component			
CC	of the aerobic respiratory chain that predominates when cells are			
CC	grown at high aeration (By similarity).			
CC	-1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).			
CC	-1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.			
CC	BUT LACK HEME-BINDING DOMAIN.			
CC	-----			
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CC	or send an email to <a href="mailto:license@1eb-sib.ch">license@1eb-sib.ch</a> ).			
CC	-----			
DR	EMBL; AE014121; AAM67999.1; -.			
DR	InterPro; IPR001505; Copper_CUA.			
DR	InterPro; IPR006333; CyOA_II.			
DR	InterPro; IPR002429; Cyt_c ox 2. '			
DR	InterPro; IPR000437; Prok_Lipoprot.			
DR	Pfam; PF00116; COX2.1.			
DR	PRINTS; PR01166; CYCOXIDASEBII.			
DR	ProDom; PD000131; Copper_CUA; 1.			
DR	TIGRFAMs; TIGR01433; CyOA_1.			
DR	PROSITE; PS00013; PROKAR_LIPOPROTEIN; FALSE NEG.			
KW	Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;			
KW	Signal; Lipoprotein; Complete proteome.			
FT	SIGNAL	1	24	POTENTIAL.
FT	CHAIN	25	290	UBIQUINOL OXIDASE POLYPEPTIDE II.
FT	LIPID	25	25	N-ACTYL DIGLYCERIDE (POTENTIAL).
FT	DOMAIN	25	42	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	43	63	POTENTIAL.
FT	DOMAIN	64	87	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	88	108	POTENTIAL.
FT	DOMAIN	109	290	EXTRACELLULAR (POTENTIAL).
SO	SEQUENCE	290 AA;	33730 MW;	3D80A028A4732963 CRC64;



Query Match 87.84; Score 36; DB 1; Length 290;  
 Best Local Similarity 83.34; Pred. No. 48;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 LDMEWL 6  
 134 LDMRWL 139

RESULT 11  
 IKK-HUMAN STANDARD; PRT; 745 AA.

ID IKK-HUMAN STANDARD; PRT; 745 AA.  
 AC 01511; 014666; Q13132; G92467;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Inhibitor of nuclear factor kappa-B kinase subunit (IC 2.7.1.-)  
 DE (1-kappa-B kinase alpha) (IKK- $\alpha$ ) (IKK- $\alpha$ ) (Ikappab kinase  
 DE (Ikappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous  
 DE Kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKB1KA)  
 DE CHUK OR IKK- $\alpha$ .  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.  
 RC TISSUE=T-cell;  
 RA MEDLINE=97386461; PubMed=9244310;  
 RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;  
 RT "Identification and characterization of an Ikappab kinase.";  
 RL Cell 90:373-383(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC MEDLINE=97394468; PubMed=9252186;  
 RA DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;  
 RT "A cytokine-responsive Ikappab kinase that activates the transcription  
 RT factor NF-kappaB.";  
 RL Nature 368:548-554(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND  
 RP SER-176.  
 RC TISSUE=Cervical carcinoma;  
 RA MEDLINE=98008813; PubMed=9346484;  
 RA Mercutio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,  
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;  
 RT "IKK-1 and IKK-2: cytokine-activated Ikappab kinases essential for  
 RT NF-kappaB activation.";  
 RL Science 278:860-866(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RA MEDLINE=99032998; PubMed=9813230;  
 RA Hu M.C.-T., Wang Y.-P.;  
 RT "Ikappab kinase alpha and -beta genes are coexpressed in adult and  
 RT embryonic tissues but localized to different human chromosomes.";  
 RL Gene 223:31-40(1998).  
 RN [5]  
 RP SEQUENCE OF 32-745 FROM N.A.  
 RC TISSUE=Cervical carcinoma;  
 RA MEDLINE=96258427; PubMed=8777433;  
 RA Connelly M.A., Marcu K.B.;  
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper  
 RT families of interacting proteins, contains a serine-threonine kinase  
 RT catalytic domain.";  
 RL Cell. Mol. Biol. Res. 41:537-549(1995).  
 RN [6]  
 RP PHOSPHORYLATION BY MAPK14/NIK, AND MUTAGENESIS OF SER-176; THR-179  
 RP AND SER-180.  
 RA MEDLINE=98188283; PubMed=9520446;  
 RA Ling L., Cao Z., Goeddel D.V.;  
 RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of

RT Ser-176.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).  
 RN [7]  
 RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.  
 RA MEDLINE=99413720; PubMed=10485710;  
 RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,  
 RA Donner D.B.;  
 RT "NF-kappaB activation by tumour necrosis factor requires the Akt  
 RT serine-threonine kinase.";  
 RL Nature 401:82-85(1999).  
 RN [8]  
 RP IKK- $\alpha$  BINDING.  
 RA MEDLINE=99212441; PubMed=10195894;  
 RA Delnase M., Hayakawa M., Chen Y., Karin M.;  
 RT "Positive and negative regulation of Ikappab kinase activity through  
 RT IKK- $\alpha$  subunit phosphorylation.";  
 RL Science 284:309-313(1999).  
 RN [9]  
 RP IKK PHOSPHORYLATION.  
 RA MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., DiDonato J.A., Lin A.;  
 RT "Coordinate regulation of Ikappab kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [10]  
 RP REVIEW.  
 RA MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 RT inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 RN [11]  
 RP SUBUNIT OF A COMPLEX CONTAINING CREBBP, NCOA2, NCOA3, IKK- $\alpha$  AND IKK- $\beta$ .  
 RA MEDLINE=21968797; PubMed=11971985;  
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,  
 RA O'Malley B.W.;  
 RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator  
 RT activity by I kappa B kinase.";  
 RL Mol. Cell. Biol. 22:3549-3561(2002).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 CC the dissociation of the inhibitor/NF-kappa-B complex and  
 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3.  
 CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated  
 CC when dephosphorylated.  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but  
 CC also as an homodimer. Directly interacts with IKK-GAMMA/IKK- $\gamma$ .  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MAPK14/NIK, MEK1, IKAP and IKK-alpha-P65-P50  
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of  
 CC a complex composed of NCOA2, NCOA3, IKK- $\alpha$ , IKK- $\beta$  and CREBBP.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Widely expressed.  
 CC -1- PTM: Phosphorylated by MAPK14/NIK, AKT and to a lesser extent by  
 CC MEK1. And dephosphorylated by PP2A. Auto-phosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPAB KINASE SUBFAMILY.  
 CC  
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 CC  
 CC EMBL; AF012890; AAC51662.1; -  
 CC EMBL; AF009325; AAC51671.1; -  
 CC EMBL; AF080157; AAD08996.1; -  
 CC EMBL; U22512; AAC50713.1; -  
 CC HSSP; O63450; 1A06.  
 CC GeneW; HGNC:1974; CHUK.  
 CC MIM; 600664; -

DR GO: GO:0005737; C:cytoplasm; TAS.  
 DR GO: GO:0008384; P:kinase activity; TAS.  
 DR GO: GO:0007345; P:embryogenesis and morphogenesis; TAS.  
 DR GO: GO:0007352; P:I-kappaB phosphorylation; TAS.  
 DR GO: GO:0006955; P:immune response; TAS.  
 DR InterPro: IPR000719; P:kinase.  
 DR InterPro: IPR002290; Ser\_Thr\_kinase.  
 DR InterPro: IPR01245; Tyr\_kinase.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR ProDom: PD000001; P:kinase; 1.  
 DR SMART: SM00220; S\_TKc; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR TRANSFAC: Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation.  
 FT DOMAIN 15 302 PROTEIN KINASE.  
 FT 455 476 LEUCINE-ZIPPER (POTENTIAL).  
 FT 738 743 NEMO-BINDING.  
 FT NP\_BIND 21 29 ATP (BY SIMILARITY).  
 FT 44 44 ATP (BY SIMILARITY).  
 FT BINDING 21 29 BY SIMILARITY.  
 FT ACT\_SITE 144 144 PHOSPHORYLATION (BY PKB/AKT1).  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY MAP3K14).  
 FT MOD\_RES 176 176  
 FT MUTAGEN 23 23 T->A: LOSS OF PHOSPHORYLATION AND  
 FT MUTAGEN 44 44 DECREASE OF KINASE ACTIVITY.  
 FT MUTAGEN 44 44 K->M: LOSS OF KINASE ACTIVITY.  
 FT MUTAGEN 176 176 S->A: LOSS OF AUTOPHOSPHORYLATION.  
 FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF  
 FT MUTAGEN 176 176 ACTIVITY.  
 FT MUTAGEN 176 176 S->E: FULL ACTIVATION.  
 FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.  
 FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.  
 FT CONFLICT 543 543 E -> G (IN REF. 2).  
 FT CONFLICT 604 604 L -> R (IN REF. 5).  
 FT CONFLICT 679 680 TS -> AY (IN REF. 5).  
 FT CONFLICT 684 684 P -> A (IN REF. 3 AND 5).  
 FT CONFLICT 684 684 TS -> DL (IN REF. 5).  
 FT CONFLICT 686 686  
 FT SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;  
 Query Match 87.8%; Score 36; DB 1; Length 745;  
 Best local Similarity 83.3%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 LDMEWL 6  
 Db 738 LDMSWL 743

RESULT 12  
 ID IKKA\_MOUSE STANDARD; PRT; 745 AA.  
 AC Q06680; Q9D2X3;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)  
 DE (I kappa-B kinase alpha) (IKBA) (IKK-A) (Ikkappa kinase)  
 DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous  
 DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFIKBA).  
 GN CHUK OR IKKA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=BALB/c;  
 RX MEDLINE=9604444; PubMed=7558004;  
 RA Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.,  
 RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human  
 RT chromosome 10 and mouse chromosome 19.";

RL Genomics 27:348-351(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=BALB/c;  
 RX MEDLINE=96258427; PubMed=8777433;  
 RA Connolly M.A., Marcu K.B.,  
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper  
 RT families of interacting proteins, contains a serine-threonine kinase  
 RT catalytic domain.";  
 RL Cell. Mol. Biol. Res. 41:537-549(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RC STRAIN=C57BL/6J; TISSUE=Colon;  
 RX MEDLINE=2108560; PubMed=11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Ishii Y.,  
 RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,  
 RA Saito T., Okazaki Y., Gojohori T., Hono H., Kanakawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischnann W., Gasteierland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carlini P., de Bonaldo M.F.,  
 RA Brownstein M.S., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilmberg L.,  
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohno S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [4]  
 RP ALTERNATIVE SPLICING.  
 RX MEDLINE=20198447; PubMed=10733566;  
 RA McKenzie F.R., Connolly M.A., Balzarano D., Mueller J.R.,  
 RA Gelezinas R., Marcu K.B.,  
 RT "Functional isoforms of Ikkappa kinase alpha (IKKalpha) lacking  
 RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and  
 RT IKKbeta have different activation requirements.";  
 RL Mol. Cell. Biol. 20:2635-2649(2000).  
 RN [5]  
 RP PHOSPHORYLATION BY MAP3K14/NIK.  
 RX MEDLINE=98188238; PubMed=9520401;  
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,  
 RA Okumura K.,  
 RT "Differential regulation of Ikkappa kinase alpha and beta by two  
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated  
 RT protein kinase/ERK kinase-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).  
 RN [6]  
 RP IKKA-IKKB BINDING.  
 RX MEDLINE=99212141; PubMed=10195894;  
 RA Delhaese M., Hayakawa M., Chen Y., Karin M.,  
 RT "Positive and negative regulation of Ikkappa kinase activity through  
 RT IKKbeta subunit phosphorylation.";  
 RL Science 284:309-313(1999).  
 RN [7]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., DiDonato J.A., Lin A.,  
 RT "Coordinate regulation of Ikkappa kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [8]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.,  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 RT inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).



RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzyzaniak M.I., Skalska U., Smalins D.E.,  
 RA Scherach A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [6]  
 RP IKK PHOSPHORYLATION.  
 RP MEDLINE=99038238; PubMed=9819420;  
 RX Nemoto S., DiDonato J.A., Lin A.;  
 RA "Coordinate regulation of I-kappaB kinases by mitogen-activated protein  
 RT kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RT Mol. Cell. Biol. 18:7336-7343(1998).  
 [7]  
 RN REVIEW.  
 RP MEDLINE=20178139; PubMed=10712233;  
 RX Jobin C., Sartor R.B.;  
 RA "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 RT inflammation and protection.";  
 RT Am. J. Physiol. 278:C451-C462(2000).  
 [8]  
 RN IDENTIFICATION IN A COMPLEX WITH CREBBP, NCOA2, NCOA3, IKKA AND IKKB.  
 RX MEDLINE=21968797; PubMed=1971985;  
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,  
 RA O'Malley B.W.;  
 RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator  
 RT activity by I kappa B kinase.";  
 RT Mol. Cell. Biol. 22:3549-3561(2002).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 CC the dissociation of the inhibitor/NF-kappa-B complex and  
 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3 (By similarity).  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MEK1, MAP3K14/NIK, IKAP and IKB-alpha-P65-P50  
 CC complex. Phosphorylated IKB-alpha is further released from the  
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB  
 CC and CREBBP.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal  
 CC muscle, kidney, pancreas, spleen, thymus, prostate, testis and  
 CC peripheral blood.  
 CC -1- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.  
 CC Weakly autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPPAB KINASE SUBFAMILY.  
 CC  
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DR GO:0006468; P:protein amino acid phosphorylation; NAS.  
 DR InterPro: IPR000719; Prot\_kinase.  
 DR InterPro: IPR002290; Ser\_thr\_kinase.  
 DR Pfam: PF00069; kinase; 1.  
 DR Pfam: PF00240; ubiquitin; 1.  
 DR ProDom: PD000001; Prot\_kinase; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP, FALSE\_NEG.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW transferase; Serine/threonine-protein kinase; ATP-binding;  
 KW phosphorylation.  
 FT DOMAIN 15 300 PROTEIN KINASE.  
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 FT DOMAIN 737 742 NEMO-BINDING.  
 FT NP\_BIND 21 29 ATP (BY SIMILARITY).  
 FT BINDING 44 44 ATP (BY SIMILARITY).  
 FT ACT\_SITE 145 145 BY SIMILARITY.  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 177 177 PHOSPHORYLATION.  
 FT MOD\_RES 181 181 PHOSPHORYLATION.  
 FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO  
 FT MUTAGEN 177 177 EFFECT ON BINDING TO NIK.  
 FT MUTAGEN 177 177 S->A: DECREASE OF ACTIVITY.  
 FT MUTAGEN 181 181 S->E: FULL ACTIVATION.  
 FT MUTAGEN 181 181 S->A: DECREASE OF ACTIVITY.  
 FT CONFLICT 231 255 WHISKYRSEVDIVSEDLNGVTKP -> CYRMPTGVNHS  
 FT CONFLICT 231 255 CNPSTLGRGRWVI (IN REF. 5).  
 FT CONFLICT 425 425 Q -> H (IN REF. 1).  
 SQ SEQUENCE 756 AA; 8653 MW; F9CADF671AE9E14E CRC64;  
 Query Match 87.8%; Score 36; DB 1; Length 756;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 LDMEWL 6  
 Db 737 LDMSWL 742  
 RESULT 14  
 ID IKKB MOUSE STANDARD. PRT; 757 AA.  
 AC 088351; Q9RLJ6;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (BC 2.7.1.-)  
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase  
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).  
 GN IKKB OR IKKB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. AND PHOSPHORYLATION BY MEK1.  
 RC STRAIN=C57BL/6; TISSUE=Spleen;  
 RX MEDLINE=98188238; PubMed=9520401;  
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,  
 RA Okumura K.;  
 RT "Differential regulation of I-kappaB kinase alpha and beta by two  
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated  
 RT protein kinase/ERK kinase kinase-1.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;  
 RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that  
 RT constitutively phosphorylates serine residues of Ikb.";  
 RT Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.  
 [3]  
 RN DEVELOPMENTAL STAGE.

RX MEDLINE=99455228; PubMed=10523828;  
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;  
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling  
 RT pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a  
 RT developmentally regulated protein kinase.";  
 RL Oncogene 18:5514-5524(1999).  
 RN (4)  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., Didonato J.A., Lin A.;  
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [5]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 RT inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 CC the dissociation of the inhibitor/NF-kappa-B complex and  
 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3.  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MEK1, MAP3K14/NIK, IKAP and IKK-ALPHA-P65-P50  
 CC complex. Phosphorylated IKK-alpha is further released from the  
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB  
 CC and CREBBP (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.  
 CC -1- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout  
 CC the mouse embryo, at E9.5 day its expression begins to be  
 CC localized to the brain, neural ganglia, neural tube, and in liver  
 CC at E12.5 day. At E15.5 day, the expression is further restricted  
 CC to specific tissues of the embryo.  
 CC -1- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.  
 CC Weakly autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPPAB KINASE SUBFAMILY.  
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 CC -----  
 DR EMBL; AF026524; AAC23557.1; -  
 DR EMBL; AF088910; AAD52095.1; -  
 DR HSP; G63450.1A06.  
 DR MGI; MGI:338071; Ikbb.  
 DR InterPro; IPR000719; Prot. kinase.  
 DR InterPro; IPR002290; Ser Thr kinase.  
 DR InterPro; IPR001245; Tyr kinase.  
 DR Pfam; PF00069; PKINASE.1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PROSITE; PD000001; Prot. Kinase.1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP. FALSE NEG.  
 DR PROSITE; PS00108; PROTEIN KINASE ST.1.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM.1.  
 KM Transerase; Serine/threonine-protein kinase; ATP-binding;  
 FT Phosphorylation.  
 FT DOMAIN 15 300 PROTEIN KINASE.  
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 FT DOMAIN 737 742 NEMO-BINDING.  
 FT NP\_BIND 21 29 ATP (BY SIMILARITY).  
 FT BINDING 44 44 ATP (BY SIMILARITY).  
 FT ACT\_SITE 145 145 BY SIMILARITY.  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 CC -----

FT MOD\_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).  
 FT CONFLICT 56 56 N -> D (IN REF. 2).  
 FT CONFLICT 343 343 N -> D (IN REF. 2).  
 FT CONFLICT 356 356 K -> E (IN REF. 2).  
 FT CONFLICT 390 390 L -> F (IN REF. 2).  
 FT CONFLICT 406 406 P -> Q (IN REF. 2).  
 FT CONFLICT 406 406 K -> R (IN REF. 2).  
 FT CONFLICT 573 573 K -> R (IN REF. 2).  
 FT CONFLICT 736 757 TLDMWSLQWEDERCSLEQACD -> VTA (IN REF. 2).  
 SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5B CRC64;  
 Query Match Score 36; DB 1; Length 757;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LDMWML 6  
 DB 737 LDMWML 742  
 RESULT 15  
 ID IKKB RAT STANDARD; PRT; 757 AA.  
 AC 09078;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (BC 2.7.1.-)  
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase  
 DE 2) (IKK) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).  
 GN IKKB OR IKKB.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid:10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang Y., Sun S., Ravid K.;  
 RT "IKK beta in megakaryocyte differentiation.";  
 RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., Didonato J.A., Lin A.;  
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [3]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 RT inflammation and protection.";  
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 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3.  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MEK1, MAP3K14/NIK, IKAP and IKK-ALPHA-P65-P50  
 CC complex. Phosphorylated IKK-alpha is further released from the  
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB  
 CC and CREBBP (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
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 CC Weakly autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPPAB KINASE SUBFAMILY.  
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CC -----  
 DR EMBL; AF115282; AAF21978.1; -  
 DR HSSP; Q63450; 1A06.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00069; Kinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KM Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KM phosphorylation.  
 FT DOMAIN 15 300 PROTEIN KINASE.  
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 FT DOMAIN 737 742 NEMO-BINDING.  
 FT NP\_BIND 21 29 ATP (BY SIMILARITY).  
 FT BINDING 44 44 ATP (BY SIMILARITY).  
 FT ACT\_SITE 145 145 BY SIMILARITY.  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 757 AA; 86866 MW; 3AFBE46A7DF91F9C CRC64;

Query March 87.8%; Score 36; DB 1; Length 757;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMEWL 6  
 |||  
 |||  
 Db 737 LDMSGWL 742

Search completed: February 18, 2004, 14:28:14  
 Job time : 4.55263 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09, Search time 6.5921 Seconds  
(without alignment)  
87.531 Million cell updates/sec

Title: US-09-643-260-17

Perfect score: 41

Sequence: 1 LDMEWL 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	95.1	501	2 S45914	probable glucan 1,
2	37	90.2	210	2 T41553	thymidylate kinase
3	37	90.2	210	2 S28955	dTMP kinase (EC 2.
4	37	90.2	242	2 T27590	hypothetical prote
5	37	90.2	277	1 JCS900	bo-type ubiquinol
6	37	90.2	281	2 S73517	MG373 homolog G12
7	37	90.2	296	2 A84985	cytochrome o ubiqn
8	37	90.2	307	1 A36885	bo-type ubiquinol
9	37	90.2	318	2 AD0384	cytochrome o ubiqn
10	37	90.2	331	2 D83480	cytochrome o ubiqn
11	37	90.2	344	2 AG3489	cytochrome o ubiqn
12	37	90.2	353	2 A87469	ubiquinol oxidase
13	37	90.2	377	2 B71184	probable sarcosine
14	37	90.2	379	2 F75144	sarcosine oxidase,
15	37	90.2	386	2 C96006	probable cytochrom
16	37	90.2	404	2 A71213	alanine-tRNA ligase
17	37	90.2	405	2 G75027	alanine-tRNA synthet
18	37	90.2	488	2 S40706	hypothetical prote
19	37	90.2	1275	2 T18556	O-antigen biosynth
20	36	87.8	82	2 C69013	hypothetical prote
21	36	87.8	162	2 C70829	hypothetical prote
22	36	87.8	270	2 I40724	hypothetical prote
23	36	87.8	332	2 A13395	NADH2 dehydrogenas
24	36	87.8	348	2 AE2733	NADH ubiquinone ox
25	36	87.8	348	2 G97514	NADH dehydrogenase
26	36	87.8	414	2 B82408	hypothetical prote
27	36	87.8	443	2 AE0309	probable sugar tra
28	36	87.8	745	1 I49101	conserved helix-10
29	36	87.8	764	2 AD3144	formate dehydrogen

30	36	87.8	764	2 H98143	cbhbc protein (U60
31	36	87.8	1120	2 A10561	integral membrane
32	35	85.4	332	2 A42593	cytochrome o ubiqn
33	35	85.4	377	2 B97376	cytochrome ba(3) (
34	35	85.4	378	2 T12895	hypothetical prote
35	35	85.4	385	2 F69941	conserved hypothet
36	35	85.4	420	2 A54759	cytochrome ba(3) c
37	35	85.4	451	2 G82218	benzox histidine k
38	35	85.4	480	2 T24087	hypothetical prote
39	35	85.4	660	2 S66708	probable membrane
40	35	85.4	700	2 T24092	hypothetical prote
41	35	85.4	723	2 T32136	hypothetical prote
42	35	85.4	765	2 T35719	chitinase - Strept
43	35	85.4	783	2 F88808	protein R09E10.3 (
44	35	85.4	854	2 C83905	hypothetical prote
45	35	85.4	903	2 T20804	hypothetical prote

## ALIGNMENTS

## RESULT 1

S45914  
probable glucan 1,3-beta-glucosidase (EC 3.2.1.58) YBR056w - yeast (Saccharomyces cerev

N.Alternate names: hypothetical protein YBR0510

C.Species: Saccharomyces cerevisiae

C.Date: 26-Aug-1994 #sequence\_revision 09-Sep-1994 #text\_change 19-Apr-2002

C.Accession: S45914; S49511; S55855

R.Aljinovic, G.; Pohl, F.M.; Pohl, T.M.

submitted to the Protein Sequence Database, August 1994

A.Reference number: S45906

A.Accession: S45914

A.Molecule type: DNA

A.Residues: 1-501 <AL2>

A.Cross-references: EMBL:Z35925; NID:G536292; PID:G536293; MIPS:YBR056w

A.Experimental source: strain S288C

A.Description: Sequence and analysis of 24 kb on chromosome II of Saccharomyces cerevisiae

A.Reference number: S49503

A.Accession: S49511

A.Molecule type: DNA

A.Residues: 1-501 <AL2>

A.Cross-references: EMBL:Z46260; NID:G559942; PID:G559952

A.Experimental source: strain S288C

R.Aljinovic, G.; Pohl, T.M.

Yeast 11, 475-479, 1995

A.Title: Sequence and analysis of 24 kb on chromosome II of Saccharomyces cerevisiae.

A.Reference number: S55846; MUID:95321020; PMID:7597852

A.Accession: S55855

A.Status: nucleic acid sequence not shown; translation not shown

A.Molecule type: DNA

A.Residues: 1-501 <AL2>

A.Cross-references: EMBL:Z46260; NID:G559942; PID:CA06399.1; PID:G559952

A.Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994

C.Genetics:

A.Cross-references: SGD:S0000260

A.Map position: 2R

C.Keywords: glycosidase; hydrolase

Query Match 95.1% Score 39; DB 2; Length 501;  
Best Local Similarity 83.3% Pred No. 63;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMEWL 6  
:|||||  
Db 109 IDMEWL 114

## RESULT 2

T41553  
thymidylate kinase - fission yeast (Schizosaccharomyces pombe)  
C.Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jan-2000  
 C/Accession: T41553  
 R/Mood: V.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Hartley, D.  
 Submitted to the EMBL Data Library, June 1998  
 A/Reference number: Z22001  
 A/Accession: T41553  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-210 <MOO>  
 A/Cross-references: EMBL:AL023794; PIDN:CAA19357.1; GSPDB:GN00068; SPDB:SPCC70.07c  
 A/Experimental source: strain 972h-; cosmid c70  
 C/Genetics:  
 A/Gene: SPDB:SPCC70.07c  
 A/Map position: 3  
 A/Intons: 45/1; 110/3  
 C/Superfamily: dtwp kinase

Query Match 90.2%; Score 37; DB 2; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 52;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMEW 5  
 |||||  
 DB 112 LDMEW 116

RESULT 3  
 S28955  
 dtwp kinase (EC 2.7.4.9) - fission yeast (Schizosaccharomyces pombe)  
 C/Species: Schizosaccharomyces pombe  
 C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 19-Jan-2001  
 C/Accession: S28955  
 R/Abalgar, L.T.; Yeh, Y.I.S.; Jong, A.Y.  
 Biochim. Biophys. Acta 1132, 222-224, 1992  
 A/Title: Functional and structural conservation of Schizosaccharomyces pombe dtwp kinase  
 A/Reference number: S28955; MUID:93003330; PMID:1137149  
 A/Accession: S28955  
 A/Molecule type: mRNA  
 A/Residues: 1-210 <ABA>  
 A/Cross-references: EMBL:X65868; NID:94973; PIDN:CAA46698.1; PID:94974  
 C/Species: dtwp kinase  
 C/Keywords: ATP; nucleotide binding; nucleotide biosynthesis; P-loop; phosphotransferase  
 F;14-21/Region: nucleotide-binding motif A (P-loop)

Query Match 90.2%; Score 37; DB 2; Length 210;  
 Best Local Similarity 100.0%; Pred. No. 52;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMEW 5  
 |||||  
 DB 111 LDMEW 115

RESULT 4  
 T27590  
 hypothetical protein ZC47.13 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000  
 C/Accession: T27590  
 R/McMurray, A.  
 submitted to the EMBL Data Library, October 1996  
 A/Reference number: Z20391  
 A/Accession: T27590  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-242 <WIL>  
 A/Cross-references: EMBL:Z81141; PIDN:CA03488.1; CESP:ZC47.13  
 A/Experimental source: clone ZC47  
 C/Genetics:  
 A/Gene: CESP:ZC47.13  
 A/Intons: 172/3  
 C/Superfamily: Caenorhabditis elegans hypothetical protein ZC47.9

Query Match 90.2%; Score 37; DB 2; Length 242;  
 Best Local Similarity 83.3%; Pred. No. 60;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMEWL 6  
 |||||  
 DB 226 LDMEWL 231

RESULT 5  
 JCS900  
 bo-type ubiquinol oxidase (EC 1.10.3.-) chain II - Bradyrhizobium japonicum  
 C/Species: Bradyrhizobium japonicum  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C/Accession: JCS900  
 R/Surpin, M.A.; Luebben, M.; Møller, R.J.  
 Gene 183, 201-206, 1996  
 A/Title: The Bradyrhizobium japonicum COXKXZ gene cluster encodes a bo3-type ubiquinol  
 A/Reference number: JCS900; MUID:97149299; PMID:8996107  
 A/Accession: JCS900  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: DNA  
 A/Residues: 1-277 <SUR>  
 C/Genetics:  
 A/Gene: coxX  
 C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain  
 C/Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; re

Query Match 90.2%; Score 37; DB 1; Length 277;  
 Best Local Similarity 83.3%; Pred. No. 69;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMEWL 6  
 |||||  
 DB 108 LDMEWL 113

RESULT 6  
 S73617  
 MG373 homolog G12.orf281 - Mycoplasma pneumoniae (strain ATCC 29342)  
 C/Species: Mycoplasma pneumoniae  
 A/Variety: ATCC 29342  
 C/Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 07-Dec-1999  
 C/Accession: S73617  
 R/Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirk, E.; Li, B.C.; Herrmann, R.  
 Nucleic Acids Res. 24, 4420-4449, 1996  
 A/Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae  
 A/Reference number: S73327; MUID:97105885; PMID:8948633  
 A/Accession: S73617  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-281 <HIM>  
 A/Cross-references: EMBL:AE000027; GB:U00089; NID:91673941; PIDN:AAB95939.1; PID:91673;  
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
 C/Genetics:  
 A/Genetic code: SGC3

Query Match 90.2%; Score 37; DB 2; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 70;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWEMWL 6  
 |||||  
 DB 271 DWEMWL 275

RESULT 7  
 AB4985  
 cytochrome o ubiquinol oxidase subunit II [imported] - Buchnera sp. (strain APS)  
 C/Species: Buchnera sp.  
 C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 02-Apr-2001  
 C/Accession: AB4985  
 R/Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.



Nature 407, 81-86, 2000  
A>Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A  
A:Reference number: AB4930; MUID:20445173; PMID:10993077  
A:Accession: AB4985  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-296 <STO>  
A:Cross-references: GB:AP000398; GSPDB:GN00144  
A:Experimental source: strain APS  
C:Genetics:  
A:Gene: cyoA; BU472  
C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain  
C:Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match  
Best Local Similarity 90.2%; Score 37; DB 2; Length 296;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWML 6  
DB 125 LDMKML 130

RESULT 8  
A:Accession: A36885  
bo-type ubiquinol oxidase (EC 1.10.3.-) chain II precursor - Acetobacter aceti  
N:Alternate names: cytochrome a1 chain II  
C:Species: Acetobacter aceti  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
C:Accession: A36885  
R:Pukaya, M.; Tayama, K.; Tamaki, T.; Ebisuya, H.; Okumura, H.; Kawamura, Y.; Horinouchi, J.; Bacteriol. 175, 4307-4314, 1993  
A>Title: Characterization of a cytochrome a-1 that functions as a ubiquinol oxidase in A  
A:Reference number: A36885; MUID:9332308; PMID:8392509  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-307 <FTK>  
A:Cross-references: GB:D13185; NID:9409064; PIDN:BA02480.1; PID:9433186  
A:Experimental source: isolate 1023  
C:Genetics:  
A:Gene: cybB  
C:Complex: heterotetramer; chains I, II, III and IV  
C:Function:  
A:Description: terminal oxidase for ethanol oxidation  
C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain  
C:Keywords: copper; electron transfer; heterotetramer; membrane-associated complex; oxid  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-307/Product: bo-type ubiquinol oxidase chain II #status predicted <MAT>  
F:48-64/Domain: transmembrane #status predicted <TM1>  
F:89-105/Domain: transmembrane #status predicted <TM2>

Query Match  
Best Local Similarity 90.2%; Score 37; DB 1; Length 307;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWML 6  
DB 135 LDMKML 140

RESULT 9  
A:Accession: AD0384  
cytochrome O ubiquinol oxidase chain II (EC 1.10.3.-) [imported] - Yersinia pestis (stre  
C:Species: Yersinia pestis  
C>Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AD0384  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.  
deno-Terraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
Hill, M.; Rutherford, K.; Simmonds, M.; Skellon, J.; Stevens, K.; Whitehead, S.; Barrall,  
Nature 413, 523-527, 2001  
A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AD0384  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-318 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC92399.1; PID:915981102; GSPDB:GN00175  
C:Genetics:  
A:Gene: cyoA  
C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chat  
C:Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; re

Query Match  
Best Local Similarity 90.2%; Score 37; DB 2; Length 318;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWML 6  
DB 135 LDMKML 140

RESULT 10  
A:Accession: D83480  
cytochrome O ubiquinol oxidase subunit II PA1317 [imported] - Pseudomonas aeruginosa (C  
C:Species: Pseudomonas aeruginosa  
C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: D83480  
R:Stover, C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Liu, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat  
A:Reference number: AB2950; MUID:20437337; PMID:10984043  
A:Accession: D83480  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-331 <STO>  
A:Cross-references: GB:AE004561; GB:AE004091; NID:9947253; PIDN:AA04706.1; GSPDB:GN0  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: cyoA; PA1317  
C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chat  
C:Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match  
Best Local Similarity 90.2%; Score 37; DB 2; Length 331;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWML 6  
DB 133 LDMKML 138

RESULT 11  
A:Accession: AG3489  
cytochrome O ubiquinol oxidase chain II (EC 1.10.3.-) [imported] - Brucella melitensis  
C:Species: Brucella melitensis  
C>Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 22-Mar-2002  
C:Accession: AG3489  
R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Loe, T.; Ivanova, .; Mazur, M.; Goltzman, B.; Selkov, E.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Leter Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A>Title: The genome sequence of the facultative intracellular pathogen Brucella melite  
A:Reference number: AB3252; PMID:11756688  
A:Accession: AG3489  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-344 <KUR>  
A:Cross-references: GB:AE00917; PIDN:AAL53082.1; PID:917983945; GSPDB:GN00190  
A:Experimental source: strain 16M  
C:Genetics:  
A:Gene: BME11901  
A:Map position: I  
C:Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chat  
C:Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; re

Query Match 90.2%; Score 37; DB 2; Length 344;  
Best Local Similarity 83.3%; Pred. No. 87;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMEW 6  
DB 141 LDMEW 146

## RESULT 12

ubiquinol oxidase subunit II [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 24-May-2001  
C:Accession: A87469

R:Nieman, W.C.; Feldlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eison, J.; Heidelberg, J.B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hatt, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87469; MUID:21173698; PMID:11259647  
A:Accession: A87469

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-353 <STO>  
A:Cross-references: GB:AE005673; NID:g13423199; PIDN:AAK23749.1; GSPDB:GN00148  
C:Genetics:

A:Gene: CCI773  
C:Superfamily: bc-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain C;Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match 90.2%; Score 37; DB 2; Length 353;  
Best Local Similarity 83.3%; Pred. No. 89;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMEW 6  
DB 146 LDMEW 151

## RESULT 13

probable sarcosine oxidase - Pyrococcus horikoshii  
C:Species: Pyrococcus horikoshii  
C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 21-Jul-2000  
C:Accession: B71184

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekir, M.; Ohnuki, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushiida, N.; Oguchi, DNA Res. 5, 55-76, 1998  
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A

A:Reference number: A71000; MUID:98344137; PMID:9679194  
A:Accession: B71184

A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA

A:Residues: 1-377 <KAM>  
A:Cross-references: GB:AP000007; NID:g3236134; PIDN:BA30865.1; PID:g3358182

A:Experimental source: strain Q73  
A:Note: this accession replaces an interim accession for a sequence replaced by Genbank

C:Genetics:

A:Gene: PH1751  
C:Superfamily: sarcosine oxidase

Query Match 90.2%; Score 37; DB 2; Length 377;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMEW 5  
DB 354 LDMEW 358

## RESULT 14

F75144  
sarcosine oxidase, chain beta (soxb) PAB0214 - Pyrococcus abyssi (strain Orsay)  
C:Species: Pyrococcus abyssi  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000  
C:Accession: F75144

R:anonymous, Genoscope  
Submitted to the EMBL Data Library, July 1999  
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome st.

A:Reference number: A75001  
A:Accession: F75144

A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-379 <KAM>  
A:Cross-references: GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAN49237.1; PID:g5457

A:Experimental source: strain Orsay  
C:Genetics:

A:Gene: soxb; PAB0214  
C:Superfamily: sarcosine oxidase  
Query Match 90.2%; Score 37; DB 2; Length 379;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMEW 5  
DB 356 LDMEW 360

## RESULT 15

probable cytochrome o ubiquinol oxidase chain II protein (EC 1.10.3.-) [imported] - St.

C:Species: Stenotrophobium meliloti  
C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
C:Accession: C96006

R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hern Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing en

A:Reference number: A95842; MUID:21396508; PMID:11481431  
A:Accession: C96006

A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-386 <KUR>  
A:Cross-references: GB:AL591985; PIDN:CAK49715.1; PID:g15141202; GSPDB:GN00167

A:Experimental source: strain 1021, megaplasmid pSymB  
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubbe, D.; Chain, P.; Cowley, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F. L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kise, E.; Komp, C.; Lelaux, hebullet, P.; Vandemol, M.; Vorholter, F.J.; Weidner, S.; Keller, D.H.; Wong, K.; Yeh, A:Title: The composite genome of the legume symbiont Stenotrophobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation

C:Genetics:

A:Gene: cyoA; SMD21487  
A:Genome: plasmid

C:Superfamily: bc-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain C;Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; re

Query Match 90.2%; Score 37; DB 2; Length 386;  
Best Local Similarity 83.3%; Pred. No. 98;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMEW 6  
DB 141 LDMEW 146

Search completed: February 18, 2004, 14:38:52  
Job time : 6.5921 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds  
(without alignments)  
75.239 Million cell updates/sec

Title: US-09-643-260-17  
Sequence: 1 LDWEML 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues  
Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: Published Applications AA:  
2: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubppa/PTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep.\*  
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11: /cgn2\_6/ptodata/1/pubppa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubppa/US09C\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubppa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubppa/US10C\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	6	10	US-09-847-940B-17
2	41	100.0	6	11	US-09-847-946A-17
3	41	100.0	6	11	US-09-847-946A-45
4	41	100.0	6	11	US-09-847-946A-117
5	41	100.0	6	11	US-09-847-946A-117
6	41	100.0	6	11	US-09-847-946A-117
7	41	100.0	6	11	US-09-847-946A-117
8	41	100.0	6	11	US-09-847-946A-117
9	41	100.0	6	11	US-09-847-946A-117
10	41	100.0	6	11	US-09-847-946A-117
11	41	100.0	6	11	US-09-847-946A-117
12	41	100.0	6	11	US-09-847-946A-117
13	41	100.0	6	11	US-09-847-946A-117
14	41	100.0	6	11	US-09-847-946A-117
15	39	95.1	471	12	US-10-369-493-12414

15	37	90.2	20	12	US-09-962-756-939	Sequence 939, App
17	37	90.2	20	12	US-10-253-471-939	Sequence 939, App
18	37	90.2	70	9	US-09-864-761-46514	Sequence 46514, A
19	37	90.2	219	12	US-10-369-493-19572	Sequence 19572, A
20	37	90.2	259	12	US-10-369-493-22800	Sequence 22800, A
21	37	90.2	280	12	US-10-369-493-3354	Sequence 3354, App
22	37	90.2	354	15	US-10-166-087-6	Sequence 6, App1
23	37	90.2	462	12	US-10-369-493-8244	Sequence 8244, App
24	36	87.8	6	10	US-09-847-940B-2	Sequence 2, App1
25	36	87.8	6	11	US-09-847-946A-2	Sequence 2, App1
26	36	87.8	7	11	US-09-847-946A-33	Sequence 33, App1
27	36	87.8	6	11	US-09-847-946A-37	Sequence 37, App1
28	36	87.8	8	11	US-09-847-946A-37	Sequence 37, App1
29	36	87.8	8	11	US-09-847-946A-38	Sequence 38, App1
30	36	87.8	9	11	US-09-847-946A-39	Sequence 39, App1
31	36	87.8	9	11	US-09-847-946A-32	Sequence 32, App1
32	36	87.8	9	11	US-09-847-946A-35	Sequence 35, App1
33	36	87.8	9	11	US-09-847-946A-36	Sequence 36, App1
34	36	87.8	10	11	US-09-847-946A-31	Sequence 31, App1
35	36	87.8	10	11	US-09-847-946A-34	Sequence 34, App1
36	36	87.8	11	11	US-09-847-946A-28	Sequence 28, App1
37	36	87.8	11	11	US-09-847-946A-132	Sequence 132, App1
38	36	87.8	11	11	US-09-847-946A-140	Sequence 140, App1
39	36	87.8	13	11	US-09-847-946A-143	Sequence 143, App1
40	36	87.8	13	11	US-09-847-946A-144	Sequence 144, App1
41	36	87.8	13	11	US-09-847-946A-145	Sequence 145, App1
42	36	87.8	13	11	US-09-847-946A-148	Sequence 148, App1
43	36	87.8	17	11	US-09-847-946A-141	Sequence 141, App1
44	36	87.8	17	11	US-09-847-946A-142	Sequence 142, App1
45	36	87.8	17	11	US-09-847-946A-146	Sequence 146, App1

#### ALIGNMENTS

RESULT 1  
US-09-847-940B-17  
Sequence 17, Application US/09847940B  
Patent No. US2002015600A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J.  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-117CP  
CURRENT APPLICATION NUMBER: US/09/847,940B  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 17  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-17

Query Match 100.0% ; Score 41 ; DB 10 ; Length 6 ;  
Best Local Similarity 100.0% ; Pred. No. 7e+05 ;  
Matches 6 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

Db 1 LDWEML 6  
US-09-847-946A-17  
Sequence 17, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J

```

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-17

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```

Query Match          100.0%; Score 41; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LDWEML 6
Db 1 LDWEML 6

```

```

RESULT 3
US-09-847-946A-45
; Sequence 45, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-45

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```

Query Match          100.0%; Score 41; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 LDWEML 6
Db 1 LDWEML 6

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RESULT 4
US-09-847-946A-117
; Sequence 117, Application US/09847946A
; Publication No. US20030054999A1

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; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 117
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-117

```

```

Query Match          100.0%; Score 41; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LDWEML 6
Db 1 LDWEML 6

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```

RESULT 5
US-09-847-946A-121
; Sequence 121, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-121

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```

Query Match          100.0%; Score 41; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LDWEML 6
Db 1 LDWEML 6

```

```

RESULT 6

```

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US-09-847-946A-114
; Sequence 114, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Pindels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-114

Query Match          100.0%; Score 41; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEML 6
Db 3 LDWEML 8

RESULT 7
US-09-847-946A-122
; Sequence 122, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Pindels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 122
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-122

Query Match          100.0%; Score 41; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEML 6
Db 1 LDWEML 6
```

```
RESULT 8
US-09-847-946A-113
; Sequence 113, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Pindels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-113

Query Match          100.0%; Score 41; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEML 6
Db 1 LDWEML 6

RESULT 9
US-09-847-946A-116
; Sequence 116, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Pindels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847, 946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-116

Query Match          100.0%; Score 41; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LDWEML 6  
| | | | |  
Db 1 LDWEML 6

## RESULT 10

US-09-847-946A-119  
; Sequence 119, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 119  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-119

Query Match 100.0%; Score 41; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEML 6  
| | | | |  
Db 3 LDWEML 8

## RESULT 11

US-09-847-946A-120  
; Sequence 120, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 120  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-120

Query Match 100.0%; Score 41; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEML 6  
| | | | |  
Db 2 LDWEML 7

## RESULT 12

US-09-847-946A-115  
; Sequence 115, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 115  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-115

Query Match 100.0%; Score 41; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEML 6  
| | | | |  
Db 2 LDWEML 7

## RESULT 13

US-09-847-946A-118  
; Sequence 118, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 118  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-118

US-09-847-946A-118

Query Match 100.0%; Score 41; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6  
 DB 3 LDWEWL 8

RESULT 14

US-09-847-946A-112  
 ; Sequence 112, Application US/09847946A  
 ; Publication No. US200305499A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: May, Michael J  
 ; APPLICANT: Ghosh, Sankar  
 ; APPLICANT: Finkelstein, Mark A  
 ; APPLICANT: Phillips, Kathryn  
 ; APPLICANT: Hamlin, Gerard  
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
 ; FILE REFERENCE: PPI-119  
 ; CURRENT APPLICATION NUMBER: US/09/847, 946A  
 ; PRIOR FILING DATE: 2001-05-02  
 ; PRIOR APPLICATION NUMBER: 60/201,261  
 ; PRIOR FILING DATE: 2000-05-02  
 ; PRIOR APPLICATION NUMBER: 09/643,260  
 ; PRIOR FILING DATE: 2000-08-22  
 ; NUMBER OF SEQ ID NOS: 160  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 112  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
 ; US-09-847-946A-112

Query Match 100.0%; Score 41; DB 11; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6  
 DB 3 LDWEWL 8

RESULT 15  
 US-10-369-493-12414  
 ; Sequence 12414, Application US/10369493  
 ; Publication No. US20030233675A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Chen, Xianfeng  
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
 ; FILE REFERENCE: 38-10(52052)B  
 ; CURRENT APPLICATION NUMBER: US/10/369,493  
 ; PRIOR FILING DATE: 2003-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/360,039  
 ; PRIOR FILING DATE: 2002-02-21  
 ; NUMBER OF SEQ ID NOS: 47374  
 ; SEQ ID NO 12414  
 ; LENGTH: 471  
 ; TYPE: PRT  
 ; ORGANISM: Aspergillus nidulans  
 ; FEATURE:  
 ; NAME/KEY: unsure

; LOCATION: (1)..(471)  
 ; OTHER INFORMATION: unsure at all Xaa locations  
 ; US-10-369-493-12414

Query Match 95.1%; Score 39; DB 12; Length 471;  
 Best Local Similarity 83.3%; Pred. No. 47+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6  
 DB 119 LDWEWL 124

Search completed: February 18, 2004, 15:42:01  
 Job time: 16.7529 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds  
(without alignments)  
35.929 Million cell updates/sec

Title: US-09-643-260-17

Perfect score: 41

Sequence: 1 LDWEWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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1: Issued\_Patents\_AA:\*  
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6: /cgn2\_6/ptodata/1/1aa/BACKFILES1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	36	87.8	745	2	US-09-023-321-3
5	36	87.8	745	2	US-08-890-853-4
6	36	87.8	745	2	US-09-032-475-3
7	36	87.8	745	2	US-09-099-125A-4
8	36	87.8	745	2	US-09-032-476-4
9	36	87.8	745	3	US-08-890-854-4
10	36	87.8	745	3	US-09-023-324-4
11	36	87.8	745	3	US-09-168-629-2
12	36	87.8	745	3	US-08-910-820-10
13	36	87.8	745	3	US-08-810-131A-2
14	36	87.8	745	4	US-09-109-986-4
15	36	87.8	745	4	US-09-844-908-10
16	36	87.8	745	2	US-08-887-518-4
17	36	87.8	756	2	US-09-023-321-4
18	36	87.8	756	2	US-08-890-853-2
19	36	87.8	756	2	US-09-032-475-4
20	36	87.8	756	2	US-09-099-125A-2
21	36	87.8	756	2	US-09-032-475-4
22	36	87.8	756	2	US-09-099-125A-2
23	36	87.8	756	2	US-09-032-476-2
24	36	87.8	756	3	US-08-890-854-2
25	36	87.8	756	3	US-09-023-324-2
26	36	87.8	756	3	US-09-168-629-15
27	36	87.8	756	3	US-09-168-629-15

28	36	87.8	756	3	US-08-910-820-9	Sequence 9, Appl1
29	36	87.8	756	4	US-09-109-986-2	Sequence 2, Appl1
30	36	87.8	756	4	US-09-844-908-9	Sequence 9, Appl1
31	36	87.8	756	4	US-09-868-758-4	Sequence 4, Appl1
32	36	87.8	997	4	US-09-417-123-123	Sequence 123, App
33	36	87.8	997	4	US-09-417-123-121	Sequence 121, App
34	34	82.9	38	2	US-08-488-161-55	Sequence 55, Appl1
35	34	82.9	38	5	US-09-273-685-55	Sequence 55, Appl1
36	34	82.9	138	5	PCT-US95-11934-55	Sequence 55, Appl1
37	34	82.9	138	4	US-08-686-878A-33	Sequence 33, Appl1
38	34	82.9	138	4	US-09-175-928-33	Sequence 33, Appl1
39	34	82.9	470	4	US-09-107-352A-4517	Sequence 4517, Ap
40	33	80.5	25	3	US-09-082-279B-1275	Sequence 1275, Ap
41	33	80.5	25	4	US-09-315-304B-1275	Sequence 1275, Ap
42	33	80.5	25	4	US-09-834-784-1275	Sequence 1275, Ap
43	33	80.5	162	4	US-09-199-637A-161	Sequence 161, App
44	33	80.5	162	4	US-09-199-637A-162	Sequence 162, App
45	33	80.5	177	4	US-09-252-991A-20614	Sequence 20614, A

#### ALIGNMENTS

RESULT 1  
US-09-252-991A-22395  
Sequence 22395, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 22395  
LENGTH: 334  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-22395

Query Match 90.2% Score 37; DB 4; Length 334;  
Best Local Similarity 83.3% Pred. No. 1.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWEWL 6  
DB 136 LDWKWL 141

RESULT 2  
US-09-172-952-14  
Sequence 14, Application US/09172952  
Patent No. 6368793  
GENERAL INFORMATION:  
APPLICANT: Hoch, James  
TITLE OF INVENTION: METABOLIC SELECTION METHODS  
FILE REFERENCE: 234/191  
CURRENT APPLICATION NUMBER: US/09/172,952  
CURRENT FILING DATE: 1998-10-14  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 14  
LENGTH: 439  
TYPE: PRT  
ORGANISM: Y1ax2  
US-09-172-952-14



Query Match 87.8%; Score 36; DB 4; Length 439;  
Best Local Similarity 83.3%; Pred. No. 3.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMWML 6  
DB 171 LDMWML 176

## RESULT 3

US-08-887-518-3  
Sequence 3, Application US/08887518  
Patent No. 5843721  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-887-518-3

Query Match 87.8%; Score 36; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMWML 6  
DB 738 LDMWML 743

US-09-023-321-3  
Sequence 3, Application US/09023321  
Patent No. 5844073  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA

QY 1 LDMWML 6  
DB 738 LDMWML 743

COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,321  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-321-3

Query Match 87.8%; Score 36; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMWML 6  
DB 738 LDMWML 743

RESULT 5  
US-08-890-853-4  
Sequence 4, Application US/08890853  
Patent No. 5851812  
GENERAL INFORMATION:  
APPLICANT: Goedel, David V.  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-853-4

Query Match 87.8%; Score 36; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMEWL 6  
DB 738 LDMSWL 743

RESULT 6  
US-09-032-475-3  
Sequence 3, Application US/09032475  
Patent No. 5854003

GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
ATTORNEY/AGENT INFORMATION:  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032.475  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/887,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-032-475-3

Query Match 87.8%; Score 36; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMEWL 6  
DB 738 LDMSWL 743

RESULT 7  
US-09-099-125A-4  
Sequence 4, Application US/09099125A  
Patent No. 5916760

GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
ATTORNEY/AGENT INFORMATION:  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099.125A  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-099-125A-4

Query Match 87.8%; Score 36; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMEWL 6  
DB 738 LDMSWL 743

RESULT 8  
US-09-099-124A-4  
Sequence 4, Application US/09099124A  
Patent No. 5939302

GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
ATTORNEY/AGENT INFORMATION:  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099.124A  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-099-124A-4

Query Match 87.8%; Score 36; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWMTL 6  
DB 738 LDWMTL 743

RESULT 9  
US-09-032-476-4  
Sequence 4, Application US/09032476  
Patent No. 6235492  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
APPLICANT: Cao, Zhaoan  
APPLICANT: R gnier, Catherine  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,476  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/890,854  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-032-476-4

Query Match 87.8%; Score 36; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWMTL 6  
DB 738 LDWMTL 743

RESULT 10  
US-08-890-854-4  
Sequence 4, Application US/08890854  
Patent No. 6235512  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
APPLICANT: Cao, Zhaoan  
APPLICANT: R gnier, Catherine  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,854  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-854-4

Query Match 87.8%; Score 36; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWMTL 6  
DB 738 LDWMTL 743

RESULT 11  
US-09-023-324-4  
Sequence 4, Application US/09023324  
Patent No. 6235513  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
APPLICANT: Cao, Zhaoan  
APPLICANT: R gnier, Catherine  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,324  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/890,854  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-324-4

Query Match      87.8%; Score 36; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 LDWMTL 6  
         ||| ||  
DB      738 LDWMTL 743

RESULT 12  
US-09-168-629-2  
; Sequence 2, Application US/09168629  
; Patent No. 6242253  
; GENERAL INFORMATION:  
; APPLICANT: Karin, Michael  
; APPLICANT: Didonato, Joseph A.  
; APPLICANT: Rothwarf, David M.  
; APPLICANT: Hayakawa, Makio  
; APPLICANT: Zandi, Ebrahim  
; TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same  
; FILE REFERENCE: P-UD 1395  
; CURRENT APPLICATION NUMBER: US/09/168,629  
; CURRENT FILING DATE: 1998-10-08  
; EARLIER APPLICATION NUMBER: 60/061,470  
; EARLIER FILING DATE: 1997-10-09  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 745  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-168-629-2

Query Match      87.8%; Score 36; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 LDWMTL 6  
         ||| ||  
DB      738 LDWMTL 743

RESULT 13  
US-08-910-820-10  
; Sequence 10, Application US/08910820  
; Patent No. 6258579  
; GENERAL INFORMATION:  
; APPLICANT: Mercurio, Frank  
; APPLICANT: Zhu, Hengyi  
; APPLICANT: Barbosa, Miguel  
; APPLICANT: Li, Gfan  
; APPLICANT: Murray, Brian W.  
; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE  
; TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,820  
FILING DATE: 12-AUG-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 860098.413C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-910-820-10

Query Match      87.8%; Score 36; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 LDWMTL 6  
         ||| ||  
DB      738 LDWMTL 743

RESULT 14  
US-08-810-131A-2  
; Sequence 2, Application US/08810131A  
; Patent No. 6268194  
; GENERAL INFORMATION:  
; APPLICANT: Karin, Michael  
; APPLICANT: Didonato, Joseph A.  
; APPLICANT: Rothwarf, David M.  
; APPLICANT: Hayakawa, Makio  
; APPLICANT: Zandi, Ebrahim  
; TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using  
; TITLE OF INVENTION: Same  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California

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; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,131A
; FILING DATE: 25-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-810-131A-2

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Query Match      87.8%; Score 36; DB 3; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 LDWEWL 6
DB      738 LDMSWL 743

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RESULT 15
US-09-109-986-4
; Sequence 4, Application US/09109986
; Patent No. 6479266
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; APPLICANT: Cao, Zhaden
; APPLICANT: R. gnter, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,986
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: 197-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-109-986-4

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Query Match      87.8%; Score 36; DB 4; Length 745;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 LDWEWL 6
DB      738 LDMSWL 743

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Search completed: February 18, 2004, 14:41:51
JOD time : 7.06579 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds  
(without alignment)  
79.423 Million cell updates/sec

Title: US-09-643-260-16

Perfect score: 40

Sequence: 1 LDRAWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	745	1	IKKA_HUMAN
2	37	92.5	745	1	IKKA_MOUSE
3	37	92.5	756	1	IKKB_HUMAN
4	37	92.5	757	1	IKKB_MOUSE
5	37	92.5	757	1	IKKB_RAT
6	36	90.0	524	1	CP72_CATRO
7	36	90.0	656	1	VEHE_SALTI
8	36	90.0	840	1	VPHI_YEAST
9	35	87.5	290	1	CYOA_BUCAR
10	35	87.5	296	1	CYOA_BUCAT
11	35	87.5	307	1	QOX2_ACEAC
12	35	87.5	314	1	CYOA_PBBPU
13	34	85.0	99	1	NOS3_SHEEP
14	34	85.0	262	1	LY4A_MOUSE
15	34	85.0	263	1	KLRA_MOUSE
16	34	85.0	914	1	GUX2_CLOSR
17	34	85.0	1167	1	ITAE_MOUSE
18	34	85.0	1201	1	NOS3_MOUSE
19	34	85.0	1202	1	NOS3_HUMAN
20	34	85.0	1204	1	NOS3_BOVIN
21	34	85.0	1204	1	NOS3_PIG
22	33	82.5	220	1	Y132_METUA
23	33	82.5	300	1	Y223_HAEIN
24	33	82.5	362	1	DCUP_YEAST
25	33	82.5	411	1	CYB_CHRVI
26	33	82.5	480	1	MTHE_DROME
27	33	82.5	501	1	YB06_YEAST
28	33	82.5	578	1	YC20_METUA
29	33	82.5	593	1	EPB3_CHICK
30	33	82.5	593	1	EPB3_HUMAN
31	33	82.5	983	1	EPB3_MOUSE
32	33	82.5	984	1	EPB3_RAT
33	33	82.5	1002	1	EPB5_CHICK

34	33	82.5	1039	1	GUNB_CALSA	P10474 c endoglucanase
35	32	80.0	83	1	VG41_BPML5	Q05252 mycobacteriophage
36	32	80.0	94	1	VG41_BPMD2	Q05253 mycobacteriophage
37	32	80.0	269	1	BAS1_HUMAN	P35613 h basigin p
38	32	80.0	315	1	T2S1_STRAL	O53608 streptomyces
39	32	80.0	336	1	NOSO_BACSU	O34453 bacillus su
40	32	80.0	339	1	RRA1_ECOLI	P27128 escherichia
41	32	80.0	343	1	ZDH4_MOUSE	Q96655 mus musculus
42	32	80.0	344	1	ZDH4_HUMAN	Q96656 homo sapien
43	32	80.0	366	1	GCST_SYNEI	O84656 synecococcus
44	32	80.0	380	1	APV_MACMU	O97666 macaca mula
45	32	80.0	387	1	MANA_RHIME	P29954 rhizobium m

## ALIGNMENTS

RESULT 1  
IKKA\_HUMAN STANDARD; PRT; 745 AA.  
AC 015111; 014666; Q13132; Q92467;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 15-SEP-2003 (Rel. 42, Last sequence update)  
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)  
DE (I-kappa-B kinase alpha) (IKK- $\alpha$ ) (IKK-A) (Ikkapab kinase)  
DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIXA).  
GN CHUK OR IKKA.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.  
RC TISSUE=T-cell;  
RX MEDLINE=97386461; PubMed=9244310;  
RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Roche M.;  
RT "Identification and characterization of an Ikappab kinase."; Cell 90:373-383(1997).  
RN [2]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=97394468; PubMed=9252186;  
RA D'Onofrio J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;  
RT "A cytokine-responsive Ikappab kinase that activates the transcription factor NF-kappaB."; Nature 388:548-554(1997).  
RN [3]  
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND SER-176.  
RX MEDLINE=97394468; PubMed=9252186;  
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L., Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;  
RT "IKK-1 and IKK-2: cytokine-activated Ikappab kinases essential for NF-kappaB activation."; Science 278:860-866(1997).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99032998; PubMed=9813230;  
RA Hu M.C.-T., Wang Y.-P.;  
RT "Ikappab kinase-alpha and -beta genes are coexpressed in adult and embryonic tissues but localized to different human chromosomes."; Gene 222:31-40(1998).  
RN [5]  
RP SEQUENCE OF 32-745 FROM N.A.  
RX TISSUE=Cervical carcinoma;  
RX MEDLINE=96258427; PubMed=8777433;  
RA Connelly M.A., Marcu K.B.;  
RT "CHUK, a new member of the helix-loop-helix and leucine zipper families of interacting proteins, contains a serine-threonine kinase catalytic domain.";

RL Cell. Mol. Biol. Res. 41:537-549(1995).  
 RN [6]  
 RP PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179  
 RP AND SER-180.  
 RX MEDLINE=98188283; PubMed=9520446;  
 RA Ling L., Cao Z., Goeddel D.V.;  
 RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of  
 Ser-176.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).  
 RN [7]  
 RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.  
 RX MEDLINE=99433720; PubMed=10485710;  
 RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,  
 RA Donner D.B.;  
 RT "NF-kappaB activation by tumor necrosis factor requires the Akt  
 serine-threonine kinase.";  
 RL Nature 401:82-85(1999).  
 RN [8]  
 RP IKKA-IKKB BINDING.  
 RX MEDLINE=99212141; PubMed=10195894;  
 RA Delhase M., Hayakawa M., Chen Y., Karin M.;  
 RT "Positive and negative regulation of IkappaB kinase activity through  
 IkappaB subunit phosphorylation.";  
 RL Science 284:309-313(1999).  
 RN [9]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., Didonato J.A., Lin A.;  
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein  
 kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [10]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 RN [11]  
 RP SUBUNIT OF A COMPLEX CONTAINING CREBBP, NCOA2, NCOA3, IKKB AND IKBK.  
 RX MEDLINE=21968797; PubMed=11971985;  
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,  
 RA O'Malley B.W.;  
 RT "Regulation of SRC-3 (pC1E/ACTR/AIB-1/RAC-3/TRAM-1) coactivator  
 activity by I kappa B kinase.";  
 RL Mol. Cell. Biol. 22:3549-3561(2002).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 the dissociation of the inhibitor/NF-kappa-B complex and  
 ultimately the degradation of the inhibitor. Also phosphorylates  
 NCOA3.  
 CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated  
 when dephosphorylated.  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but  
 also as an homodimer. Directly interacts with IKK-GAMMA/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 also bind to MAP3K14/NIK, MEKK1, IKAP and IKK-alpha-P65-P50  
 complex. A weak interaction with TRAF2 cannot be excluded. Part of  
 a complex composed of NCOA2, NCOA3, IKKB, IKBK and CREBBP.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Widely expressed.  
 CC -1- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by  
 MEKK1, and dephosphorylated by PP2A. Autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPAB KINASE SUBFAMILY.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL; AF012890; AAC51662.1; -  
 DR EMBL; AF009225; AAC51671.1; -  
 DR EMBL; AF080157; AAD08996.1; -  
 DR EMBL; U22512; AAC50713.1; -  
 DR HSRP; Q63450; 1A06.  
 DR Genew; HGNC:1974; CHUK.  
 DR MIM; 600664; -  
 DR GO; GO:0005737; Cytoplasm; TAS.  
 DR GO; GO:0008384; FikappaB kinase activity; TAS.  
 DR GO; GO:0007345; Plemryogenesis and morphogenesis; TAS.  
 DR GO; GO:0007252; P-I-kappaB phosphorylation; TAS.  
 DR GO; GO:0006955; P-immune response; TAS.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR Prodom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 DR KX Transferrase; Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation.  
 KM DOMAIN 15 302  
 FT 15  
 FT DOMAIN 455 476  
 FT 476  
 FT DOMAIN 738 743  
 FT 743  
 FT NP BIND 21 29  
 FT 29  
 FT BINDING 44 44  
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 FT 680  
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 FT 687  
 SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;  
 Query Match 92.5%; Score 37; DB 1; Length 745;  
 Best Local Similarity 83.3%; Pred. No. 76;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LDMAML 6  
 Db 738 LDMAML 743  
 RESULT 2  
 IKKA MOUSE STANDARD; PRT; 745 AA.  
 AC Q60680; Q9D2X3;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)  
 DE (I kappa-B kinase alpha) (IKK-alpha) (IKK-A) (IkappaB kinase)  
 DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous  
 kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKIKK).  
 GN CHUK OR IKKA.  
 OS MUS MUSCULUS (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.  
 NX NCBI\_TaxID=10090;





FT VARSPLIC 452 471 MSLIRYANITKKNITLIS -> IFRKNVKNERNKRGKH  
 FT SLP (in isoform 2).  
 FT VARSPLIC 472 745 Missing (in isoform 2).  
 FT VARSPLIC 577 584 DHLYSDST -> GTTLQSQY (in isoform 3).  
 FT VARSPLIC 585 745 /FtId=VSP\_004868.  
 FT VARSPLIC 585 745 /FtId=VSP\_004869.  
 FT CONFLICT 236 236 K -> E (in REF. 3).  
 FT CONFLICT 400 400 S -> Y (in REF. 3).  
 FT SEQUENCE 745 AA; 84728 MW; 3PEF5582AF92233 CRC64;  
 Query Match 92.5%; Score 37; DB 1; Length 745;  
 Best Local Similarity 83.3%; Pred. No. 76;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LDRAWL 6  
 Db 738 LDWMSWL 743  
 RESULT 3  
 IKKB HUMAN STANDARD; PRT; 756 AA.  
 ID IKKB HUMAN STANDARD; PRT; 756 AA.  
 AC 014920; 075327;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)  
 DE 1-kappa-B kinase beta (IKKB) (IKK-beta) (IKK-B) (1-kappa-B kinase  
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).  
 GN IKKB OR IKKB.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.  
 RC TISSUE=Cervical carcinoma;  
 RX MEDLINE=98008813; PubMed=9346484;  
 RA Mercutio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,  
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;  
 RT "IKK-1 and IKK-2: cytosolic-activated Ikkappa kinases essential for  
 RT NF-kappaB activation.";  
 RL Science 278:860-866(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.  
 RX MEDLINE=98008814; PubMed=9346485;  
 RA Wotoniak J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;  
 RT "IkappaB kinase-beta: NF-kappaB activation and complex formation with  
 RT IkappaB kinase-alpha and NIK.";  
 RL Science 278:866-869(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RX MEDLINE=99032998; PubMed=9913330;  
 RA Hu M.C.-T., Wang Y.-P.;  
 RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and  
 RT embryonic tissues but localized to different human chromosomes.";  
 RL Gene 222:31-40(1998).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND GENE MAPPING.  
 RX MEDLINE=98438415; PubMed=9763654;  
 RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;  
 RT "Assignment of IkappaB kinase beta (IKKB) to human chromosome band  
 RT 8p12-7p11 by in situ hybridization.";  
 RL Cytogenet. Cell Genet. 82:32-33(1998).  
 RN [5]  
 RP SEQUENCE OF 1-256 FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Straubeberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
 RA Altschul S.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schreier T.E.,  
 RA Brownstein M.J., Ueda T.B., Tohilyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., DiDonato J.A., Lin A.;  
 RT "Coordinate regulation of I-kappaB kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [7]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 RT inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 RN [8]  
 RP IDENTIFICATION IN A COMPLEX WITH CREBBP; NCOA2; NCOA3; IKKA AND IKKB.  
 RX MEDLINE=21968797; PubMed=11971985;  
 RA Wu R.C., Qin U., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,  
 RA O'Malley B.W.;  
 RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator  
 RT activity by I kappa B kinase.";  
 RL Mol. Cell. Biol. 22:3549-3561(2002).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 CC the dissociation of the inhibitor/NF-kappa-B complex and  
 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3 (By similarity).  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKB-alpha-P65-P50  
 CC complex. Phosphorylated IKB-alpha is further released from the  
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB  
 CC and CREBBP.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal  
 CC muscle, kidney, pancreas, spleen, thymus, prostate, testis and  
 CC peripheral blood.  
 CC -1- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.  
 CC Weakly autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPAB KINASE SUBFAMILY.  
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 CC -----  
 CC EMBL; AF029684; AAC51860.1; -  
 CC EMBL; AF080158; AAD08997.1; -  
 CC EMBL; AF031416; AAC64675.1; -  
 CC EMBL; BC006231; AA06231.1; -

DR HSP; 063450; 1A06.  
 DR Genew; HGNC:5960; IKKB.  
 DR MIM; 603258; --  
 DR GO; GO:0005737; C:cytoplasm; NAS.  
 DR GO; GO:0005524; F:ATP binding activity; NAS.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.  
 DR GO; GO:0016563; F:transcriptional activator activity; NAS.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00069; pkinase.1.  
 DR Pfam; PF00240; ubiquitin.1.  
 DR Prodom; PD000001; Prot\_kinase.1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KM Transferrase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation.  
 FT DOMAIN 15 300 PROTEIN KINASE.  
 FT 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 FT DOMAIN 737 742 NEMO-BINDING.  
 FT NP BIND 21 29 ATP (BY SIMILARITY).  
 FT BINDING 44 44 ATP (BY SIMILARITY).  
 FT ACT SITE 145 145 BY SIMILARITY.  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 177 177 PHOSPHORYLATION.  
 FT MOD\_RES 181 181 PHOSPHORYLATION.  
 FT MOD\_RES 181 181 K-2A: LOSS OF KINASE ACTIVITY AND NO EFFECT ON BINDING TO NIK.  
 FT MOD\_RES 44 44 S-2A: DECREASE OF ACTIVITY.  
 FT MUTAGEN 177 177 S-2E: FULL ACTIVATION.  
 FT MUTAGEN 177 177 S-2A: DECREASE OF ACTIVITY.  
 FT MUTAGEN 181 181 S-2E: FULL ACTIVATION.  
 FT MUTAGEN 181 181 S-2A: DECREASE OF ACTIVITY.  
 FT CONFLICT 231 255 WHSKVRKSEVDIVSDELNGTYVF -> CVRMMPGVVHNS  
 FT CONFLICT 231 255 CNSTLGGGRGMI (IN REF. 5).  
 FT CONFLICT 425 425 Q -> H (IN REF. 1).  
 SQ SEQUENCE 756 AA; 86563 MW; P9CADF671A3B3E14E CRC64;

Query Match 92.5%; Score 37; DB 1; Length 756;  
 Best Local Similarity 83.3%; Pred. No. 77;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWAWL 6  
 Db 737 LDWAWL 742

RESULT 4  
 IKKB\_MOUSE  
 ID IKKB\_MOUSE STANDARD; PRT; 757 AA.  
 AC 088351; Q9RIJ6;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)  
 DE (1-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase  
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).  
 GN IKKB OR IKKB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sclerogastrea; Muridae; Murinae; Mus.  
 OC NBI\_TaxID=10090;  
 RX MEDLINE=98188238; PubMed=9520401;  
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEK1.  
 RC STRAIN=C57BL/6; TISSUE=Spleen;  
 RA Okumura K., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,  
 RA "Differential regulation of IkappaB kinase alpha and beta by two  
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated  
 RT protein kinase/ERK kinase kinase-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).  
 RN [2]

RP SEQUENCE FROM N.A.,  
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.,  
 RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that  
 RT constitutively phosphorylates serine residues of Ikb.";  
 RL Submitted (Aug-1998) to the EMBL/Genbank/DDB databases.  
 RN [3]  
 RP DEVELOPMENTAL STAGE.  
 RX MEDLINE=99455228; PubMed=10523828;  
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.,  
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling  
 RT pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a  
 RT developmentally regulated protein kinase.";  
 RL Oncogene 18:5514-5524(1999).  
 RN [4]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., Diodato J.A., Lin A.,  
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [5]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.,  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 RT inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B complex and  
 CC the dissociation of the inhibitor/NF-kappa-B complex and  
 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3.  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MEK1, MAPK14/NIK, IKAP and IKB-ALPHA-P65-P50  
 CC complex. Phosphorylated IKB-alpha is further released from the  
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB  
 CC and CREBBP (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.  
 CC -1- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout  
 CC the mouse embryo, at E9.5 day its expression begins to be  
 CC localized to the brain, neural ganglia, neural tube, and in liver  
 CC at E12.5 day. At E15.5 day, the expression is further restricted  
 CC to specific tissues of the embryo.  
 CC -1- PTM: Phosphorylated by MEK1 and probably also by MAPK14/NIK.  
 CC -1- Weakly autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPPAB KINASE SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AF026524; AAC23557.1; --  
 DR EMBL; AF088910; AAD52095.1; --  
 DR HSP; 063450; 1A06.  
 DR MGD; MGI:1338071; IKKb.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; pkinase.1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR Prodom; PD000001; Prot\_kinase.1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KM Transferrase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation.

FT DOMAIN 15 300 PROTEIN KINASE.  
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 FT DOMAIN 737 742 NEMO-BINDING.  
 FT NP\_BIND 21 29 ATP (BY SIMILARITY).  
 FT BINDING 44 44 ATP (BY SIMILARITY).  
 FT ACT\_SITE 145 145 BY SIMILARITY.  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).  
 FT CONFLICT 56 56 N -> D (IN REF. 2).  
 FT CONFLICT 343 343 N -> D (IN REF. 2).  
 FT CONFLICT 356 356 K -> E (IN REF. 2).  
 FT CONFLICT 390 390 L -> F (IN REF. 2).  
 FT CONFLICT 406 406 P -> Q (IN REF. 2).  
 FT CONFLICT 573 573 K -> R (IN REF. 2).  
 FT CONFLICT 736 757 TLDMSWTQMEDERCSLEQACD -> VTA (IN REF. 2).  
 SQ SEQUENCE 757 AA; 86690 MW; PED962F095449C5E CRC64;  
 Query Match Best local Similarity 92.5%; Score 37; DB 1; Length 757;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LDMAWL 6  
 Db 737 LDMSWL 742  
 RESULT 5  
 ID IKKB\_RAT STANDARD; PRT; 757 AA.  
 AC 09QY78;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)  
 DE (1-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase  
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).  
 GN IKKB OR IKKB.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RA Zhang Y., Sun S., Ravid K.;  
 RT "IKK beta in megakaryocyte differentiation";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN 12;  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., Didonato J.A., Lin A.;  
 RT "Coordinate regulation of Ikkappa kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN 13;  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 RT inflammation and protection";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 CC the dissociation of the inhibitor/NF-kappa-B complex and  
 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3.  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MEK1, MAP3K14/NIK, IKAP and IKK-alpha-P65-P50  
 CC complex. Phosphorylated IKK-alpha is further released from the  
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB  
 CC and CREBBP (by similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.  
 CC Weakly autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPAB KINASE SUBFAMILY.  
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 CC -----  
 CC EMBL; AF15282; AAF21978.1; -.  
 DR HSSP; Q63450; 1A06.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PRODOM; PD000001; Prot kinase; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KM Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KM Phosphorylation.  
 FT DOMAIN 15 300 PROTEIN KINASE.  
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 FT DOMAIN 737 742 NEMO-BINDING.  
 FT NP\_BIND 21 29 ATP (BY SIMILARITY).  
 FT BINDING 44 44 ATP (BY SIMILARITY).  
 FT ACT\_SITE 145 145 BY SIMILARITY.  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 757 AA; 86866 MW; 3AFB46A7DF919C CRC64;  
 Query Match Best local Similarity 92.5%; Score 37; DB 1; Length 757;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LDMAWL 6  
 Db 737 LDMSWL 742  
 RESULT 6  
 ID CP72\_CATRO STANDARD; PRT; 524 AA.  
 AC 005047;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome P450 72A1 (EC 1.3.3.9) (CYP7A1) (Secoiooganin synthase)  
 DE (SL5).  
 GN CYP72A1 OR CYP72 OR P450CR3.  
 OS Catharanthus roseus (Rose periwinkle) (Madagascar periwinkle).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; Lamiales; Gentianales; Apocynaceae; Rauvolfiaceae; Vinaceae;  
 CC Catharanthus.  
 OX NCBI\_TaxID=4058;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RA Vetter H.-P., Mangold U., Schroeder G., Warner F.-J.,  
 RA Werck-Reichardt D., Schroeder U.;  
 RT "Molecular analysis and heterologous expression of an inducible  
 RT cytochrome P-450 protein from periwinkle (Catharanthus roseus L.).";  
 RL Plant Physiol. 100:998-1007(1992).  
 RN 12;  
 SQ SEQUENCE OF 469-524 FROM N.A.

RC STRAIN=cv. G. Don;  
 RX MEDLINE=93283641; PubMed=8507838;  
 RA Medjfer A.H., Souer E., Verpoorte R., Hoge J.H.C.;  
 RT "Isolation of cytochrome P-450 cDNA clones from the higher plant  
 RL Catharanthus roseus by a PCR strategy.";   
 RN Plant Mol. Biol. 22:379-383(1993).  
 RP [3]  
 RC FUNCTION.  
 RP STRAIN=cv. CPA,  
 RX MEDLINE=20575722; PubMed=11135113;  
 RA Imler S., Schroeder G., St-Pierre B., Crouch N.P., Hotze M.,  
 RT Schmidt J., Strack D., Matern U., Schroeder J.;  
 RL "Indole alkaloid biosynthesis in Catharanthus roseus: new enzyme  
 RT activities and identification of cytochrome P450 CYP72A1 as  
 RL secologanin synthase.";   
 RL Plant J. 24:797-804(2000).  
 CC -1- FUNCTION: Converts loganin into secologanin.  
 CC -1- CATALYTIC ACTIVITY: loganin + NADPH + O(2) = secologanin + NADP(+) + 2 H(2)O.  
 CC -1- PATHWAY: Indole alkaloids biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: Vacuolar membrane (Probable).  
 CC -1- TISSUE SPECIFICITY: Upper and lower leaf epidermis.  
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.  
 CC -----  
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 CC -----  
 DR EMBL: L10081; AAA33106.1; -;  
 DR EMBL: X69775; CA849430.1; -;  
 DR PIR: S35168; S35168.  
 DR HSSP: P14779; IJPZ.  
 DR InterPro: IPR001128; Cytochrome\_P450.  
 DR Pfam: PR00067; P450.1.  
 DR PRINTS: PR00385; P450.  
 DR PROSITE: PS00086; CYTOCHROME\_P450; 1.  
 KW Oxidoreductase; Monooxygenase; Electron transport; Transmembrane;  
 KW NADP; Heme; Alkaloid metabolism.  
 FT TRANSMEM 12 32  
 FT METAL 470 470  
 FT VARIANT 190 190  
 FT VARIANT 194 194  
 FT VARIANT 223 223  
 FT VARIANT 312 312  
 FT VARIANT 318 318  
 FT VARIANT 403 403  
 FT VARIANT 405 405  
 FT VARIANT 411 411  
 SQ SEQUENCE 524 AA; 60557 MW; EF5D864B43C751E8 CRC64;  
 Query Match 90.0%; Score 36; DB 1; Length 524;  
 Best Local Similarity 100.0%; Pred. No. 77;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OS Salmonella typh.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OC NCBI\_TaxId=601;  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GIU 10007;  
 RX MEDLINE=93322324; PubMed=8331073;  
 RA Hashimoto Y., Li N., Yokoyama H., Ezaki T.;  
 RT "Complete nucleotide sequence and molecular characterization of Viab  
 RL region encoding Vi antigen in Salmonella typh.";   
 RL J. Bacteriol. 175:4456-4465(1993).  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CT18;  
 RX MEDLINE=21534947; PubMed=11677608;  
 RA Parhill J., Dougan G., James K.D., Holden M.T.G., Sebathia M.,  
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebathia M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagsels K.,  
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrett B.G.;  
 RT "Complete genome sequence of a multiple drug resistant Salmonella  
 RT enterica serovar Typh CT18.";   
 RL Nature 413:848-852(2001).  
 RL [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Ty2 / ATCC 700931;  
 RX MEDLINE=2531367; PubMed=12644504;  
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,  
 RA Burland V., Kodyanski V., Schwartz D.C., Blattner F.R.;  
 RT "Comparative genomics of Salmonella enterica serovar Typh strains Ty2  
 and CT18.";   
 RL J. Bacteriol. 185:2330-2337(2003).  
 CC -1- FUNCTION: MAY BE INVOLVED IN TRANSLOCATION OF THE VI ANTIGEN.  
 CC -----  
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 CC -----  
 DR EMBL: D14156; BAA03200.1; -;  
 DR EMBL: AL627283; CAD06771.1; -;  
 DR EMBL: AE016848; AA071797.1; -;  
 DR PIR: A56975; A56975.  
 DR InterPro: IPR001440; TPR.  
 KW Polysaccharide transport; Transport; Complete proteome.  
 KW Polyaccharide export protein VEXE.  
 SQ SEQUENCE 656 AA; 73652 MW; 26097F9D6F51CED CRC64;  
 Query Match 90.0%; Score 36; DB 1; Length 656;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAM 5  
 DB 28 LDMAM 32

QY 1 LDMAM 5  
 DB 411 LDMAM 415

RESULT 7  
 VEXE\_SALT1  
 ID VEXE\_SALT1 STANDARD; PRT; 656 AA.  
 AC P43112;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE VI polyaccharide export protein VEXE.  
 GN VEXE OR STY4651 OR T4344.

RESULT 8  
 VP11\_YEAST  
 ID VP11\_YEAST STANDARD; PRT; 840 AA.  
 AC P32563;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Vacuolar ATP synthase 95 kDa subunit (Vacuolar ATPase 95 kDa subunit).  
 GN VP11 OR YOR270C.  
 OS Saccharomyces cerevisiae (Baker's yeast).



Query Match 87.5%; Score 35; DB 1; Length 290;  
Best Local Similarity 83.3%; Pred. No. 63;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMAML 6  
DB 134 LDMRWL 139

```
RESULT 10
CYOA_BUCAI STANDARD; PRT; 296 AA.
ID CYOA_BUCAI
AC P57344;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase
subunit 2).
GN CYOA OR BU472.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 symbiotic bacterium).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=118099;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT Buchnera sp. AS-1;
RL Nature 407:81-86(2000).
CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
GROWN AT HIGH AERATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.
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CC -----
DR EMBL, AF001119; BAB13169.1; -.
DR HSSP, P18400; 1CYW.
DR InterPro: IPR001505; Copper_CuA.
DR InterPro: IPR006333; CyOA_II.
DR InterPro: IPR002429; Cyt_c_ox_2.
DR InterPro: IPR000437; Prok_IIPprot.
DR Pfam: PF00116; COX2, 1.
DR ProDom: PD000131; Copper_CuA; 1.
DR PROSITE: PS00143; CyOA; 1.
DR PROSITE: PS00013; PROKAR LIPOPROTEIN; FALSE_NEG.
DR OXidoreductase; Respiratory chain; Electron transport; Transmembrane;
KW signal; Lipoprotein; Complete proteome.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 296 UBIQUINOL OXIDASE POLYPEPTIDE II.
FT LIPID 16 16 N-ACYL DIGLYCERIDE (POTENTIAL).
FT DOMAIN 16 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 54 POTENTIAL.
FT DOMAIN 55 78 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 79 99 POTENTIAL.
FT DOMAIN 100 296 EXTRACELLULAR (POTENTIAL).
SQ SEQUENCE 296 AA; 34180 MW; 1AB2BAF0408FFBAC CRC64;
```

Query Match 87.5%; Score 35; DB 1; Length 296;

Best Local Similarity 83.3%; Pred. No. 64;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMAML 6  
DB 125 LDMRWL 130

```
RESULT 11
COX2_ACEAC STANDARD; PRT; 307 AA.
ID COX2_ACEAC
AC P50653;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome
DE A1 subunit 2) (Oxidase BA(3) subunit 2).
GN CYAB.
OS Acetobacter aceti.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Acetobacter.
OX NCBI_TaxID=435;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=1023;
RX MEDLINE=9332308; PubMed=8392509;
RA Fukaya M., Tayama K., Tamaki T., Ebisuya H., Okumura H.,
RA Kawamura Y., Horinouchi S., Beppu T.;
RT Characterization of a cytochrome at that functions as a ubiquinol
oxidase in Acetobacter aceti.
RL J. Bacteriol. 175:4307-4314(1993).
CC -1- PATHWAY: TERMINAL OXIDASE FOR ETHANOL OXIDATION.
CC -1- SUBUNIT: HETEROTETRAMER OF THE SUBUNITS 1, 2, 3 AND 4.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL, D13185; BAA02480.1; -.
DR PIR, A36885; A36885.
DR HSSP, P18400; 1CYW.
DR InterPro: IPR001505; Copper_CuA.
DR InterPro: IPR006333; CyOA_II.
DR InterPro: IPR002429; Cyt_c_ox_2.
DR Pfam: PF00116; COX2, 1.
DR PRINTS: PR01166; CYCOXIDASEII.
DR ProDom: PD000131; Copper_CuA; 1.
DR PROSITE: PS00143; CyOA; 1.
DR PROSITE: PS00013; PROKAR LIPOPROTEIN; 1.
DR OXidoreductase; Transmembrane; Respiratory chain; signal;
KW Lipoprotein.
FT SIGNAL 2 23 POTENTIAL.
FT CHAIN 24 307 UBIQUINOL OXIDASE POLYPEPTIDE II.
FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).
FT TRANSMEM 46 66 POTENTIAL.
FT TRANSMEM 87 107 POTENTIAL.
SQ SEQUENCE 307 AA; 33921 MW; E66734B84410996D CRC64;
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Query Match 87.5%; Score 35; DB 1; Length 307;  
Best Local Similarity 83.3%; Pred. No. 67;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMAML 6  
DB 135 LDMRWL 140

```

RESULT 12
CYOA_PSEPU STANDARD; PRT; 314 AA.
ID CYOA_PSEPU
AC 09MWR1;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O
subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase
subunit 2).
GN CYOA.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxId=303;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=IH-2000; PubMed=9868765;
RA Hiraizawa H., Takami H., Inoue A., Horikoshi K.;
RT "Isolation and characterization of toluene-sensitive mutants from
Pseudomonas putida IH-2000."
RT Pseudomonas putida IH-2000."
RL FEMS Microbiol Lett. 169:219-225 (1998).
CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
GROWN AT HIGH AERATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: SOME TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.
-----
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-----
DR EMBL; AB016787; BAA76356.1; -.
DR HSSP; P18400; ICYM.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR006333; CyOA_II.
DR InterPro; IPR002429; Cyt_cox_2.
DR Pfam; PF00116; COX2; 1.
DR ProDom; PD000131; Copper_CuA; 1.
DR TIGRfam; TIGR01433; CyOA; 1.
DR PROSITE; PS00013; PROXKA_LIPOPROTEIN; 1.
KW Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
KW Inner membrane; Signal; Lipoprotein.
FT SIGNAL 1 23
FT CHAIN 1 314
FT LIPID 24 24
FT DOMAIN 24 42
FT TRANSMEM 43 63
FT DOMAIN 64 86
FT TRANSMEM 87 107
FT DOMAIN 108 314
FT DOMAIN 314 34702 MM; 96EB04FC3AA77F07 CRC64;
SQ SEQUENCE 314 AA; 34702 MM; 96EB04FC3AA77F07 CRC64;

Query Match 87.5%; Score 35; DB 1; Length 314;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

AC P79209;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type
II) (NOSII) (Endothelial NOS) (eNOS) (constitutive NOS) (cNOS)
DE (Fragment).
GN NOS3 OR ENOS.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxId=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Endothelial cells;
RA Aguan K., Weiner C.P.;
RT "Effect of hypoxia on the microvasculature of developing fetal
brain of sheep: a studies on the expression pattern of
constitutive forms of nitric oxide synthase."
RT Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN
VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A cGMP-MEDIATED SIGNAL
TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH
FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND
PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS (BY
SIMILARITY).
CC -1- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
nitric oxide + N NADP(+).
CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF PAD AND FMN. ALSO REQUIRES
TETRAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
THE ENZYME (BY SIMILARITY).
CC -1- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN (BY
SIMILARITY).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.
-----
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-----
DR EMBL; U76738; AAB40705.1; -.
DR HSSP; P29473; IDOC.
DR InterPro; IPR004030; NO synthase.
DR Pfam; PF02898; NO synthase; 1.
DR PROSITE; PS60001; NOS; PARTIAL.
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Calcium-binding;
KW Heme; Multigene family.
FT NON TER 1 1
FT NON TER 99 99
SQ SEQUENCE 99 AA; 11034 MM; 82C3C765557031DA CRC64;

Query Match 85.0%; Score 34; DB 1; Length 99;
Best Local Similarity 80.0%; Pred. No. 33;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 LDMAWL 6
DB 133 LDMAWL 138

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RESULT 14
LY4A_MOUSE STANDARD; PRT; 262 AA.
ID LY4A_MOUSE
AC P20937;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE T-cell surface glycoprotein YEL/48 (T lymphocyte antigen A1) (LY49-A

```

QY	2	DWAWL	6	:
DE	antigen)			
DR	KLRA1 OR LY49A OR LY-49A OR LY49 OR LY-49.			
OS	Mus musculus (Mouse).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=89140367; PubMed=2783949;			
RT	Chan P.-Y., Takeda F.;			
RT	"Molecular cloning and characterization of a novel murine T cell			
RL	surface antigen, Y51/48."			
RL	J. Immunol. 142:1727-1736(1989).			
CC	[2]			
CC	SEQUENCE FROM N.A.			
CC	MEDLINE=89309828; PubMed=2787364;			
CC	Yokoyama W.M., Jacobs L., Kanggawa O., Shevach E.M., Cohen D.I.;			
CC	"A murine T lymphocyte antigen belongs to a supergene family of type			
CC	II integral membrane proteins."			
CC	J. Immunol. 143:1379-1386(1989).			
CC	- I FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR H-2D			
CC	ALLELES. INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING			
CC	CELL LYSIS.			
CC	- I SUBUNIT: Homodimer; disulfide-linked.			
CC	- I SUBCELLULAR LOCATION: Type II membrane protein.			
CC	- I TISSUE SPECIFICITY: HIGH, IN T LYMPHOMA LINES, VERY LOW IN			
CC	NORMAL LYMPHOCYTES.			
CC	- I SIMILARITY: Contains 1 C-type lectin family domain.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL; M25775; AAA40578.1; ALT_SEQ.			
DR	EMBL; M25812; AAA37242.1; -.			
DR	PIR; A30573; A30573.			
DR	PIR; A45813; A45813.			
DR	PDB; 1QO3; 02-JAN-00.			
DR	MGI; MGI:101907; Klrcl.			
DR	InterPro; IPR001304; Lectin_C.			
DR	Pfam; PF00059; Lectin_c1.			
DR	SMART; SM00034; CLECT; 1.			
DR	PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.			
DR	PROSITE; PS50041; C_Type_Lectin_2; 1.			
KM	T-cell; Glycoprotein; Antigen; Transmembrane; Cell adhesion;			
KM	Signal-anchor; Lectin; Receptor; Multigene family; 3D-structure.			
FT	DOMAIN	1	44	CYTOPLASMIC (PROBABLY).
FT	TRANSMEM	45	66	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT				(POTENTIAL).
FT	DOMAIN	67	262	EXTRACELLULAR (PROBABLY).
FT				C-TYPE LECTIN (LONG FORM).
FT	DISULFID	167	253	BY SIMILARITY.
FT	DISULFID	232	245	BY SIMILARITY.
FT	SITE	137	139	CELL ATTACHMENT SITE.
FT	CARBOHYD	86	86	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	103	103	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	123	123	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	76	78	NCE -> KIQ (IN REF. 2).
FT	CONFLICT	106	106	I -> M (IN REF. 2).
FT	CONFLICT	166	166	A -> T (IN REF. 2).
FT	CONFLICT	223	223	G -> R (IN REF. 2).
FT	SEQUENCE	262 AA;	30498 MM;	3CJ328D265F71B5E CRC64;
Query Match		85.0%;	Score 34;	DB 1; Length 262;
Best Local Similarity		80.0%;	Pred. No. 82;	
Matches	4; Conservative	1;	Mismatches	0; Indels 0; Gaps 0;

Db 207 DNAMEI 211

```
RESULT 15
ID KLR4_MOUSE STANDARD; PRT; 263 AA.
AC 060651; 078026; Q9EP45;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Killer cell lectin-like receptor 4 (T-cell surface glycoprotein
DE LY-49) (LY49-D antigen).
GN KLR4 OR LY49D OR LY-49D OR LY49-D.
OS Mus musculus (Mouse).
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM D2).
RC STRAIN=C57BL/6; TISSUE=Spleen;
RX MEDLINE=94300066; PubMed=8027540;
RA Smith H.R.C., Karloher F.M., Yokoyama W.M.;
RT "Ly-49 multigene family expressed by IL-2-activated NK cells.";
RN Immunol. 153:1068-1079(1994).
RN [2]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RC STRAIN=C57BL/6;
RX MEDLINE=96421544; PubMed=8824161;
RA Silver E.T., Elliott J.P., Kane K.P.;
RT "Alternatively spliced Ly-49d and H transcripts are found in IL-2-
RT activated NK cells.";
RN Immunogenetics 44:478-482(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM D1).
RC STRAIN=NOD, and NOR;
RX MEDLINE=20384764; PubMed=10925254;
RA Silver E.T., Gong D.-E., Chang C.S., Amrani A., Santamaria P.,
RA Kane K.P.;
RT "Ly-49d activates NK-mediated lysis by recognizing H-2dd.";
RN J. Immunol. 165:1771-1781(2000).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR CLASS I MHC.
CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=D1;
CC IsoId=Q60651-1; Sequence=Displayed;
CC Name=D2;
CC IsoId=Q60651-2; Sequence=VSP_003068;
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL, U10090; AAA50218.1; -
DR EMBL, U78247; AAC33667.1; -
DR EMBL, AF218079; AAF99592.1; -
DR EMBL, AF218078; AAF99591.1; -
DR PIR, I49049; I49049.
DR MGD; MGI:101904; Klr4d.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; FALSE_NEG.
DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
KW T-cell; Glycoprotein; Antigen; Transmembrane; Cell adhesion;
KW Signal-anchor; Lectin; Receptor; Multigene family;
KW Alternative splicing; Polymorphism
```



```

FT DOMAIN 1 44 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 45 65 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 66 263 (POTENTIAL).
FT DOMAIN 139 258 EXTRACELLULAR (POTENTIAL).
FT DISULFID 168 254 C-TYPE LECTIN (LONG FORM).
FT DISULFID 233 246 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 222 222 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 39 41 Missing (in isoform D2).
FT VARIANT 5 5 /Ftd=VSP_003068.
FT VARIANT 29 5 E -> K (IN STRAINS NOD AND NOR).
FT VARIANT 32 29 R -> W (IN STRAINS NOD AND NOR).
FT VARIANT 35 35 E -> Q (IN STRAINS NOD AND NOR).
FT VARIANT 45 45 R -> G (IN STRAINS NOD AND NOR).
FT VARIANT 60 45 L -> F (IN STRAINS NOD AND NOR).
FT VARIANT 79 60 T -> I (IN STRAINS NOD AND NOR).
FT VARIANT 132 79 K -> Q (IN STRAINS NOD AND NOR).
FT VARIANT 189 132 Y -> S (IN STRAINS NOD AND NOR).
FT VARIANT 189 189 L -> F (IN STRAINS NOD AND NOR).
SQ SEQUENCE 263 AA; 30872 MM; DOA940A089A9F42D CRC64;

```

```

Query Match 85.0%; Score 34; DB 1; Length 263;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 2 DWAWL 6
DB 208 DWAWI 212

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Search completed: February 18, 2004, 14:28:13  
 Job time : 3.55263 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds

(without alignments)  
87.531 Million cell updates/sec

Title: US-09-643-260-16

Perfect score: 40

Sequence: 1 LDMAML 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76: \*  
2: PIR1: \*  
3: PIR2: \*  
4: PIR3: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	92.5	745	1	conserved helix-lo
2	36	90.0	215	2	purine phosphoribo
3	36	90.0	251	2	probable phosphotr
4	36	90.0	304	2	probable cytochrom
5	36	90.0	316	2	hypothetical prote
6	36	90.0	316	2	dipeptide ABC tran
7	36	90.0	516	2	cytochrome P450 (C
8	36	90.0	524	2	cytochrome P450 -
9	36	90.0	524	2	probable cytochrom
10	36	90.0	656	2	VI polysaccharide
11	36	90.0	656	2	VI polysaccharide
12	36	90.0	840	1	H+-exporting ATPas
13	36	90.0	1212	2	probable two-compo
14	36	90.0	1575	2	lysobactin synthe
15	35	87.5	162	2	hypothetical prote
16	35	87.5	204	2	hypothetical prote
17	35	87.5	277	1	bo-type ubiquinol
18	35	87.5	296	2	cytochrome o ubiq
19	35	87.5	299	2	hypothetical prote
20	35	87.5	307	1	bo-type ubiquinol
21	35	87.5	318	2	cytochrome o ubiq
22	35	87.5	331	2	cytochrome o ubiq
23	35	87.5	337	2	hypothetical prote
24	35	87.5	337	2	probable integral
25	35	87.5	344	2	cytochrome o ubiq
26	35	87.5	353	2	ubiquinol oxidase
27	35	87.5	366	2	probable cytochrom
28	35	87.5	394	2	hypothetical prote
29	35	87.5	418	2	hypothetical prote

30	35	87.5	443	2	AE0309	probable sugar tra
31	35	87.5	1139	2	A10379	probable potassium
32	35	85.0	260	2	A19049	Ly-49D-GE antigen
33	34	85.0	262	2	I49361	natural killer cel
34	34	85.0	262	2	A10573	T-cell surface gly
35	34	85.0	262	2	A45813	T-cell surface gly
36	34	85.0	267	2	I55686	LgA-1 - mouse
37	34	85.0	322	2	A13395	NADH2 dehydrogenas
38	34	85.0	348	2	AE2733	NADH ubiquinone ox
39	34	85.0	348	2	G97514	NADH dehydrogenase
40	34	85.0	395	2	E90438	hypothetical prote
41	34	85.0	395	2	B96610	hypothetical prote
42	34	85.0	616	2	C69226	type I restriction
43	34	85.0	1202	2	S71424	nitric-oxide synth
44	34	85.0	1203	1	A47501	nitric-oxide synth
45	34	85.0	1205	1	A38943	nitric-oxide synth

#### ALIGNMENTS

##### RESULT 1

149101

conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.1-) CHUK - mouse

C/Species: Mus musculus (house mouse)

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C/Accession: 149101

R/Mock: B.A.; Connolly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.

A/Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome

A/Reference number: 149101; PMID:96044444; PMID:7558004

A/Accession: 149101

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-745 <RES>

A/Cross-references: EMBL:U12473; NID:g1079492; PIRN:AAC52589.1; PID:g1079493

C/Genetics:

A/Gene: CHUK

C/Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homo

C/Keywords: ATP; phosphotransferase

F/13-283/Domain: protein kinase homology <KIN>

Query Match 92.5%; Score 37; DB 1; Length 745;

Best Local Similarity 83.3%; Pred. No. 1.4e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6

DB 738 LDMAML 743

##### RESULT 2

D75215

putine phosphoribosyltransferase PAB2405 - Pyrococcus abyssi (strain Orsay)

C/Species: Pyrococcus abyssi

C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999

C/Accession: D75215

R/anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome st:

A/Reference number: A75001

A/Accession: D75215

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-215 <RAM>

A/Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIRN:CA849171.1; PID:e1515

A/Experimental source: strain Orsay

C/Genetics:

A/Gene: gpta; PAB2405

Query Match 90.0%; Score 36; DB 2; Length 215;

Best Local Similarity 66.7%; Pred. No. 57;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 6  
 :||||:  
 Db 141 IDMAW 146

RESULT 3  
 E70521  
 Probable phosphotransferase - Mycobacterium tuberculosis (strain H37Rv)  
 C/Species: Mycobacterium tuberculosis  
 C/Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
 C/Accession: E70521  
 R/Col: S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellton, S.; Squares, S.; Nature 393, 537-544, 1998  
 A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.  
 A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A/Reference number: A70500; PMID:98295987; PMID:9634230  
 A/Accession: E70521  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-251 <COL>  
 A/Cross-references: GB:A004449; GB:AL123456; NID:g3261805; PIDN:CAM10016.1; PID:g2224828  
 A/Experimental source: Strain H37Rv  
 C/Genetics:  
 A/Gene: RV3817  
 C/Superfamily: kanamycin kinase

Query Match 90.0%; Score 36; DB 2; Length 251;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMAMW 6  
 :||||:  
 Db 86 DMAMW 90

RESULT 4  
 F83632  
 Probable cytochrome c oxidase assembly factor PA0113 [imported] - Pseudomonas aeruginosa  
 C/Species: Pseudomonas aeruginosa  
 C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C/Accession: F83632  
 R/Steuer, C.K.; Plam, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
 A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
 A/Reference number: A82950; PMID:20437337; PMID:10984043  
 A/Accession: F83632  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-304 <STO>  
 A/Cross-references: GB:A004449; GB:A004091; NID:g9945928; PIDN:AA03503.1; GSPDB:GN001  
 A/Experimental source: Strain PA01  
 C/Genetics:  
 A/Gene: PA0113  
 C/Superfamily: heme O synthase

Query Match 90.0%; Score 36; DB 2; Length 304;  
 Best Local Similarity 100.0%; Pred. No. 81;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5  
 :||||:  
 Db 259 LDMAW 263

RESULT 5  
 AB2931  
 hypochloral protein Atu3048 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
 C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
 C/Accession: AB2931  
 R/Mood, D.W.; Sebubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, erage, G.; Giller, W.; Grant, C.; Guenther, D.; Kuyavlin, T.; Levy, R.; Li, M.; McCle ; Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm ster, B.W.  
 A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A/Reference number: AB2577; PMID:21608550; PMID:11743193  
 A/Accession: AB2931  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-316 <KUR>  
 A/Cross-references: GB:A008689; PIDN:AA143864.1; PID:g17741409; GSPDB:GN00187  
 A/Experimental source: strain C58 (Dupont)  
 C/Genetics:  
 A/Gene: Atu3048  
 A/Map position: linear chromosome

Query Match 90.0%; Score 36; DB 2; Length 316;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5  
 :||||:  
 Db 67 LDMAW 71

RESULT 6  
 D98351  
 dipeptide ABC transporter, dipeptide-binding protein PAB0092 [imported] - Agrobacteriu  
 C/Species: Agrobacterium tumefaciens  
 C/Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 18-Nov-2002  
 C/Accession: D98351  
 R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Gurolo, B.; Goldma A.; Liu, P.; Wolam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappe, C.; Markelz, B Science 294, 2323-2328, 2001  
 A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium t  
 A/Reference number: A97359; PMID:21608551; PMID:11743194  
 A/Accession: D98351  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-316 <KUR>  
 A/Cross-references: GB:A007870; PIDN:AAK90334.1; PID:g15160371; GSPDB:GN00170  
 C/Genetics:  
 A/Gene: AGR L 3514  
 A/Map position: linear chromosome

Query Match 90.0%; Score 36; DB 2; Length 316;  
 Best Local Similarity 100.0%; Pred. No. 84;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5  
 :||||:  
 Db 67 LDMAW 71

RESULT 7  
 T10000  
 cytochrome P450 (CYP72C) - Madagascarc periwinkle (fragment)  
 C/Species: Catharanthus roseus (Madagascarc periwinkle)  
 C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Feb-2001  
 C/Accession: T10000  
 R/Mangold, U.; Eichel, J.; Bateshauser, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Weic Plant Sci. 96, 129-136, 1994  
 A/Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from Catharan  
 A/Reference number: Z16915  
 A/Accession: T10000  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-516 <MAN>  
 A/Cross-references: EMBL:U19075; NID:g404689; PID:g404690

A:Experimental source: cv. cp3

C:Genetics:

A:Gene: CYP72C

C:Superfamily: unassigned cytochrome P450; cytochrome P450 homology

C:Keywords: heme; iron; metalloprotein

F:318-481/Domain: cytochrome P450 homology <P45>

F:459/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match

90.0%; Score 36; DB 2; Length 516;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5

Db 17 LDMAW 21

RESULT 8

T09999

Cytochrome P450 - Madagascari periwinkle

C:Species: Catharanthus roseus (Madagascari periwinkle)

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Feb-2001

C:Accession: T09999

R:Margold, U.; Bichel, J.; Betschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Werck-

plant Sci. 96, 129-136, 1994

A:Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from Catharanth

A:Reference number: Z16915

A:Accession: T09999

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-524 <MAN>

A:Cross-references: EMBL:L19074; NID:g404687; PID:g404688

A:Experimental source: cv. cp3

C:Genetics:

A:Gene: CYP72B

A:Introns: 96/1; 170/3; 252/2; 381/3

C:Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology

C:Keywords: heme; iron; metalloprotein

F:329-492/Domain: cytochrome P450 homology <P45>

F:470/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match

90.0%; Score 36; DB 2; Length 524;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5

Db 28 LDMAW 32

RESULT 9

T09944

probable cytochrome P450 protein - Madagascari periwinkle

N:Alternate names: CYP72 protein

C:Species: Catharanthus roseus (Madagascari periwinkle)

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Feb-2001

C:Accession: T09944

R:Vetter, H.P.; Margold, U.; Schroeder, G.; Marner, F.J.; Werck-Reichhart, D.; Schroeder

Plant Physiol. 100, 998-1007, 1992

A:Title: Molecular analysis and heterologous expression of an inducible cytochrome P-450

A:Reference number: Z16902

A:Accession: T09944

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-524 <VERT>

A:Cross-references: EMBL:L10081; NID:g167483; PID:g167484

C:Genetics:

A:Gene: CYP72

C:Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology

C:Keywords: heme; iron; metalloprotein

F:329-492/Domain: cytochrome P450 homology <P45>

F:470/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 90.0%; Score 36; DB 2; Length 524;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5

Db 28 LDMAW 32

RESULT 10

A56975

Vi polysaccharide capsule transporter Vexx - Salmonella typhi

C:Species: Salmonella typhi

C:Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 11-Jan-2000

C:Accession: A56975

R:Hashimoto, Y.; Li, N.; Yokoyama, H.; Ezaki, T.

J. Bacteriol. 175, 4456-4465, 1993

A:Title: Complete nucleotide sequence and molecular characterization of ViAB region en

A:Reference number: A56975; MUID:9332324; PMID:8331073

A:Accession: A56975

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-656 <HAS>

A:Cross-references: GB:D14156; NID:g426443; PIDN:BAA03200.1; PID:d1003709; PID:g426453

C:Genetics:

A:Gene: vexx

C:Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat

F:284-317/Domain: tetratricopeptide repeat homology <TR1>

F:318-351/Domain: tetratricopeptide repeat homology <TR2>

Query Match

90.0%; Score 36; DB 2; Length 656;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5

Db 411 LDMAW 415

RESULT 11

AF1040

Vi polysaccharide export protein [imported] - Salmonella enterica subsp. enterica sero

C:Species: Salmonella enterica subsp. enterica serovar Typhi

A:Note: This species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002

C:Accession: AF1040

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churchel

th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar

, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AF1040

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-556 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD06771.1; PID:g16505421; GSPDB:GN00176

C:Genetics:

A:Gene: vexx

C:Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat

Query Match 90.0%; Score 36; DB 2; Length 656;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5

Db 411 LDMAW 415

RESULT 12

AA2970

H+-exporting ATPase (EC 3.6.3.6) 95k chain, vacuolar - yeast (*Saccharomyces cerevisiae*)  
 N:Alternate names: protein O5430c; protein YOR270C  
 C:Species: *Saccharomyces cerevisiae*  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 03-Jun-2002  
 C/Accession: A42970, S67167, S67172, S72041  
 R:Manolson, M.P.; Proteau, D.; Preston, R.A.; Stembit, A.; Roberts, B.T.; Hoyt, M.A.; P.  
 J. Biol. Chem. 267, 14294-14303, 1992  
 A:Title: The VPH1 gene encodes a 95-kDa integral membrane polypeptide required for in v  
 A/Reference number: A42970; MUID:92332542; PMID:1385813  
 A/Accession: A42970  
 A:Molecule type: DNA  
 A:Residues: 1-840 <MAN>  
 A/Cross-references: GB:M89778, NID:g173172, PIDN:AAA35211.1, PID:g173173  
 A:Experimental source: strain X2180-1b; vacuolar acidification-defective mutants  
 A:Note: sequence extracted from NCBI backbone (NCBIN:108529, NCBI:P.108530)  
 R:Jumlaux, J.C.; Polrey, R.  
 A:Submitted to the Protein Sequence Database, July 1996  
 A/Reference number: S67143  
 A/Accession: S67167  
 A:Molecule type: DNA  
 A:Residues: 1-840 <JAU>  
 A/Cross-references: EMBL:Z75178; NID:g1420605; PIDN:CAA9494.1; PID:g1420606; GSPDB:GN0  
 A:Experimental source: strain S288C  
 R:Cheret, G.; Sor, F.  
 A:Submitted to the Protein Sequence Database, July 1996  
 A/Reference number: S67169  
 A/Accession: S67172  
 A:Molecule type: DNA  
 A:Residues: 1-840 <CHE>  
 A/Cross-references: EMBL:Z75178; NID:g1420605; PIDN:CAA9494.1; PID:g1420606; GSPDB:GN0  
 A:Experimental source: strain S288C  
 R:Cheret, G.; Bernardi, A.; Sor, F.  
 A:Yeast 12, 1059-1064, 1996  
 A:Title: DNA sequence analysis of the VPH1-SNF2 region on chromosome XV of *Saccharomyces*  
 A/Reference number: S72039; MUID:97051594; PMID:8896271  
 A/Accession: S72041  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-840 <CHM>  
 A/Cross-references: EMBL:X89633; NID:g1279694; PIDN:CAA61776.1; PID:g1279697  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995  
 C:Genetics:  
 A:Gene: SGD:VPH1, MIPS:YOR270C  
 A/Cross-references: MIPS:YOR270C; SGD:S0005796  
 A:Map position: 15R  
 C:Function:  
 A:Description: hydrogen ion transport; hydrolase; required for assembly and activity of  
 C:Superfamily: vacuolar ATP synthase 95k chain  
 C:Keywords: ATP; glycoprotein; hydrogen ion transport; hydrolase; membrane-associated co  
 F/407-441/Domain: transmembrane #status predicted <TM1>  
 F/457-478/Domain: transmembrane #status predicted <TM2>  
 F/539-558/Domain: transmembrane #status predicted <TM3>  
 F/565-591/Domain: transmembrane #status predicted <TM4>  
 F/635-656/Domain: transmembrane #status predicted <TM5>  
 F/733-795/Domain: transmembrane #status predicted <TM6>

Query Match 90.0%; Score 36; DB 1; Length 840;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5  
 Db 518 LDMAW 522

RESULT 13  
 F83153  
 Probable two-component sensor PA3946 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
 C/Species: *Pseudomonas aeruginosa*  
 C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C/Accession: F83153  
 R:Stover, C.K.; Pham, X.O.; Ewlyn, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lhm.

.; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pat.  
 A/Reference number: A82950; MUID:20437337; PMID:10984043  
 A/Accession: F83153  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1212 <STO>  
 A/Cross-references: GB:AE004812; GB:AE004091; NID:g9950125; PIDN:AA07333.1; GSPDB:GN0  
 A:Experimental source: strain PA01  
 C:Genetics:  
 A:Gene: PA3946  
 C:Superfamily: evgs protein; response regulator homology

Query Match 90.0%; Score 36; DB 2; Length 1212;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWAML 6  
 Db 47 DWAML 51

RESULT 14  
 T18545  
 Lysoactin synthetase - *Lysoacter* sp. (ATCC 53042) (fragment)  
 C/Species: *Lysoacter* sp.  
 A/Variety: ATCC 53042  
 C>Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 01-Dec-2000  
 C/Accession: T18545  
 R:Bernhard, F.  
 A:Submitted to the EMBL Data Library, March 1996  
 A:Description: Identification of genes encoding for peptide synthetases from Gram-nega  
 A/Reference number: Z18962  
 A/Accession: T18545  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1575 <BER>  
 A/Cross-references: EMBL:X96558; NID:e991096; PID:e236566; PIDN:CAA65394.1  
 A:Experimental source: ATCC 53042  
 C:Superfamily: acyl carrier protein homology; acetate-CoA ligase homology  
 C:Keywords: carrier protein; phosphopantetheine; phosphoprotein  
 F/468-924/Domain: acetate-CoA ligase homology <AC1>  
 F/942-1010/Domain: acyl carrier protein homology <ACP>  
 F/974/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 90.0%; Score 36; DB 2; Length 1575;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAW 5  
 Db 601 LDMAW 605

RESULT 15  
 C70829  
 hypochlorite protein Rv0471c - *Mycobacterium tuberculosis* (strain H37Rv)  
 C/Species: *Mycobacterium tuberculosis*  
 C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 28-Jul-2000  
 C/Accession: C70829  
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,  
 Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd,  
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
 Nature 393, 537-544, 1998  
 A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.  
 A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genom  
 A/Reference number: A70500; MUID:98295987; PMID:9634230  
 A/Accession: C70829  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-162 <COL>  
 A/Cross-references: GB:AL021933; GB:AL123456; NID:g3261529; PIDN:CAA17426.1; PID:e1252;

A:Experimental source: strain H37Rv  
C:Genetics:  
A:Gene: RV0471c  
C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV0471c

Query Match 87.5%; Score 35; DB 2; Length 162;  
Best Local Similarity 83.3%; Pred. No. 62;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDNAML 6  
|||  
Db 63 LDMRWL 68

Search completed: February 18, 2004, 14:38:52  
Job time : 7.5921 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds  
(without alignments)  
35.929 Million cell updates/sec

Title: US-09-643-260-16

Perfect score: 40  
Sequence: 1 LDMAWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTCUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backflite1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	38	95.0	223	4	US-09-107-532A-5762
2	37	92.5	745	2	US-08-887-518-3
3	37	92.5	745	2	US-09-023-321-3
4	37	92.5	745	2	US-08-890-853-4
5	37	92.5	745	2	US-09-032-475-3
6	37	92.5	745	2	US-09-099-125A-4
7	37	92.5	745	3	US-09-099-125A-4
8	37	92.5	745	3	US-09-032-475-4
9	37	92.5	745	3	US-08-890-854-4
10	37	92.5	745	3	US-09-023-324-4
11	37	92.5	745	3	US-09-168-629-2
12	37	92.5	745	3	US-08-810-131A-2
13	37	92.5	745	4	US-09-109-986-4
14	37	92.5	745	4	US-09-844-908-10
15	37	92.5	745	4	US-09-868-758-3
16	37	92.5	745	4	US-08-887-518-4
17	37	92.5	745	2	US-09-023-321-4
18	37	92.5	745	2	US-08-890-853-2
19	37	92.5	745	2	US-09-032-475-4
20	37	92.5	745	2	US-09-099-125A-2
21	37	92.5	745	2	US-09-099-125A-2
22	37	92.5	745	2	US-09-032-476-2
23	37	92.5	745	3	US-08-890-854-2
24	37	92.5	745	3	US-09-023-324-2
25	37	92.5	745	3	US-09-168-629-15
26	37	92.5	745	3	US-08-910-820-9
27	37	92.5	745	3	US-08-910-820-9

28	37	92.5	745	4	US-09-109-986-2	Sequence 2, Appl1
29	37	92.5	745	4	US-09-844-908-9	Sequence 9, Appl1
30	37	92.5	745	4	US-09-868-758-4	Sequence 4, Appl1
31	37	92.5	996	4	US-09-417-197-123	Sequence 123, App
32	37	92.5	997	4	US-09-417-197-121	Sequence 121, App
33	36	90.0	316	4	US-09-252-991A-17312	Sequence 17312, A
34	36	90.0	1627	4	US-09-252-991A-20395	Sequence 20395, A
35	35	87.5	302	4	US-09-252-991A-21655	Sequence 21655, A
36	35	87.5	334	4	US-09-252-991A-22395	Sequence 22395, A
37	35	87.5	439	4	US-09-172-952-14	Sequence 14, Appl1
38	34	85.0	1205	1	US-07-908-245-2	Sequence 2, Appl1
39	34	85.0	1205	2	US-08-319-866-10	Sequence 10, Appl1
40	34	85.0	1205	3	US-09-123-708-6	Sequence 6, Appl1
41	34	85.0	1205	3	US-09-123-624-6	Sequence 6, Appl1
42	34	85.0	1257	3	US-08-750-152A-2	Sequence 2, Appl1
43	33	82.5	100	1	US-08-241-853-28	Sequence 28, Appl1
44	33	82.5	100	1	US-08-241-853-29	Sequence 29, Appl1
45	33	82.5	100	2	US-08-850-917-28	Sequence 28, Appl1

## ALIGNMENTS

RESULT 1  
US-09-107-532A-5762  
Sequence 5762, Application US/09107532A  
Patent No. 6583275

## GENERAL INFORMATION:

APPLICANT: LYNN A Doucette-Stramm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts

COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A

PRIOR APPLICATION DATA:  
FILING DATE: 30-Jun-1998  
APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:  
NAME: Ariadello, Pamela Deneke  
REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-8277

TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 5762:

SEQUENCE CHARACTERISTICS:  
LENGTH: 223 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES

ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:

NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...223  
SEQUENCE DESCRIPTION: SEQ ID NO: 5762:  
US-09-107-532A-5762

Query Match 95.0%; Score 38; DB 4; Length 223;  
Best Local Similarity 83.3%; Pred. No. 80;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6  
DB 184 LDMAML 189

## RESULT 2

US-08-887-518-3  
Sequence 3, Application US/08887518  
Patent No. 5843721  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Wu, Lin  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-887-518-3  
Query Match 92.5%; Score 37; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6  
DB 738 LDMAML 743

## RESULT 3

US-09-023-321-3  
Sequence 3, Application US/09023321  
Patent No. 5844073  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Wu, Lin  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO

STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,321  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-321-3

Query Match 92.5%; Score 37; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6  
DB 738 LDMAML 743

RESULT 4  
US-08-890-853-4  
Sequence 4, Application US/08890853  
Patent No. 5851812  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Moronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:



SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-853-4

Query Match 92.5%; Score 37; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6  
DB 738 LDWAWL 743

RESULT 5  
US-09-032-475-3

Sequence 3, Application US/09032475  
Patent No. 5854003  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032.475  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/887,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-032-475-3

Query Match 92.5%; Score 37; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6  
DB 738 LDWAWL 743

RESULT 6  
US-09-099-125A-4  
Sequence 4, Application US/09099125A

Patent No. 5916760  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Moronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,125A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-099-125A-4

Query Match 92.5%; Score 37; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6  
DB 738 LDWAWL 743

RESULT 7  
US-09-099-124A-4  
Sequence 4, Application US/09099124A  
Patent No. 5939302  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Moronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,124A

;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/890,853  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: OSMAN, RICHARD A  
;; REGISTRATION NUMBER: 36,627  
;; REFERENCE/DOCKET NUMBER: T97-006-1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 343-4341  
;; TELEFAX: (415) 343-4342  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 745 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-09-099-124A-4

Query Match 92.5%; Score 37; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6  
|||:|  
Db 738 LDMSWL 743

## RESULT 8

US-09-032-476-4  
; Sequence 4, Application US/09032476  
; Patent No. 6235492  
; GENERAL INFORMATION:  
; APPLICANT: Roche, Mike  
; APPLICANT: Cao, Zhaoan  
; APPLICANT: R gnier, Catherine  
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/032,476  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/890,854  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: T97-006-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 745 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-09-032-476-4

Query Match 92.5%; Score 37; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAWL 6  
|||:|  
Db 738 LDMSWL 743

## RESULT 9

US-08-890-854-4  
; Sequence 4, Application US/08890854  
; Patent No. 6235512  
; GENERAL INFORMATION:  
; APPLICANT: Roche, Mike  
; APPLICANT: Cao, Zhaoan  
; APPLICANT: R gnier, Catherine  
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/890,854  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: T97-006-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 745 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

QY 1 LDWAWL 6  
|||:|  
Db 738 LDMSWL 743

## RESULT 10

US-09-023-324-4  
; Sequence 4, Application US/09023324  
; Patent No. 6235513  
; GENERAL INFORMATION:  
; APPLICANT: Roche, Mike  
; APPLICANT: Cao, Zhaoan  
; APPLICANT: R gnier, Catherine  
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,324  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/890,854  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-324-4

Query Match 92.5%; Score 37; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 3,4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAML 6  
DB 738 LDMSWL 743

RESULT 11  
US-09-168-629-2  
Sequence 2, Application US/09168629  
GENERAL INFORMATION:  
APPLICANT: Karin, Michael  
APPLICANT: Didonato, Joseph A.  
APPLICANT: Rothwarf, David M.  
APPLICANT: Hayakawa, Makio  
APPLICANT: Zandi, Ebrahim  
TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same  
FILE REFERENCE: P-UD 3295  
CURRENT APPLICATION NUMBER: US/09/168,629  
CURRENT FILING DATE: 1998-10-08  
EARLIER APPLICATION NUMBER: 60/061,470  
EARLIER FILING DATE: 1997-10-09  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 745  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-168-629-2

Query Match 92.5%; Score 37; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 3,4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAML 6  
DB 738 LDMSWL 743

DB 738 LDMSWL 743

RESULT 12  
US-08-910-820-10  
Sequence 10, Application US/08910820  
Patent No. 6258579  
GENERAL INFORMATION:  
APPLICANT: Mercutio, Frank  
APPLICANT: Zhu, Hengyi  
APPLICANT: Barbosa, Miguel  
APPLICANT: Li, Gian  
APPLICANT: Murray, Brian W.  
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE  
TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,820  
FILING DATE: 12-AUG-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 860098.413C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-910-820-10

Query Match 92.5%; Score 37; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 3,4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWAML 6  
DB 738 LDMSWL 743

RESULT 13  
US-08-810-131A-2  
Sequence 2, Application US/08810131A  
Patent No. 6268194  
GENERAL INFORMATION:  
APPLICANT: Karin, Michael  
APPLICANT: Didonato, Joseph A.  
APPLICANT: Rothwarf, David M.  
APPLICANT: Hayakawa, Makio  
APPLICANT: Zandi, Ebrahim  
TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using  
TITLE OF INVENTION: Same  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego

STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/810,131A  
FILING DATE: 25-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 2408  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-810-131A-2

Query Match 92.5%; Score 37; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMAWL 6  
Db 738 LDMSWL 743

RESULT 14  
US-09-109-986-4  
Sequence 4, Application US/09109986  
Patent No. 6479266  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Cao, Zhaoen  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/109,986  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/990,854  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-109-986-4

Query Match 92.5%; Score 37; DB 4; Length 745;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMAWL 6  
Db 738 LDMSWL 743

RESULT 15  
US-09-844-908-10  
Sequence 10, Application US/09844908  
Patent No. 6576437  
GENERAL INFORMATION:  
APPLICANT: Mercutio, Frank  
APPLICANT: Zhu, Hengyi  
APPLICANT: Bardoe, Miguel  
APPLICANT: Li, Gian  
Murray, Brian W.  
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE  
COMPLEX AND METHODS OF USE THEREFOR  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESS: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/844,908  
FILING DATE: 27-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,820  
FILING DATE: 12-AUG-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 860098.413C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-844-908-10

Query Match 92.5%; Score 37; DB 4; Length 745;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMAWL 6  
Db 738 LDMSWL 743

Search completed: February 18, 2004, 14:41:51  
Job time : 7.06579 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds

(without alignments)  
79.423 Million cell updates/sec

Title: US-09-643-260-15

Perfect score: 36

Sequence: 1 LDMSYL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	94.4	98	1 YDAS_ECOLI	P76063 echerichia
2	33	91.7	330	1 YETK_BACSU	O1540 bacillus su
3	32	88.9	265	1 RAD1_SCHPO	O74841 schizosach
4	32	88.9	445	1 KXAB_BACPT	P30268 bacillus fi
5	32	88.9	476	1 CLS_CLOPE	P3266 clostridium
6	32	88.9	517	1 SEST_CABSL	Q9466 caenorhabdi
7	32	88.9	707	1 ORCI_SCHPO	P4789 schizosach
8	32	88.9	734	1 GYS1_RABIT	P13834 coryciolagu
9	32	88.9	737	1 GYS1_HUMAN	P13807 homo sapien
10	32	88.9	737	1 GYS1_MACMU	Q8mj46 macaca mula
11	32	88.9	737	1 GYS1_MOUSE	P54859 mus musculu
12	32	88.9	738	1 GYS1_MOUSE	Q9214 mus musculu
13	32	88.9	2245	1 MYSJ_DICDI	P54697 dictyostei
14	31	86.1	223	1 RM49_CABSL	Q21939 caenorhabdi
15	31	86.1	385	1 O46A_DROME	P81919 drosophila
16	31	86.1	506	1 POFB_SCHPO	Q09855 schizosach
17	31	86.1	703	1 GYS2_HUMAN	P54840 homo sapien
18	31	86.1	703	1 GYS2_RAT	P17625 rattus norv
19	31	86.1	745	1 IKKA_HUMAN	O5111 h inhibitor
20	31	86.1	745	1 IKKA_MOUSE	O60680 m inhibitor
21	31	86.1	755	1 IKKB_HUMAN	O14920 homo sapien
22	31	86.1	757	1 IKKB_MOUSE	O88351 mus musculu
23	31	86.1	757	1 IKKB_RAT	Q8qy78 rattus norv
24	31	86.1	758	1 VKGC_BOVIN	Q07175 bos taurus
25	31	86.1	758	1 VKGC_HUMAN	P38435 homo sapien
26	31	86.1	758	1 VKGC_RAT	O88496 rattus norv
27	31	86.1	1161	1 CYGE_DROME	O07553 drosophila
28	30	83.3	97	1 PIXX_RHISN	Q33207 rhizobium s
29	30	83.3	121	1 YCF2_VICPA	P15821 vicia faba
30	30	83.3	266	1 UPK_FUSNN	O8186 fusobacteri
31	30	83.3	364	1 KITH_ILTVT	P33983 infectiosa
32	30	83.3	366	1 ALP_NEUCR	P33444 neurospora
33	30	83.3	417	1 CPB2_HUMAN	P48052 homo sapien

34	30	83.3	419	1 CBPA_BOVIN	P00730 bos taurus
35	30	83.3	446	1 PIV2_ADE40	P48752 human adeno
36	30	83.3	452	1 PIV2_ADE12	P12540 human adeno
37	30	83.3	482	1 AR12_CABSL	Q22431 caenorhabdi
38	30	83.3	492	1 AR12_MOUSE	Q92166 mus musculu
39	30	83.3	493	1 AR12_HUMAN	O95376 homo sapien
40	30	83.3	509	1 AR12_DROME	O76924 drosophila
41	30	83.3	528	1 YCT9_MYCTU	O11038 mycobacteri
42	30	83.3	675	1 CPAA_BACTJ	O87906 bacillus th
43	30	83.3	691	1 TOKI_YEAST	P40310 saccharomyc
44	30	83.3	1179	1 ATX1_ARATH	Q91022 arabidopsis
45	29	80.6	103	1 Y131_METUA	Q57595 methanococc

## ALIGNMENTS

RESULT 1  
YDAS\_ECOLI STANDARD; PRT; 98 AA.  
AC P76063;  
DT 15-JUN-1998 (Rel. 36, Last sequence update)  
DT 15-JUN-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein ydas precursor.  
OS YDAS OR B1357.  
GN Bacterichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Bacterichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; Pubmed=9278503;  
RA Blatner F.R., Plunkett G. III, Bloch C.A., Berna N.T., Burland V.,  
RA Riley M., Colado-Vides J., Glaeser J.D., Rode C.K., Mayhew G.P.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Bacterichia coli K-12.";  
RL Science 277:1453-1474(1997).  
CC -----  
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CC -----  
CC DR EMBL; AE000233; AAC74439.1; -.  
CC DR PIR; H64885; H64885.  
CC DR Ecogene; EG1361; Ydas.  
CC KM Hypothetical protein; Signal; Complete proteome.  
CC FT STGNL 1 32  
CC CHAIN 23 98  
CC SQ SEQUENCE 98 AA; 10975 MW; 397F00BA459E3BC4 CRC64;  
Query Match 94.4%; Score 34; DB 1; Length 98;  
Best local similarity 83.3%; Pred. No. 10;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSYL 6  
Db 67 IDMSYL 72  
RESULT 2  
YETK\_BACSU STANDARD; PRT; 330 AA.  
AC Y1540;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Hypoetical transport protein yekK.

OS Bacillus subtilis.

CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI\_taxid=1423;

XP [1]

RP SEQUENCE FROM N.A.

RC STRAIN=168;

RC MEDLINE=98044033; PubMed=9384377;

RX Kunat P., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borria R., Bouvier L., Brans A., Braun M., Brigelli S.C., Bron S., Brouillet S., Brusch C.V., Caldwell J., Capuano V., Carter N.M., Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A., Denizot P., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T., Ertian K.D., Errington J., Fabre C., Ferrati E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghm S.Y., Glaeser P., Goffeau A., Golightly E.J., Grand G., Ra Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henauc A., Halbert H., Holsteppel S., Hosono S., Hulio M.F., Itaya M., Jones L., Joris B., Karamata D., Kashara Y., Klaer-Blandford M., Klein C., Kobayashi Y., Koester P., Koningsberg G., Krogh S., Kumano M., Kunita K., Lapidus A., Lardinis S., Laber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portetelle D., Porrolik S., Prescott A.M., Priesgen E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivoletta C., Rocha E., Roche B., Rose M., Sadate Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F., Serighi J., Sekowka A., Seror S.J., Serro P., Shin B.S., Soldo B., Socorin A., Taccori E., Takagi T., Takahashi H., Takemaru K., Teneuchi M., Tanakoshi A., Tanaka T., Terpestra P., Tognoni A., Totsato V., Uchiyama S., Vandendol M., Vannier F., Vaeserott A., Vardi A., Wandut R., Wedler E., Wedler H., Wellenreger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.

RT "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis".

RL Nature 390:249-256(1997).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).

CC -1- SIMILARITY: BELONGS TO THE ENA TRANSPORTER FAMILY.

CC -----

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CC -----

DR EMBL: Z99107; CAB12540.1; -.

DR PIR: H69798; H69798.

DR Subtilisin; Bg12867; yekK.

DR InterPro: IPR000620; DUF6.

DR Pfam: PF00892; DUF6; 2.

KW Hypoetical protein; Transport; Transmembrane; Complete proteome.

FT TRANSMEM 27 47 POTENTIAL.

FT TRANSMEM 56 76 POTENTIAL.

FT TRANSMEM 90 110 POTENTIAL.

FT TRANSMEM 119 139 POTENTIAL.

FT TRANSMEM 147 167 POTENTIAL.

FT TRANSMEM 176 196 POTENTIAL.

FT TRANSMEM 206 226 POTENTIAL.

FT TRANSMEM 243 263 POTENTIAL.

FT TRANSMEM 270 290 POTENTIAL.

FT TRANSMEM 294 314 POTENTIAL.

SO SEQUENCE 330 AA; 35758 MW; 7C6C65F1EDB276B5 CRC64;

Query Match 91.7%; Score 33; DB 1; Length 330;

Best local Similarity 83.3%; Pred. No. 51;

Matches 5; Conservative 1; Identical 0; Gaps 0;

1 LDM5YL 6  
 |||||:  
 Db 239 LDM5YL 244

RESULT 3  
 FAD1 SCPO  
 ID \_FAD1 SCPO STANDARD; PART; 265 AA.

AC 074841:  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Probable FAD synthetase (EC 2.7.7.2) (FAD adenyllyltransferase) (FAD  
 pyrophosphorylase) (FAD adenine dinucleotide synthetase).  
 OS Schizosaccharomyces pombe (fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 CX NCBI\_TaxID=4896;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RC MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouris J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,  
 RA Brooke K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Shelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Voickert G., Aert R., Robben J., Gymnopoulos B.,  
 RA Welteers I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moesli D., Hilbert H.,  
 RA Borzym K., Langier I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mortier S.,  
 RA Gilbert R., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rocher M., Gallardin C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Bento J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,  
 RA Cerinetti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Spakovskii G.V., Uesary D., Barrett B.G., Nurse P.;  
 RL The genome sequence of Schizosaccharomyces pombe.";  
 RL Nature 415:871-880(2002).

CC -1 FUNCTION: ADENYLATES FMN TO FAD (BY SIMILARITY).  
 CC -1 CATALYTIC ACTIVITY: ATP + FMN = diphosphate + FAD.  
 CC -1 SIMILARITY: BELONGS TO THE PAPS REDUCTASE FAMILY. FAD1 SUBFAMILY.

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CC EMBL; AL031764; CAA21108.1; -;  
 DR PIR; T40878; T40878.  
 DR GenBank; SPC01235.04c; -;  
 DR InterPro; IPR002500; PAPS\_reduct.  
 DR Pfam; PF01507; PAPS\_reduct.1.  
 DR Trnaseq; NucleotideLyticTransferase; FAD; FMN.  
 DR TRANSFERASE; NucleotideLyticTransferase; FAD; FMN.  
 DR SEQUENCE 265 AA; 30608 MW; BC6C62B6F43A6F3 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 265;  
 Best Local Similarity 100.0%; Pred. NO. 62;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSY 5  
 Db 173 LDMSY 177

## RESULT 4

YKAB\_BACFI STANDARD; PRT; 445 AA.  
 ID YKAB\_BACFI  
 AC P30268;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Probable aminotransferase in kata 3 region (EC 2.6.-.-) (ORF B).  
 OS Bacillus firmus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 NCBI\_TaxId=1399;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Quirk P.G., Krulwich T.A.;  
 RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.  
 CC -1- COFACTOR: Pyridoxal phosphate (Potential).  
 CC -1- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent  
 CC aminotransferases.

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CC -----  
 DR EMBL; L02548; AAA22560.1; -.  
 DR PIR; S27492; S27492.  
 DR HSP; P12995; I0J3.  
 DR InterPro: IPR005814; AminoTrans\_3.  
 DR Pfam; PF00202; AminoTrans\_3; 1.  
 DR PROSITE; PS00600; AA\_TRANSFERS\_CLASS\_3; 1.  
 DR KMW Hypothetical protein; AminoTransferase; Transferase;  
 KM Pyridoxal phosphate.  
 FT BINDING 280  
 FT SEQUENCE 445 AA; 48849 MM; SC921199BC2244C CRC64;

Query Match 88.9%; Score 32; DB 1; Length 445;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSYL 6  
 Db 4 DMSYL 8

RESULT 5  
 CLS\_CLOPE STANDARD; PRT; 476 AA.  
 ID CLS\_CLOPE  
 AC Q9ZNC6;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cardiolipin synthetase (EC 2.7.8.-) (Cardiolipin synthase) (CL  
 DE synthase).  
 GN CLS OR CLSD OR CPE1430.  
 OS Clostridium perfringens.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 NCBI\_TaxId=1502;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCTC 8237 / ATCC 13124 / CN 1491 / Type A;  
 RX MEDLINE=20049836; PubMed=10585141;  
 RA Koyama M., Katayama S., Kaji M., Taniguchi Y., Matsushita O.,  
 Minami J., Morita S., Okabe A.;

RT "A Clostridium perfringens hem gene cluster contains a cysG (B)  
 RT homologue that is involved in cobalamin biosynthesis."  
 RL Microbiol. Immunol. 43:947-957(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN=13 / Type A;  
 RX MEDLINE=21664373; PubMed=11792842;  
 RA Shimizu T., Ohtani K., Hirakawa H., Onohima K., Yamashita A.,  
 RA Shiba T., Ogasawara N., Hattori M., Kohara S., Hayashi H.;  
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic  
 RT flesh-eater."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).  
 CC -1- FUNCTION: Catalyzes the reversible phosphatidyl group transfer  
 CC from one phosphatidylglycerol molecule to another to form  
 CC cardiolipin (CL) (diphosphatidylglycerol) and glycerol (By  
 CC similarity).  
 CC -1- CATALYTIC ACTIVITY: 2 Phosphatidylglycerol =  
 CC diphosphatidylglycerol + glycerol.  
 CC -1- SUBCELLULAR LOCATION: Membrane-bound (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE D FAMILY. CARDIOLIPIN  
 CC SYNTHASE SUBFAMILY.  
 CC -1- SIMILARITY: Contains 2 PLD phospholipase domains.

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CC -----  
 DR EMBL; AB017186; BAA74786.1; -.  
 DR EMBL; AP003190; BAB81136.1; -.  
 DR PIR; T43863; T43863.  
 DR HAMAP; MF\_00190; -; 1.  
 DR InterPro: IPR001736; PLD.  
 DR Pfam; PF00614; PLDC; 2.  
 DR SMART; SM00155; PLDC; 2.  
 DR PROSITE; PS0035; PLD; 2.  
 DR KMW Transferrase; Phospholipid biosynthesis; Transmembrane;  
 KM Repeat; Complete proteome.  
 FT TRANSMEM 2  
 FT TRANSMEM 31  
 FT DOMAIN 207  
 FT DOMAIN 389  
 FT ACT SITE 212  
 FT ACT SITE 394  
 FT ACT SITE 394  
 FT CONFLICT 469  
 FT SEQUENCE 476 AA; 55040 MM; 8EC32FC113F0A5CB CRC64;

Query Match 88.9%; Score 32; DB 1; Length 476;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSY 5  
 Db 265 LDMSY 269

RESULT 6  
 SBST\_CAEEL STANDARD; PRT; 517 AA.  
 ID SBST\_CAEEL  
 AC Q9N4D6;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Putative seestrin.  
 GN Y74C9A.5.  
 OS Caenorhabditis elegans.  
 OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 NCBI\_TaxId=6239;  
 RN [1]



RP SEQUENCE FROM N.A.  
 RC STRAIN=Br18101 N2;  
 RA Du H., Woldmann P., Ames M.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP CONCEPTUAL TRANSLATION.  
 RA Axelsson K., Baltoch A.;  
 RL Unpublished observations. (MAR-2001).  
 CC -1- SUBCELLULAR LOCATION: Nuclear (by similarity).  
 CC -1- SIMILARITY: Belongs to the seestrin family.  
 CC -1- CAUTION: Ref.1 sequence differs from that shown due to erroneous  
 CC gene model prediction.  
 CC -----  
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 CC -----  
 DR EMBL: AC024206; AAF36051.1; ALT\_SEQ.  
 DR Wormpep: Y74C9A.5; CE24663.  
 DR InterPro: IPR006730; PA26.  
 DR Pfam: PF04636; PA26; 1.  
 KW Hypothetical protein; Nuclear protein.  
 SQ SEQUENCE 517 AA; 60881 MW; D7BC041916D0E205 CRC64;  
 Query March 88.9%; Score 32; DB 1; Length 517;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSYL 6  
 DB 156 IDMSYM 161  
 RESULT 7  
 ORC1\_SCHPO STANDARD; PRT; 707 AA.  
 AC P54789;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Origin recognition complex subunit 1.  
 GN ORC1 OR ORP1 OR SPBC29A10.15.  
 OS Schizosaccharomyces pombe (Fission Yeast).  
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 CC Schizosaccharomycetes.  
 OC NCBI\_TaxID=4896;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=9609401; PubMed=750207;  
 RA Gavin K.A., Hidaka M., Stillman B.D.;  
 RT "Conserved initiator proteins in eukaryotes."  
 RL Science 270:1667-1671(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=96109289; PubMed=8618924;  
 RA Muzi-Falconi M., Kelly T.J.;  
 RT "Orp1, a member of the Cdc18/Cdc6 family of S-phase regulators, is  
 RT homologous to a component of the origin recognition complex."  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:12475-12479(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgroves J., Peat N., Haylee J., Basham D., Bowman S.,  
 RA Brooke K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsis K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbitts C.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Stevens S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckaert G., Aert R., Robben J., Gymnopoulos B.,  
 RA Wajsbjerg I., Vansireels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer C., Moesl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Medler H., Wandt R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leleure V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas R., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Amatrone J., Forburg S.L.,  
 RA Carrut L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,  
 RA Shipatovskii G.V., Ussery D., Barrell B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe."  
 RL Nature 415:871-880(2002).  
 RN [4]  
 RP SUBUNIT.  
 RX MEDLINE=20006240; PubMed=10535928;  
 RA Moon K.Y., Kong D., Lee J.K., Raychaudhuri S., Hurwitz J.;  
 RT "Identification and reconstitution of the origin recognition complex  
 RT from Schizosaccharomyces pombe."  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:12367-12372(1999).  
 CC -1- FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAT  
 CC BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSOMAL  
 CC REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BINDS TO  
 CC THE ARS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION.  
 CC -1- SUBUNIT: ORC IS COMPOSED OF SIX SUBUNITS.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED CONSTITUTIVELY DURING THE CELL  
 CC CYCLE.  
 CC -1- SIMILARITY: BELONGS TO THE ORC1 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: U40378; AAC49141.1; -;  
 DR EMBL: U43392; AAB38247.1; -;  
 DR EMBL: U38522; AAC49129.1; -;  
 DR EMBL: AL034463; CAA22443.1; -;  
 DR PIR: T40070; T40070.  
 DR GeneDB Spombe; SPBC29A10.15; -;  
 DR InterPro: IPR003593; AAA\_ATPase.  
 DR InterPro: IPR003595; AAA\_ATPase.  
 DR InterPro: IPR000637; AT\_hook.  
 DR InterPro: IPR001025; BAH.  
 DR Pfam: PF00004; AAA; 1.  
 DR Pfam: PF02178; AT\_hook; 1.  
 DR Pfam: PF01426; BAH; 1.  
 DR SMART: SM00382; AAA; 1.  
 DR SMART: SM00384; AT\_hook; 1.  
 DR SMART: SM00439; BAH; 1.  
 KW DNA replication; Nuclear protein; DNA-binding; ATP-binding.  
 FT NP BIND 368 375 ATP (POTENTIAL).  
 SQ SEQUENCE 707 AA; 80514 MW; D056018159A40A44 CRC64;  
 Query March 88.9%; Score 32; DB 1; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSY 5  
 DB 156 IDMSYM 161

Db 193 LDMSY 197

RESULT 8

CC GYS1\_RABIT STANDARD; PRT; 734 AA.

AC PI3834; 018817; 13, Created

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Glycogen [starch] synthase, muscle (EC 2.4.1.11).

GN GYS1 OR GYS.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OC NCBI\_TaxID=9986;

OK NCBI\_TaxID=9986;

RM SEQUENCE FROM N.A.

RC STRAIN=New Zealand white; TISSUE=Skeletal muscle;

RX MEDLINE=9003911; PubMed=2509275;

RA Zhang W.M., Browner M.F., Fletcher R.J., Depauli-Roach A.A., Roach P.J.;

RT "Primary structure of rabbit skeletal muscle glycogen synthase deduced from cDNA clones."

RT PASEB J. 3:2532-2536(1989).

RL [2]

RP SEQUENCE OF 1-29 AND 611-734.

RX MEDLINE=86242253; PubMed=3087361;

RA Cohen P., Holmes C.F.B.;

RT "Identification of the C-terminus of rabbit skeletal muscle glycogen synthase."

RT Biochem. Biophys. Res. Commun. 137:542-545(1986).

RL [3]

RP SEQUENCE OF 1-29, AND PHOSPHORYLATION SITES.

RX MEDLINE=80246030; PubMed=6772446;

RA Rylatt D.B., Alken A., Billham T., Condon G.D., Embi N., Cohen P.;

RT "Glycogen synthase from rabbit skeletal muscle. Amino acid sequence at the sites phosphorylated by glycogen synthase kinase-3, and extension of the N-terminal sequence containing the site phosphorylated by phosphorylase kinase."

RT Eur. J. Biochem. 107:529-537(1980).

RL [4]

RP SEQUENCE OF 1-15.

RX MEDLINE=79148665; PubMed=107043;

RA Huang T.S., Krebs E.G.;

RT "Effect of proteases on the structure and activity of rabbit skeletal muscle glycogen synthase."

RT FEBS Lett. 98:66-70(1979).

RL [5]

RP PARTIAL SEQUENCE, AND PHOSPHORYLATION SITES.

RX MEDLINE=85285012; PubMed=3928373;

RA Kuret J., Woodgett J.R., Cohen P.;

RT "Multisite phosphorylation of glycogen synthase from rabbit skeletal muscle. Identification of the sites phosphorylated by casein kinase-I."

RT Eur. J. Biochem. 151:39-48(1985).

RL [6]

RP SEQUENCE OF 664-682, AND PHOSPHORYLATION SITES.

RX MEDLINE=88326353; PubMed=3137939;

RA Mehrenholz A.M., Vocaw P., Roach P.J., Depauli-Roach A.A., Zlonchek T.F., Harrison M.L., Gebhen R.L.;

RT "Phosphorylation of glycogen synthase by a bovine thymus protein-tyrosine kinase, p40."

RT Biochem. Biophys. Res. Commun. 155:52-58(1988).

RL -1- FUNCTION: Transfers the glucosyl residue from UDP-Glc to the nonreducing end of alpha-1,4-glucan.

CC -1- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl} (N) = UDP + {(1,4)-alpha-D-glucosyl} (N+1)

CC -1- ENZYME REGULATION: ALLOSTERIC ACTIVATION BY GLUCOSE-6-PHOSPHATE, AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE.

CC -1- PATHWAY: Glycogen biosynthesis.

CC -1- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE FAMILY.

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CC -----

DR EMBL; AF017114; AAB69872.1; -

DR PIR; A33369; A33369.

KM Glycogen biosynthesis; Transferase; Glycosyltransferase;

KW Allosteric enzyme; Phosphorylation.

FT INIT MET 0 0

FT BINDING 38 38 UDP-GLUCOSE (BY SIMILARITY).

FT MOD RES 7 7 PHOSPHORYLATION (BY PKA).

FT MOD RES 10 10 PHOSPHORYLATION.

FT MOD RES 640 640 PHOSPHORYLATION.

FT MOD RES 644 644 PHOSPHORYLATION.

FT MOD RES 648 648 PHOSPHORYLATION.

FT MOD RES 652 652 PHOSPHORYLATION.

FT MOD RES 656 656 PHOSPHORYLATION.

FT MOD RES 697 697 PHOSPHORYLATION.

FT CONFLICT 691 691 B -> Q (IN REF. 2).

FT CONFLICT 725 725 P -> S (IN REF. 2).

FT CONFLICT 727 727 S -> P (IN REF. 2).

SQ SEQUENCE 734 AA; 83470 MW; 781BA6C435048C56 CRC64;

QY 1 LDMSYL 6

Db 595 LDMSYL 600

Query Match 88.9%; Score 32; DB 1; Length 734;

Best Local Similarity 83.3%; Pred. No. 1; 7e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 9

CC GYS1\_HUMAN STANDARD; PRT; 737 AA.

AC PI3807;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Glycogen [starch] synthase, muscle (EC 2.4.1.11).

GN GYS1 OR GYS.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI\_TaxID=9606;

OK NCBI\_TaxID=9606;

RM SEQUENCE FROM N.A.

RC TISSUE=Muscle;

RX MEDLINE=89160794; PubMed=2493642;

RA Browner M.F., Nakano K., Bang A.G., Fletcher R.J.;

RT "Human muscle glycogen synthase cDNA sequence: a negatively charged protein with an asymmetric charge distribution."

RT Proc. Natl. Acad. Sci. U.S.A. 86:1443-1447(1989).

RL [2]

RP SEQUENCE FROM N.A., AND VARIANT NIDDM SER-464.

RX MEDLINE=95385856; PubMed=7657035;

RA Orho M., Nikula-Ijas P., Schalin-Jantti C., Permutt M.A., Groop L.C.;

RT "Isolation and characterization of the human muscle glycogen synthase gene."

RT Diabetes 44:1099-1105(1995).

RL [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Endometrium;

RX MEDLINE=97163531; PubMed=9010351;

RA Su X., Schuler L., Shapiro S.S.;

RT "Cloning and characterization of a glycogen synthase cDNA from human endometrium."

RT J. Steroid Biochem. Mol. Biol. 59:459-465(1996).

CC -1- FUNCTION: Transfers the glycosyl residue from UDP-Glc to the  
 CC nonreducing end of alpha-1,4-glucan.  
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl} (N) =  
 CC UDP + {(1,4)-alpha-D-glucosyl} (N+1).  
 CC -1- ENZYME REGULATION: ALLOSTERIC ACTIVATION BY GLUCOSE-6-PHOSPHATE,  
 CC AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE.  
 CC -1- PATHWAY: Glycogen biosynthesis.  
 CC -1- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE  
 CC FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; J04501; AAA88046.1; -;  
 DR EMBL; Z33622; CAAB3916.1; -;  
 DR EMBL; Z33623; CAAB3916.1; JOINED.  
 DR EMBL; Z33609; CAAB3916.1; JOINED.  
 DR EMBL; Z33624; CAAB3916.1; JOINED.  
 DR EMBL; Z33625; CAAB3916.1; JOINED.  
 DR EMBL; Z33626; CAAB3916.1; JOINED.  
 DR EMBL; Z33610; CAAB3916.1; JOINED.  
 DR EMBL; Z33627; CAAB3916.1; JOINED.  
 DR EMBL; Z33628; CAAB3916.1; JOINED.  
 DR EMBL; Z33629; CAAB3916.1; JOINED.  
 DR EMBL; Z33630; CAAB3916.1; JOINED.  
 DR EMBL; Z33631; CAAB3916.1; JOINED.  
 DR EMBL; Z33633; CAAB3916.1; JOINED.  
 DR EMBL; U32573; AAB60385.1; -;  
 DR PIR; A32156; AAB60385.1; -;  
 DR Genew; HGNC:4706; GYS1.  
 DR GK; P13807; -;  
 DR MIM; 138570; -;  
 KM Glycogen biosynthesis; Transferase; Glycosyltransferase;  
 KM Allosteric enzyme; Phosphorylation; Disease mutation;  
 KW Diabetes mellitus; Polymorphism.  
 FT BINDING 39 39 UDP-GLUCOSE (BY SIMILARITY).  
 FT MOD\_RES 8 8 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).  
 FT MOD\_RES 11 11 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 641 641 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 645 645 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 649 649 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 653 653 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 657 657 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 658 658 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 710 710 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 710 710 PHOSPHORYLATION (BY SIMILARITY).  
 FT VARIANT 130 130 K -> E (IN dbSNP:5456).  
 FT VARIANT 283 283 N -> S (IN dbSNP:5461).  
 FT VARIANT 359 359 E -> G (IN dbSNP:5465).  
 FT VARIANT 416 416 M -> V (IN dbSNP:5447).  
 FT VARIANT 464 464 G -> S (IN dbSNP:5473).  
 FT VARIANT 619 619 E -> Q (IN dbSNP:5450).  
 FT VARIANT 619 619 P -> A (IN dbSNP:5453).  
 FT VARIANT 691 691 /FTID=VAR 014731.  
 FT CONFLICT 136 136 T -> I (IN REF. 1 AND 3).  
 FT CONFLICT 462 462 MISSING (IN REF. 3).  
 FT CONFLICT 608 608 A -> D (IN REF. 3).  
 FT CONFLICT 706 706 S -> R (IN REF. 1 AND 3).  
 SQ SEQUENCE 737 AA; 83785 MW; 0B321BFBDB0BD7F CRC64;  
 Query Match 88.9%; Score 32; DB 1; Length 737;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSYL 6  
 DB 596 LDWKYL 601  
 RESULT 10  
 GYS1\_MACMU STANDARD; PRT; 737 AA.  
 AC Q6M26;  
 DT 28-FEB-2003 (Rel. 41, Last created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Glycogen (starch) synthase, muscle (EC 2.4.1.11).  
 GN GYS1 OR GYS.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Carcophleciinae; Macaca.  
 OC NCBI\_TaxID=9544;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RA Ottmeyer H.K., Marciani K.R., Hansen B.C.;  
 RT "Monkey skeletal muscle glycogen synthase sequence,";  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Transfers the glycosyl residue from UDP-Glc to the  
 CC nonreducing end of alpha-1,4-glucan (By similarity).  
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl} (N) =  
 CC UDP + {(1,4)-alpha-D-glucosyl} (N+1).  
 CC -1- ENZYME REGULATION: ALLOSTERIC ACTIVATION BY GLUCOSE-6-PHOSPHATE,  
 CC AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE.  
 CC -1- PATHWAY: Glycogen biosynthesis.  
 CC -1- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE  
 CC FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AF529178; AAM93267.1; -;  
 KM Glycogen biosynthesis; Transferase; Glycosyltransferase;  
 KM Allosteric enzyme; Phosphorylation.  
 FT BINDING 39 39 UDP-GLUCOSE (BY SIMILARITY).  
 FT MOD\_RES 8 8 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).  
 FT MOD\_RES 11 11 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 641 641 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 645 645 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 649 649 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 653 653 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 657 657 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 658 658 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 698 698 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 710 710 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 710 710 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 737 AA; 83786 MW; B8B0B3114C58F56C CRC64;  
 Query Match 88.9%; Score 32; DB 1; Length 737;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Glycogen [etarch] synthase, brain [EC 2.4.1.11].  
 GN GYS3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NC NCB1\_TaxID=10090;  
 RX MEDLINE=96385248; PubMed=8793107;  
 RA Pellegrini G., Rossier C., Magistretti P.J., Martin J.L.;  
 RT "Cloning, localization and induction of mouse brain glycogen  
 synthase.";  
 RL Brain Res. Mol. Brain Res. 38:191-199(1996).  
 CC -1- FUNCTION: Transfers the glycosyl residue from UDP-Glc to the  
 CC nonreducing end of alpha-1,4-glucan.  
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl) (N) =  
 CC UDP + ((1,4)-alpha-D-glucosyl) (N+1).  
 CC -1- ENZYME REGULATION: ALLOSTERIC ACTIVATION BY GLUCOSE-6-PHOSPHATE,  
 CC AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE.  
 CC -1- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE  
 CC FAMILY.  
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 CC -----  
 DR EMBL; X94616; CAA64322.1; -.  
 DR MGD; MGI:107378; Gys3.  
 KW Glycogen biosynthesis; Transferase; Glycosyltransferase;  
 KM Allosteric enzyme; Phosphorylation.  
 FT BINDING 39 39 UDP-GLUCOSE (BY SIMILARITY).  
 FT MOD RES 8 8 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).  
 FT MOD RES 11 11 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD RES 640 640 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD RES 644 644 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD RES 648 648 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD RES 652 652 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD RES 656 656 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD RES 697 697 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD RES 710 710 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 737 AA; 83824 MW; 891A0614C8F6C085 CRC64;  
 Query Match 88.9%; Score 32; DB 1; Length 737;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LDMSYL 6  
 DB 595 LDMKYL 600

RP SEQUENCE FROM N.A.  
 RA Seidlin M.F., Xue Z., Rochelle J.M., DeBry R., Surwit R.;  
 RT "Mouse glycogen synthase gene."  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Transfers the glycosyl residue from UDP-Glc to the  
 CC nonreducing end of alpha-1,4-glucan (By similarity).  
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl) (N) =  
 CC UDP + ((1,4)-alpha-D-glucosyl) (N+1).  
 CC -1- ENZYME REGULATION: ALLOSTERIC ACTIVATION BY GLUCOSE-6-PHOSPHATE,  
 CC AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE  
 CC FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; U53218; AAD09457.1; -.  
 DR MGD; MGI:101805; Gys1.  
 KW Glycogen biosynthesis; Transferase; Glycosyltransferase;  
 KM Allosteric enzyme; Phosphorylation.  
 FT BINDING 39 39 UDP-GLUCOSE (BY SIMILARITY).  
 FT MOD RES 8 8 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).  
 FT MOD RES 11 11 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD RES 641 641 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD RES 645 645 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD RES 649 649 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD RES 653 653 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD RES 657 657 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD RES 698 698 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 738 AA; 83955 MW; 6C2C8B5D5004F1D1 CRC64;  
 Query Match 88.9%; Score 32; DB 1; Length 738;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LDMSYL 6  
 DB 596 LDMKYL 601

RESULT 13  
 MSG DICI  
 AC P54637; STANDARD; PRT; 2245 AA.  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Myosin II heavy chain.  
 GN MYOJ.  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Metazoa; Dictyostelida; Dictyostelium.  
 OC NCB1\_TaxID=44689;  
 RX MEDLINE=96215148; PubMed=8636147;  
 RC STRAIN=AX3.  
 RP SEQUENCE FROM N.A.  
 RA Hammer J.A. III, Jung G.;  
 RT "The sequence of the dictyostelium myo J heavy chain gene predicts a  
 RT novel, dimeric, unconventional myosin with a heavy chain molecular  
 RT mass of 258 kDa."  
 RL J. Biol. Chem. 271:7120-7127(1996).  
 RN [2]  
 RP SEQUENCE OF 1-1021 FROM N.A.  
 RX MEDLINE=97039016; PubMed=8884597;  
 RA Peterson M.D., Urso A.S., Titus M.A.;  
 RT "Dictyostelium discoideum myoJ: a member of a broadly defined myosin  
 RT V class or a class XI unconventional myosin?";

```

RL U. Muscle Res. Cell Motil. 17:411-424(1996).
RN [3]
RP SEQUENCE OF 182-298 FROM N.A.
RX MEDLINE=95023928; PubMed=7937787;
RA Titus M.A., Kuspa A., Loomis W.F.;
RT "Discovery of myosin genes by physical mapping in Dictyostelium.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:9446-9450(1994).
CC -1- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN AND HAS ATPASE
CC ACTIVITY THAT IS ACTIVATED BY ACTIN.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: Contains 1 myosin-like globular head domain.
CC -1- SIMILARITY: Contains 1 dimeric domain.
CC -1- SIMILARITY: Contains 3 IQ domains.
CC -----
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CC -----
DR EMBL: U42409; AAA85186.1; -.
DR EMBL: L35322; AAA79858.1; -.
DR PIR: T18278; T18278.
DR HSBP: P08799; IMND.
DR DictyDb: D001095; myoJ.
DR InterPro: IPR002710; DIL.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; myosin_N.
DR Pfam: PF01843; DIL; 1.
DR Pfam: PF00612; IQ; 6.
DR Pfam: PF00663; myosin_head; 2.
DR Pfam: PF02736; myosin_N; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD003376; DIL; 1.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 3.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PS00096; IQ; 3.
KW Myosin; ATP-binding; Actin-binding; Calmodulin-binding; Repeat;
KW Coiled coil.
FT DOMAIN 1 809 MYOSIN HEAD-LIKE.
FT DOMAIN 824 851 IQ 1.
FT DOMAIN 872 901 IQ 2.
FT DOMAIN 943 972 IQ 3.
FT DOMAIN 973 1812 COILED COIL (POTENTIAL).
FT DOMAIN 2060 2220 DILUTE.
FT NP_BIND 174 181 ATP (POTENTIAL).
FT DOMAIN 669 749 ACTIN-BINDING.
FT CONFLICT 191 191 L -> F (IN REF. 2).
FT CONFLICT 284 284 A -> T (IN REF. 2).
FT CONFLICT 291 291 G -> R (IN REF. 2).
FT CONFLICT 332 347 NKGCFEIEGVSDSEH -> IEMNELKVTYMK (IN
FT REF. 2).
FT CONFLICT 550 550 N -> K (IN REF. 2).
FT CONFLICT 865 866 HH -> QQ (IN REF. 2).
SQ SEQUENCE 2245 AA; 258478 MW; 615SEFIDLAB4SBE CRC64;
Query Match 88.9%; Score 32; DB 1; Length 2245;
Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Potential mitochondrial 60S ribosomal protein L49 (MRP-L49).
GN R1D1.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Steward C.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
CC -1- SIMILARITY: BELONGS TO THE L49EM FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL: Z75547; CA99906.1; -.
DR PIR: T24188; T24188.
DR WormPep: R1D1.9; CE06314.
DR Pfam: PF05046; Img2; 1.
DR Hypothetical protein; Ribosomal protein; Mitochondrion.
KW Hypothetical protein; Ribosomal protein; Mitochondrion.
SQ SEQUENCE 223 AA; 25862 MW; 2A8DC95C813CB3F CRC64;
Query Match 86.1%; Score 31; DB 1; Length 223;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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OY 1 LDMSYL 6
DB 530 IDMSYI 535
RESULT 14
RM49_CABEL STANDARD; PRT; 223 AA.
AC Q21939;

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OY 1 LDMSYL 6
DB 530 IDMSYI 535
RESULT 15
O46A_DROME STANDARD; PRT; 385 AA.
AC P81919; Q9U6X9; Q9V5H3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Odorant receptor 46a.
GN OR46A OR OR46F.1 OR DOR46F.1 OR AN9 OR CG17849.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99389723; PubMed=10458908;
RA Gao Q., Chess A.;
RT "Identification of candidate Drosophila olfactory receptors from
RT genomic DNA sequence.";
RL Genomes 60:31-39(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hopkins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutcliffe G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.C., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 / Search time 3.55263 Seconds

(Without alignments)  
79.423 Million cell updates/sec

Title: US-09-643-260-14

Sequence: 1 LDMSFL 6

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	91.4	404	1 YCFD_HABIN	P4663 haemophilus
2	31	88.6	135	1 VAL2_CLVK	P14976 cassava lat
3	31	88.6	135	1 VAL2_CLVN	P14968 cassava lat
4	31	88.6	135	1 VAL2_TYICV	P27282 tomato yell
5	31	88.6	204	1 HIS2_YERPE	Q82FY1 yerbina pe
6	31	88.6	240	1 LEC5_VATWA	Rel371 vatatea ma
7	31	88.6	355	1 CXAS_RAT	P28234 ratu8 norv
8	31	88.6	356	1 CXAS_CANPA	P33725 canis fami
9	31	88.6	357	1 CXAS_HUMAN	P01231 mus musculu
10	31	88.6	357	1 CXAS_MOUSE	001231 mus musculu
11	31	88.6	368	1 CXAS_CHICK	P18860 gallus gall
12	31	88.6	382	1 LYS1_CANAL	P43065 candida alb
13	31	88.6	383	1 P2C4_SCHPO	O14166 schizosacch
14	31	88.6	399	1 CXAS_CHICK	P36391 gallus gall
15	31	88.6	400	1 NUCM_PROMI	Q37619 proteobaca
16	31	88.6	405	1 CXAS_BOVIN	P41987 bos taurus
17	31	88.6	415	1 CXAS_RAT	P29414 ratu8 norv
18	31	88.6	416	1 CXAS_MOUSE	Q6448 mus musculu
19	31	88.6	432	1 CXAS_HUMAN	P48185 homo sapien
20	31	88.6	434	1 CXAS_HUMAN	Q9Y618 homo sapien
21	31	88.6	439	1 CXAS_MOUSE	P28236 mus musculu
22	31	88.6	439	1 CXAS_SHEEP	P55917 ovis aries
23	31	88.6	510	1 CXS6_CHICK	P29415 gallus gall
24	31	88.6	1363	1 ILPR_BRALA	002466 brachiolesto
25	30	85.7	98	1 YDAS_ECOLI	P76063 escherichia
26	30	85.7	225	1 TRPF_CANAL	P43073 candida alb
27	30	85.7	570	1 MKKS_HUMAN	Q9N11 homo sapien
28	30	85.7	654	1 CBP1_YEAST	P07282 saccharomyc
29	30	85.7	709	1 KRP1_SCHPO	Q09175 schizosacch
30	30	85.7	745	1 IKKA_HUMAN	O15111 h inhibitor
31	30	85.7	745	1 IKKA_MOUSE	O60680 m inhibitor
32	30	85.7	751	1 TALA_POVHA	P03075 hamster pol
33	30	85.7	756	1 IKKB_HUMAN	O14920 homo sapien

34	30	85.7	757	1 IKKB_MOUSE	O88351 mus musculu
35	30	85.7	757	1 IKKB_RAT	Q9Q78 ratu8 norv
36	30	85.7	3746	1 ACVS_PENCH	P19787 penicillium
37	30	85.7	3791	1 ACVT_PENCH	P26046 penicillium
38	29	82.9	139	1 YOR2_ADEG1	P20744 avian adeno
39	29	82.9	179	1 Y256_SUT50	Q98055 mycoplasma
40	29	82.9	228	1 Y268_MYCGE	P47510 mycoplasma
41	29	82.9	233	1 CR29_ENTHI	P19476 entamoeba h
42	29	82.9	284	1 YK62_SULTO	Q96Y66 sulfolobus
43	29	82.9	328	1 NIK3_AZOB	P45672 azospirillum
44	29	82.9	330	1 YETK_BACSU	O31540 bacillus su
45	29	82.9	344	1 METE_THERVO	Q97914 thermoplasma

## ALIGNMENTS

RESULT 1  
YCFD\_HABIN STANDARD, PRT, 404 AA.  
AC P4663;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Protein H10396.  
GN H10396.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Haemophilus.  
OX NCBI\_TaxId=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RD / KW20 / ATCC 51907;  
RX MEDLINE=95350630; PubMed=7542800;  
RA Fetschmann R.D., Adams M.D., White O., Clayton R.A., Kirtness E.F.,  
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
RA Scott J.D., Shirley R., Liu L.-I., Giedek A., Kelley J.M.,  
RA Weidman J.F., Phillips C.A., Spriggs T., Heddlom E., Cotton M.D.,  
RA Utecherback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
RA Gnehm C.L., Fritchman J.L., Fuhrmann J.L., Geochagen N.S.M.,  
RA Venter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae  
RT Rd.";  
RT Science 269:496-512(1995).  
RP IDENTIFICATION BY MASS SPECTROMETRY.  
RX MEDLINE=201337488; PubMed=10675023;  
RA Langen H., Takece B., Evers S., Berndt P., Lahm H.W., Wipf B.,  
RA Gray C., Fountoulakis M.;  
RT "Two-dimensional map of the proteome of Haemophilus influenzae";  
RT Electrophoresis 21:411-429(2000).  
CC -1-SIMILARITY: STRONG, TO E.COLI YCFD.  
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CC  
CC EMBL, U32723; AAC22055.1; -  
DR PIR; A64151; A64151.  
DR TIGR; H10396; -  
DR InterPro; IPR003347; TF\_JmjC.  
DR SMART; SM00558; JmjC; 1.  
KW Complete proteome.  
SQ  
SQ SEQUENCE 404 AA; 46419 MW; A3FF26064D3F8B4C CRC64;  
Query Match 91.4%; Score 32; DB 1; Length 404;  
Best Local Similarity 83.3%; Pred. No. 70;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DMSFL 6  
|||||

Db 366 DMSFL 371

## RESULT 2

VAL2\_CLVW STANDARD; PRT; 135 AA.

AC P14976;  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE AL2 protein (15.2 kDa protein).  
GN AC2.  
OS Cassava latent virus (strain West Kenyan 844).  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=10818;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Stanley J., Gay M.R.;  
RT "Nucleotide sequence of cassava latent virus DNA.";  
RL Nature 301:260-262(1983).  
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL2 PROTEIN FAMILY.  
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-----  
CC EMBL; J02057; -; NOT\_ANNOTATED CDS.  
DR InterPro: IPR000942; Gemin1.AL2.  
DR Pfam; PF01440; Gemin1.AL2; 1.  
DR PRINTS; PR00230; GEMCOATL2.  
DR ProDom; PD001117; Gemin1.AL2; 1.  
SQ SEQUENCE 135 AA; 15159 MW; 75D24A8CD636848 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 135;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSFL 6  
|||||

Db 128 DMSFL 132

## RESULT 3

VAL2\_CLVW STANDARD; PRT; 135 AA.

AC P14968;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE AL2 protein (15.2 kDa protein).  
GN AC2.  
OS Cassava latent virus (strain Nigerian).  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=10819;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=90174930; PubMed=2308631;  
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;  
RT "Nucleotide sequence of the infectious cloned DNA components of  
RT African cassava mosaic virus (Nigerian strain).";  
RL Nucleic Acids Res. 18:197-198(1990).  
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL2 PROTEIN FAMILY.  
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DR EMBL; X17095; CAA34952.1; -.  
DR PIR; S07593; S07593.  
DR InterPro; IPR000942; Gemin1.AL2.  
DR Pfam; PF01440; Gemin1.AL2; 1.  
DR PRINTS; PR00230; GEMCOATL2.  
DR ProDom; PD001117; Gemin1.AL2; 1.  
SQ SEQUENCE 135 AA; 15178 MW; 2825C2P42E5E1F49 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 135;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSFL 6  
|||||

Db 128 DMSFL 132

## RESULT 4

VAL2\_TYLCV STANDARD; PRT; 135 AA.

AC P27262;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE AL2 protein (C2 protein).  
GN C2.  
OS Tomato yellow leaf curl virus (TYLCV).  
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
OX NCBI\_TaxID=10832;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=92024070; PubMed=1926771;  
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;  
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus  
RT with a single genomic component.";  
RL Virology 185:151-161(1991).  
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL2 PROTEIN FAMILY.  
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-----  
CC EMBL; X15656; CAA33689.1; -.  
DR PIR; C40779; OOCVCA.  
DR InterPro; IPR000942; Gemin1.AL2.  
DR Pfam; PF01440; Gemin1.AL2; 1.  
DR PRINTS; PR00230; GEMCOATL2.  
DR ProDom; PD001117; Gemin1.AL2; 1.  
SQ SEQUENCE 135 AA; 15611 MW; F111C8C2F7E9DD32 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 135;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSFL 6  
|||||

Db 128 DMSFL 132

## RESULT 5

HIS2\_YERPE STANDARD; PRT; 204 AA.

AC Q8ZF1;



DT 28-FEB-2003 (Rel. 41, Last Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Histidine biosynthesis bifunctional protein hsisB [includes:  
 DE Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) (PRA-CH);  
 DE Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) (PRA-PH)].  
 GN HSI OR HSI8 OR YPO1542 OR Y2628.  
 OS Yersinia pestis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Yersinia.  
 OX NCBI\_TaxID=632;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CO-92 / Biovar Orientalis;  
 RX MEDLINE=21470413; PubMed=1156360;  
 RA Parikh J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,  
 RA Penrice M.B., Sebailia M., James K.D., Churcher C., Mungall K.L.,  
 RA Baker S., Baaham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,  
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
 RA Felwell T., Hamlin N., Holroyd S., Jagers K., Kariyasev A.V.,  
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,  
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.,  
 RA "Genome sequence of Yersinia pestis, the causative agent of plague";  
 RL Nature 413:523-527(2001).  
 RT [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=KIMS / Biovar Medisevalis;  
 RX MEDLINE=22137863; PubMed=12142430;  
 RA Deng W., Burland V., Plunkett G. II, Boutin A., Mayhew G.F., Liles P.,  
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,  
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,  
 RA Straley S.C., McDonough K.A., Milles M.L., Watson J.S., Blattner F.R.,  
 RA Perry R.D.;  
 RT "Genome sequence of Yersinia pestis KIM";  
 RL J. Bacteriol. 184:4601-4611(2002).  
 CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-ATP + H(2)O = 1-(5-  
 CC phosphoribosyl)-AMP + diphosphate.  
 CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-AMP + H(2)O = 1-(5-  
 CC phosphoribosyl)-5-(1-(5-phosphoribosyl)-imidazole-4-carboxamide.  
 CC -1- PATHWAY: Histidine biosynthesis; second step.  
 CC -1- PATHWAY: Histidine biosynthesis; third step.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE PRA-CH  
 CC FAMILY.  
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE PRA-PH  
 CC FAMILY.  
 CC -----  
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DT 28-FEB-2003 (Rel. 41, Last Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Histidine biosynthesis bifunctional protein hsisB [includes:  
 DE Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) (PRA-CH);  
 DE Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) (PRA-PH)].  
 GN HSI OR HSI8 OR YPO1542 OR Y2628.  
 OS Yersinia pestis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Yersinia.  
 OX NCBI\_TaxID=632;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CO-92 / Biovar Orientalis;  
 RX MEDLINE=21470413; PubMed=1156360;  
 RA Parikh J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,  
 RA Penrice M.B., Sebailia M., James K.D., Churcher C., Mungall K.L.,  
 RA Baker S., Baaham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,  
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
 RA Felwell T., Hamlin N., Holroyd S., Jagers K., Kariyasev A.V.,  
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,  
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.,  
 RA "Genome sequence of Yersinia pestis, the causative agent of plague";  
 RL Nature 413:523-527(2001).  
 RT [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=KIMS / Biovar Medisevalis;  
 RX MEDLINE=22137863; PubMed=12142430;  
 RA Deng W., Burland V., Plunkett G. II, Boutin A., Mayhew G.F., Liles P.,  
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,  
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,  
 RA Straley S.C., McDonough K.A., Milles M.L., Watson J.S., Blattner F.R.,  
 RA Perry R.D.;  
 RT "Genome sequence of Yersinia pestis KIM";  
 RL J. Bacteriol. 184:4601-4611(2002).  
 CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-ATP + H(2)O = 1-(5-  
 CC phosphoribosyl)-AMP + diphosphate.  
 CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-AMP + H(2)O = 1-(5-  
 CC phosphoribosyl)-5-(1-(5-phosphoribosyl)-imidazole-4-carboxamide.  
 CC -1- PATHWAY: Histidine biosynthesis; second step.  
 CC -1- PATHWAY: Histidine biosynthesis; third step.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE PRA-CH  
 CC FAMILY.  
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE PRA-PH  
 CC FAMILY.  
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DT 28-FEB-2003 (Rel. 41, Last Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Histidine biosynthesis bifunctional protein hsisB [includes:  
 DE Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) (PRA-CH);  
 DE Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) (PRA-PH)].  
 GN HSI OR HSI8 OR YPO1542 OR Y2628.  
 OS Yersinia pestis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Yersinia.  
 OX NCBI\_TaxID=632;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CO-92 / Biovar Orientalis;  
 RX MEDLINE=21470413; PubMed=1156360;  
 RA Parikh J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,  
 RA Penrice M.B., Sebailia M., James K.D., Churcher C., Mungall K.L.,  
 RA Baker S., Baaham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,  
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
 RA Felwell T., Hamlin N., Holroyd S., Jagers K., Kariyasev A.V.,  
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,  
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.,  
 RA "Genome sequence of Yersinia pestis, the causative agent of plague";  
 RL Nature 413:523-527(2001).  
 RT [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=KIMS / Biovar Medisevalis;  
 RX MEDLINE=22137863; PubMed=12142430;  
 RA Deng W., Burland V., Plunkett G. II, Boutin A., Mayhew G.F., Liles P.,  
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,  
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,  
 RA Straley S.C., McDonough K.A., Milles M.L., Watson J.S., Blattner F.R.,  
 RA Perry R.D.;  
 RT "Genome sequence of Yersinia pestis KIM";  
 RL J. Bacteriol. 184:4601-4611(2002).  
 CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-ATP + H(2)O = 1-(5-  
 CC phosphoribosyl)-AMP + diphosphate.  
 CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-AMP + H(2)O = 1-(5-  
 CC phosphoribosyl)-5-(1-(5-phosphoribosyl)-imidazole-4-carboxamide.  
 CC -1- PATHWAY: Histidine biosynthesis; second step.  
 CC -1- PATHWAY: Histidine biosynthesis; third step.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE PRA-CH  
 CC FAMILY.  
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE PRA-PH  
 CC FAMILY.  
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Best Local Similarity 100.0%; Pred. No. 63;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 DMSF 5  
Db 224 DMSF 228

## RESULT 7

CXAS\_RAT STANDARD; PRT; 355 AA.  
ID CXAS\_RAT  
AC P28234  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Gap junction alpha-5 protein (Connexin 40) (Cx40).  
GN GJA5 OR CXN-40.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Sprague-Dawley;  
RX MEDLINE=92112940; PubMed=1370487;  
RA Haefliger J.-A., Brizzone R., Jenkins N.A., Gilbert D.J.,  
RA Copeland N.G., Paul D.L.;  
RT "Four novel members of the connexin family of gap junction proteins.  
Molecular cloning, expression, and chromosome mapping.";  
RT J. Biol. Chem. 267:2057-2064(1992).  
RL [2]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=93021055; PubMed=1328644;  
RA Beyer E.C., Reed K.E., Westphale E.M., Kanter H.L., Larson D.M.;  
RT "Molecular cloning and expression of rat connexin40, a gap junction  
protein expressed in vascular smooth muscle.";  
RT J. Membr. Biol. 127:69-76(1992).  
RL [3]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=9806770; PubMed=9403066;  
RA Seul K.H., Taddei P.N., Beyer E.C.;  
RT "Mouse connexin40: gene structure and promoter analysis.";  
RL Genomics 46:120-126(1997).  
CC -1- FUNCTION: One gap junction consists of a cluster of closely packed  
pairs of transmembrane channels, the connexons, through which  
materials of low mw diffuse from one cell to a neighboring cell.  
CC -1- SUBUNIT: A connexon is composed of a hexamer of connexins.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: Highly expressed in lung.  
CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)  
SUBFAMILY.  
CC -----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M76535; AAA41000.1; -  
DR EMBL; M83092; AAA41194.1; -  
DR EMBL; AF021806; AAC55502.1; -  
DR EMBL; AF022136; AAC55503.1; -  
DR PIR; A42053; A42053.  
DR InterPro; IPR000500; Connexin.  
DR Pfam; PF00029; connexin.1.  
DR PRINTS; PR00206; CONNEXIN.  
DR SMART; SM00037; CNX; 1.  
DR PROSITE; PS00407; CONNEXINS\_1; 1.  
DR PROSITE; PS00408; CONNEXINS\_2; 1.  
KW Gap junction, Transmembrane.  
FT INIT\_MET 0 0 BY SIMILARITY.

FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 23 40 POTENTIAL.  
FT DOMAIN 41 75 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 76 98 POTENTIAL.  
FT DOMAIN 99 154 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 155 177 POTENTIAL.  
FT DOMAIN 178 204 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 205 227 POTENTIAL.  
FT DOMAIN 228 355 CYTOPLASMIC (POTENTIAL).  
SQ SEQUENCE 355 AA; 40102 MW; 4F8594386800B9 CRC64;  
Query Match Score 31; DB 1; Length 355;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 DMSF 6  
Db 2 DMSF 6

## RESULT 8

CXAS\_CANFA STANDARD; PRT; 356 AA.  
ID CXAS\_CANFA  
AC P33725;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Gap junction alpha-5 protein (Connexin 40) (Cx40).  
GN GJA5.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92136511; PubMed=1310450;  
RA Kanter H.L., Safitz J.E., Beyer E.C.;  
RT "Cardiac myocytes express multiple gap junction proteins.";  
RL Circ. Res. 70:438-444(1992).  
CC -1- FUNCTION: One gap junction consists of a cluster of closely packed  
pairs of transmembrane channels, the connexons, through which  
materials of low mw diffuse from one cell to a neighboring cell.  
CC -1- SUBUNIT: A connexon is composed of a hexamer of connexins.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)  
SUBFAMILY.  
CC -----  
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CC -----  
DR EMBL; M81347; AAA30838.1; -  
DR PIR; A49024; A49024.  
DR InterPro; IPR000500; Connexin.  
DR Pfam; PF00029; connexin.1.  
DR PRINTS; PR00206; CONNEXIN.  
DR SMART; SM00037; CNX; 1.  
DR PROSITE; PS00407; CONNEXINS\_1; 1.  
DR PROSITE; PS00408; CONNEXINS\_2; 1.  
KW Gap junction, Transmembrane.  
FT INIT\_MET 0 0 BY SIMILARITY.  
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 23 40 POTENTIAL.  
FT DOMAIN 41 76 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 77 99 POTENTIAL.  
FT DOMAIN 100 154 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 155 177 POTENTIAL.  
FT DOMAIN 178 204 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 205 227 POTENTIAL.

FT DOMAIN 228 356 CYTOPLASMIC (POTENTIAL).  
 SQ SEQUENCE 356 AA; 33901 MW; C8431D65CF9E78BE CRC64;  
 Query Match 88.6%; Score 31; DB 1; Length 356;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DMSFL 6  
 DB 2 DMSFL 6

RESULT 9  
 CXAS HUMAN STANDARD; PRT; 357 AA.  
 AC P36382;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Gap junction alpha-5 protein (Connexin 40) (Cx40).  
 GN Cx45.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9505780; PubMed=7966354;  
 RA Kanter H.L., Saffitz J.E., Beyer E.C.;  
 RT "Molecular cloning of two human cardiac gap junction proteins,  
 RT connexin40 and connexin45.";  
 RL J. Mol. Cell. Cardiol. 26:861-868 (1994).  
 RP [2]  
 RP REVISIONS.  
 RA Beyer E.C., Christensen E.A.;  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Hefflinger J.-A., Goy J.J., Maebler G.;  
 RT "Spontaneous cases of dilated cardiomyopathies associated with  
 RT arrionentricular conduction defects are not linked to mutation within  
 RT the connexins 40 and 43 genes.";  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,  
 RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein W.J., Udell T.B., Tomshylyk S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pabey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallie D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC -1- FUNCTION: One gap junction consists of a cluster of closely packed  
 CC pairs of transmembrane channels, the connexons, through which

CC materials of low mw diffuse from one cell to a neighboring cell.  
 CC -1- SUBUNIT: A connexon is composed of a hexamer of connexins.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)  
 CC SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: U03486; AAA60457.2; -;  
 CC EMBL: L34954; AAA91833.1; -;  
 CC EMBL: AF151979; AAD37801.1; -;  
 CC EMBL: BC013313; AAH13313.1; -;  
 CC DR Genew; HGNC:4279; GJA5.  
 CC MIM: 121013; -;  
 CC DR GO; GO:0015285; F:connexon channel activity; TAS.  
 CC DR GO; GO:0007043; P:intercellular junction assembly; TAS.  
 CC DR GO; GO:006936; P:muscle contraction; TAS.  
 CC DR InterPro; IPR000500; Connexin.  
 CC DR Pfam; PF00029; connexin; 1.  
 CC DR PRINTS; PR00206; CONNEXIN.  
 CC DR SMART; SM00037; CNX; 1.  
 CC DR PROSITE; PS00407; CONNEXINS\_1; 1.  
 CC DR PROSITE; PS00408; CONNEXINS\_2; 1.  
 CC KW Gap junction; Transmembrane.  
 CC FT INIT MET 0 0  
 CC FT DOMAIN 1 22 BY SIMILARITY.  
 CC FT TRANSMEM 23 40 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 41 75 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 76 98 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 99 163 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 164 183 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 184 205 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 206 228 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 229 357 POTENTIAL.  
 CC FT CYTOPLASMIC (POTENTIAL).  
 CC SQ SEQUENCE 357 AA; 40249 MW; 63FP9AA3CAED760 CRC64;  
 Query Match 88.6%; Score 31; DB 1; Length 357;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DMSFL 6  
 DB 2 DMSFL 6

RESULT 10  
 CXAS MOUSE STANDARD; PRT; 357 AA.  
 AC Q01231;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Gap junction alpha-5 protein (Connexin 40) (Cx40).  
 GN GJA5 OR CXN-40.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=92299686; PubMed=1318884;  
 RA Hempmann J., Suchyna T., Lichtenberg-Frate H., Jungbluth S.,  
 RA Dahl E., Schwarz J., Nicholson B.J., Willecke K.;  
 RT "Molecular cloning and functional expression of mouse connexin40, a  
 RT second gap junction gene preferentially expressed in lung.";  
 RL J. Cell Biol. 117:1299-1310 (1992).

```

CC -1- FUNCTION: One gap junction consists of a cluster of closely packed
CC pairs of transmembrane channels, the connexons, through which
CC materials of low mw diffuse from one cell to a neighboring cell.
CC -1- SUBUNIT: A connexon is composed of a hexamer of connexins.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Kidney, heart and skin, but most abundant
CC in lung.
CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL: X61675; CAA43850.1; -.
DR PIR: S23111; S23111.
DR MGI: MGI:95716; Gja5.
DR InterPro: IPR000500; Connexin.
DR Pfam: PF00029; connexin.1.
DR PRINTS: PR00206; CONNEXIN.
DR SMART: SM00037; CNX; 1.
DR PROSITE: PS00407; CONNEXINS_1; 1.
DR PROSITE: PS00408; CONNEXINS_2; 1.
KW Gap junction; Transmembrane.
FT INIT MET 0 0 BY SIMILARITY.
FT DOMAIN 23 22 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 23 40 POTENTIAL.
FT DOMAIN 41 75 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 76 98 POTENTIAL.
FT DOMAIN 99 155 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 156 178 POTENTIAL.
FT DOMAIN 179 205 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 206 228 POTENTIAL.
FT DOMAIN 229 357 POTENTIAL.
SQ SEQUENCE 357 AA; 40282 MW; 7823CDA57A9CTC90 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 357;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6
DB 2 DWSFL 6

RESULT 11
ID ID_CXAS_CHICK STANDARD; PRT; 368 AA.
AC P18860;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gap junction alpha-5 protein (Connexin 42) (Cx42).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90354434; PubMed=2167316;
RA Beyer E.C.;
RT "Molecular cloning and developmental expression of two chick embryo
RT gap junction proteins."
RL J. Biol. Chem. 265:14439-14443(1990).
CC -1- FUNCTION: One gap junction consists of a cluster of closely packed
CC pairs of transmembrane channels, the connexons, through which
CC materials of low mw diffuse from one cell to a neighboring cell.
CC -1- SUBUNIT: A connexon is composed of a hexamer of connexins.

```

```

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Mostly in heart, and in the whole embryo,
CC liver, stomach, and pectoral muscle.
CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL: M35043; AAA48716.1; -.
DR PIR: B37819; B37819.
DR InterPro: IPR000500; Connexin.
DR Pfam: PF00029; connexin.1.
DR PRINTS: PR00206; CONNEXIN.
DR SMART: SM00037; CNX; 1.
DR PROSITE: PS00407; CONNEXINS_1; 1.
DR PROSITE: PS00408; CONNEXINS_2; 1.
KW Gap junction; Transmembrane.
FT INIT MET 0 0 BY SIMILARITY.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 23 45 POTENTIAL.
FT DOMAIN 46 75 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 76 98 POTENTIAL.
FT DOMAIN 99 159 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 160 182 POTENTIAL.
FT DOMAIN 183 210 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 211 233 POTENTIAL.
FT DOMAIN 234 368 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 368 AA; 41613 MW; 853A042PFS1DACB CRC64;

Query Match 88.6%; Score 31; DB 1; Length 368;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6
DB 2 DWSFL 6

RESULT 12
ID ID_LYS1_CANAL STANDARD; PRT; 382 AA.
AC P43065;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Saccharopine dehydrogenase [NAD+], L-lysine forming] (EC 1.5.1.7)
DE (Lysine--2-oxoglutarate reductase) (SDH).
GN LYS1.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_Taxid=5476;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95012722; PubMed=7927784;
RA Garrard R.C., Schmidt T.M., Bhattacharjee J.K.;
RT "Molecular and functional analysis of the Lys1 gene of Candida
RT albicans."
RL Infect. Immun. 62:5027-5031(1994).
CC -1- CATALYTIC ACTIVITY: N(6)-(L-1,3-dicarboxypropyl)-L-lysine + NAD(+)
CC + H2O = L-lysine + 2-oxoglutarate + NADH.
CC -1- PATHWAY: Lysine biosynthesis; alpha-aminoacidic acid pathway;
CC eight (last) step.
CC -1- SUBUNIT: Monomer (by similarity).
CC -1- SIMILARITY: TO OTHER FUNGAL SACCHAROPINE DEHYDROGENASE.
CC -----
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DR EMBL, U13233; AAA21362.1; -  
 DR InterPro: IPR004002; Aladh\_PMT.  
 DR Pfam: PF01262; Aladh\_PNT\_C; 1.  
 DR Pfam: PF05222; Aladh\_PNT\_N; 1.  
 KM Lysine biosynthesis; Oxidoreductase; NAD.  
 FT ACT SITE 217 BY SIMILARITY  
 SQ SEQUENCE 382 AA; 42394 MW; A3620191DF04B8BF CRC64;

Query Match 88.6%; Score 31; DB 1; Length 382;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSF 5  
 DB 151 LDMSF 155

RESULT 13  
 P2C4\_SCHPO STANDARD; PRT; 383 AA.  
 ID P2C4\_SCHPO  
 AC 014156; Q9UR02;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Protein phosphatase 2C homolog 4 (EC 3.1.3.16) (PP2C-4).  
 GN PTC4 OR SPAC4A8.03C.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 NC NCB1\_TaxID=4896;  
 RX MEDLINE=972;  
 RN [1]  
 RP SEQUENCE FROM N.A., SUBUNIT, SUBCELLULAR LOCATION, AND FUNCTION.  
 RC STRAIN=972;  
 RX MEDLINE=99365157; PubMed=10436019;  
 RA Gaiter F., Ruseell P.;  
 RT "Vaccule fusion regulated by protein phosphatase 2C in fission  
 RL yeast." Mol. Biol. Cell 10:2647-2654(1999).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21648401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouros J., Peat N., Hayles J., Baker S., Baaham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones W., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Mount S., Mungall K., Murphy L., Niblett D., Odeil C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tiley A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volkert G., Aert R., Robben J., Gymnopre B.,  
 RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Medler H., Wandt R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Drenth S., Gloux S., Lelaure V., Mottler S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucan M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,  
 RA Cernetti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakowski G.V., Useery D., Barrell B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe.";  
 RL Nature 415:871-880(2002).  
 CC -1- FUNCTION: HAS A ROLE IN THE REGULATION OF VACUOLE FUSION.  
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +  
 CC phosphate.  
 CC -1- CORFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).  
 CC -1- SUBUNIT: Monomer.  
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND, VACUOLAR.  
 CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.  
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DR EMBL, AF140285; AAD27651.1; -  
 DR EMBL, Z98762; CAB58554.1; -  
 DR PIR, T38772; T38772.  
 DR GenedB Spombe; SPAC4A8.03C; -  
 DR InterPro: IPR001932; PP2C-like.  
 DR InterPro: IPR000222; PP2C.  
 DR Pfam: PF00481; PP2C; 1.  
 DR SMART; SM00331; PP2C\_SIG; 1.  
 DR SMART; SM00332; PP2C; 1.  
 DR PROSITE; PS01032; PP2C; 1.  
 KM Hydrolyase; Magnesium; Manganese; Membrane; Multigene family.  
 FT METAL 92  
 FT METAL 308  
 FT METAL 347  
 FT METAL 347  
 SQ SEQUENCE 383 AA; 43569 MW; 88B0C2BD4E49BF CRC64;

Query Match 88.6%; Score 31; DB 1; Length 383;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSFL 6  
 DB 299 DMSFL 303

RESULT 14  
 CXAB\_CHICK STANDARD; PRT; 399 AA.  
 ID CXAB\_CHICK  
 AC P36381; O92144;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Gap junction alpha-8 protein (Connexin 45.6) (CX45.6).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NC NCB1\_TaxID=9031;  
 RX MEDLINE=94325667; PubMed=8049527;  
 RA Jiang J.X., White T.W., Goodenough D.A., Paul D.L.;  
 RT "Molecular cloning and functional characterization of chick lens  
 RL fiber connexin 45.6." Mol. Biol. Cell 5:369-373(1994).  
 RL [2]  
 RN SEQUENCE OF 1-235 FROM N.A.  
 RC TISSUE=lens fibers;  
 RX MEDLINE=96437509; PubMed=8840185;  
 RA Sawada K., Agata K., Eguchi G.;  
 RT "Characterization of terminally differentiated cell state by  
 RT categorizing cDNA clones derived from chicken lens fibers.";  
 RL Int. J. Dev. Biol. 40:531-535(1996).

```

CC -1- FUNCTION: One gap junction consists of a cluster of closely packed
CC pairs of transmembrane channels, the connexons, through which
CC materials of low mw diffuse from one cell to a neighboring cell.
CC -1- SUBUNIT: A connexon is composed of a hexamer of connexins.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL; L24799; AAA57134.1; -
DR EMBL; D25333; BAA05381.1; -
DR PIR; I50219; I50219.
DR InterPro; IPR000500; Connexin.
DR InterPro; IPR002266; Connexin50.
DR Pfam; PF03509; Connexin50; 1.
DR Pfam; PF00029; connexin; 1.
DR PRINTS; PR00206; CONNEXIN.
DR SMART; SM00037; CNX; 1.
DR PROSITE; PS00407; CONNEXINS_1; 1.
DR PROSITE; PS00408; CONNEXINS_2; 1.
KM Gap junction; Transmembrane.
FT INIT MET 0 0 BY SIMILARITY.
FT DOMAIN 1 19 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 20 42 POTENTIAL.
FT DOMAIN 43 73 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 74 96 POTENTIAL.
FT DOMAIN 97 151 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 152 174 POTENTIAL.
FT DOMAIN 175 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 229 POTENTIAL.
FT DOMAIN 230 399 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 145 146 EG -> DL (IN REF. 2).
FT CONFLICT 187 188 WP -> D (IN REF. 2).
FT CONFLICT 233 235 IRR -> SEL (IN REF. 2).
SQ SEQUENCE 399 AA; 45485 MW; 4197392ADB6C85CA CRC64;

Query Match 88.6%; Score 31; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSFL 6
DB 2 DMSFL 6

RESULT 15
NUCM_PROWI STANDARD; PRT; 400 AA.
AC Q37619;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE NADH-ubiquinone oxidoreductase 49 kDa subunit (EC 1.6.5.3)
DE (EC 1.6.99.3) (NADH dehydrogenase subunit 7).
GN NAD7.
OS Prototheca wickerhamii.
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Prototheca.
OC NCBI_TaxID=3111;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=263-11;
RX MEDLINE=94180393; PubMed=8133522;
RA Wolff G., Planke I., Lang B.F., Kueck U., Burger G.;
RT "Complete sequence of the mitochondrial DNA of the chlorophyte alga

```

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RT Prototheca wickerhamii. Gene content and genome organization.";
RL J. Mol. Biol. 237:75-86(1994).
CC -1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC TO BE UBIQUINONE. COMPONENT OF THE IRON-SULFUR (IP) FRAGMENT OF
CC THE ENZYME.
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I 49 kDa SUBUNIT FAMILY.
CC -----
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CC -----
DR EMBL; U02970; AAD12640.1; -
DR PIR; T11921; T11921.
DR InterPro; IPR001135; Oxidored_49kDa.
DR Pfam; PF00346; complex1_49kd; 1.
DR PROSITE; PS00535; COMPLEX1_49K; 1.
DR Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
KM SEQUENCE 400 AA; 45810 MW; 7227458F8E80BC9D2 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSF 5
DB 221 LDMSF 225

Search completed: February 18, 2004, 14:28:12
Job time : 4.55263 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds  
(without alignments)  
75.239 Million cell updates/sec

Title: US-09-643-260-14

Perfect score: 35

Sequence: 1 LDMSFL 6

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubppa/PTCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubppa/PTCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubppa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubppa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubppa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubppa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubppa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubppa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	6	10 US-09-847-940B-14	Sequence 14, App1
2	35	100.0	6	11 US-09-847-946A-14	Sequence 14, App1
3	33	94.3	218	12 US-10-032-189-107	Sequence 107, App
4	33	94.3	218	12 US-09-863-776-50	Sequence 50, App1
5	33	94.3	218	12 US-09-981-151A-91	Sequence 91, App1
6	33	94.3	827	12 US-10-347-470A-26	Sequence 26, App1
7	32	91.4	6	10 US-09-847-940B-15	Sequence 15, App1
8	32	91.4	6	11 US-09-847-946A-15	Sequence 15, App1
9	32	91.4	56	10 US-09-764-877-1782	Sequence 1782, App
10	32	91.4	56	12 US-10-242-515-1782	Sequence 1782, App
11	32	91.4	743	12 US-10-104-047-2340	Sequence 2340, App
12	31	88.6	124	9 US-09-925-302-460	Sequence 460, App
13	31	88.6	157	10 US-09-738-626-4783	Sequence 4783, App
14	31	88.6	184	15 US-10-078-770-86	Sequence 86, App1
15	31	88.6	238	15 US-10-078-770-96	Sequence 96, App1

16	31	88.6	264	12 US-10-097-111-300	Sequence 300, App
17	31	88.6	305	15 US-10-078-770-90	Sequence 90, App1
18	31	88.6	317	12 US-10-032-189-32	Sequence 32, App1
19	31	88.6	358	12 US-10-438-537-4	Sequence 4, App1
20	31	88.6	358	12 US-10-295-027-1228	Sequence 1228, App
21	31	88.6	413	12 US-10-032-189-106	Sequence 106, App
22	31	88.6	416	12 US-10-032-189-105	Sequence 105, App
23	31	88.6	417	12 US-10-032-189-104	Sequence 104, App
24	31	88.6	433	12 US-09-863-776-48	Sequence 48, App1
25	31	88.6	435	12 US-10-032-189-102	Sequence 102, App
26	31	88.6	435	12 US-10-032-189-103	Sequence 103, App
27	31	88.6	515	12 US-10-108-260A-3041	Sequence 3041, App
28	31	88.6	1025	12 US-10-345-072-7	Sequence 7, App1
29	31	88.6	1025	15 US-10-195-144-7	Sequence 7, App1
30	31	88.6	1285	12 US-10-369-493-12354	Sequence 12354, App
31	30	85.7	6	10 US-09-847-940B-2	Sequence 2, App1
32	30	85.7	6	11 US-09-847-946A-2	Sequence 2, App1
33	30	85.7	6	11 US-09-847-946A-33	Sequence 33, App1
34	30	85.7	7	11 US-09-847-946A-37	Sequence 37, App1
35	30	85.7	8	11 US-09-847-946A-30	Sequence 30, App1
36	30	85.7	8	11 US-09-847-946A-38	Sequence 38, App1
37	30	85.7	9	11 US-09-847-946A-29	Sequence 29, App1
38	30	85.7	9	11 US-09-847-946A-32	Sequence 32, App1
39	30	85.7	9	11 US-09-847-946A-35	Sequence 35, App1
40	30	85.7	9	11 US-09-847-946A-36	Sequence 36, App1
41	30	85.7	10	11 US-09-847-946A-31	Sequence 31, App1
42	30	85.7	10	11 US-09-847-946A-34	Sequence 34, App1
43	30	85.7	11	11 US-09-847-946A-28	Sequence 28, App1
44	30	85.7	11	11 US-09-847-946A-132	Sequence 132, App
45	30	85.7	11	11 US-09-847-946A-140	Sequence 140, App

#### ALIGNMENTS

RESULT 1  
US-09-847-940B-14  
Sequence 14, Application US/09847940B  
Patent No. US20020156000A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J.  
APPLICANT: Ghosh, Sankar  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-117CP  
CURRENT APPLICATION NUMBER: US/09/847,940B  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-14  
Query Match 100.0%; Score 35; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7e+05; 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0;  
QY 1 LDMSFL 6  
Db 1 LDMSFL 6  
RESULT 2  
US-09-847-946A-14  
Sequence 14, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J

APPLICANT: Ghosh, Sanjay  
APPLICANT: Pindels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NBD peptide  
US-09-847-946A-14

Query Match 100.0%; Score 35; DB 11; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSFL 6  
Db 1 LDMSFL 6

RESULT 3  
US-10-032-189-107  
Sequence 107, Application US/10032189  
Publication No. US20030170630A1  
GENERAL INFORMATION:  
APPLICANT: Alsebrook II, John P  
APPLICANT: Tchernev, Velizar T  
APPLICANT: Liu, Xiaohong  
APPLICANT: Spytek, Kimberly A  
APPLICANT: Zethusen, Bryan D  
APPLICANT: Paturajan, Meera  
APPLICANT: Grose, William M  
APPLICANT: Lepley, Denise M  
APPLICANT: Burgess, Catherine E  
APPLICANT: Shinkels, Richard A  
APPLICANT: Grose, William M  
APPLICANT: Szekeres, Edward S  
APPLICANT: Vernet, Corine A.M.  
APPLICANT: Li, Li  
APPLICANT: Caeman, Stacie J  
APPLICANT: Boldog, Ferenc L  
APPLICANT: Gorman, Linda  
APPLICANT: Gangoli, Esha A  
APPLICANT: Fernandes, Elma R  
APPLICANT: Rieger, Daniel K  
APPLICANT: Edinger, Shlomit R  
APPLICANT: Gunther, Erik  
APPLICANT: Millet, Isabelle  
APPLICANT: Sciore, Paul  
APPLICANT: Ellerman, Karen  
APPLICANT: MacDougall, John R  
APPLICANT: Smithson, Glenda  
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-228  
CURRENT APPLICATION NUMBER: US/10/032,189  
CURRENT FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 60/257,495  
PRIOR FILING DATE: 2000-12-21  
PRIOR APPLICATION NUMBER: 60/258,171  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 60/269,940  
PRIOR FILING DATE: 2001-02-20

PRIOR APPLICATION NUMBER: 60/274,192  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: 60/277,826  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: 60/279,840  
PRIOR FILING DATE: 2001-03-29  
PRIOR APPLICATION NUMBER: 60/282,981  
PRIOR FILING DATE: 2001-04-11  
PRIOR APPLICATION NUMBER: 60/283,656  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/309,247  
PRIOR FILING DATE: 2001-07-31  
PRIOR APPLICATION NUMBER: 60/311,754  
PRIOR FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: 60/313,331  
PRIOR FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 260  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 107  
LENGTH: 218  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Connexin  
US-10-032-189-107

Query Match 94.3%; Score 33; DB 13; Length 218;  
Best Local Similarity 83.3%; Pred. No. 3.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSFL 6  
Db 1 LDMSFL 6

RESULT 4  
US-09-863-776-50  
Sequence 50, Application US/09863776  
Publication No. US20030198953A1  
GENERAL INFORMATION:  
APPLICANT: Spytek, Kimberly A  
APPLICANT: Majumder, Kumud  
APPLICANT: Tchernev, Velizar T  
APPLICANT: Mishra, Vishnu  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Spaderna, Steven K  
APPLICANT: Shenoy, Suresh G  
APPLICANT: Rastelli, Luca  
APPLICANT: Li, Li  
APPLICANT: Taupier, Raymond J  
APPLICANT: Gangoli, Esha  
TITLE OF INVENTION: No. US20030198953A1 Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-020  
CURRENT APPLICATION NUMBER: US/09/863,776  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: 09/540,763  
PRIOR FILING DATE: 2000-03-30  
PRIOR APPLICATION NUMBER: 60/206,679  
PRIOR FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: 60/206,688  
PRIOR FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: 60/206,829  
PRIOR FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: 60/207,748  
PRIOR FILING DATE: 2000-05-30  
PRIOR APPLICATION NUMBER: 60/207,798  
PRIOR FILING DATE: 2000-05-30  
PRIOR APPLICATION NUMBER: 60/208,263  
PRIOR FILING DATE: 2000-05-31  
PRIOR APPLICATION NUMBER: 60/208,831  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: 60/209,451



PRIOR FILING DATE: 2000-06-05  
PRIOR APPLICATION NUMBER: 60/210,060  
PRIOR FILING DATE: 2000-06-07  
PRIOR APPLICATION NUMBER: 60/219,507  
PRIOR FILING DATE: 2000-07-20  
PRIOR APPLICATION NUMBER: 60/221,337  
PRIOR FILING DATE: 2000-07-26  
PRIOR APPLICATION NUMBER: 60/221,927  
PRIOR FILING DATE: 2000-07-31  
PRIOR APPLICATION NUMBER: 60/263,135  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: 60/263,688  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: 60/263,694  
PRIOR FILING DATE: 2001-01-24  
NUMBER OF SEQ ID NOS: 155  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 50  
LENGTH: 218  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Connexin  
US-09-863-776-50

Query Match 94.3%; Score 33; DB 12; Length 218;  
Best Local Similarity 83.3%; Pred. No. 3.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
:|||||  
Db 1 MDMSFL 6

RESULT 5  
US-09-981-151A-91  
Sequence 91, Application US/09981151A  
Publication No. US20030212256A1  
GENERAL INFORMATION:  
APPLICANT: Edinger, Shlomit R  
APPLICANT: Gerlach, Valerie  
APPLICANT: MacDougall, John R  
APPLICANT: Malyankar, Muriel M  
APPLICANT: Smithson, Glenda  
APPLICANT: Miller, Isabelle  
APPLICANT: Peyman, John A  
APPLICANT: Stone, David J  
APPLICANT: Gunther, Erik  
APPLICANT: Rilleman, Karen  
APPLICANT: Shlomek, Richard A  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Guo, Xiaojia  
APPLICANT: Patturajan, Meera  
APPLICANT: Taupier Jr, Raymond J  
APPLICANT: Burgess, Catherine E  
APPLICANT: Zerhusen, Bryan D  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Spytek, Kimberly A  
APPLICANT: Gangoli, Esha A  
APPLICANT: Fernandes, Elma R  
APPLICANT: Gorman, Linda  
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-168  
CURRENT APPLICATION NUMBER: US/09/981,151A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 60/241,040  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,058  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,063  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/241,243

PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/242,152  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/242,482  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,611  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,612  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/242,880  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/242,881  
PRIOR FILING DATE: 2000-10-24  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 91  
LENGTH: 218  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Connexin  
US-09-981-151A-91

Query Match 94.3%; Score 33; DB 12; Length 218;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
:|||||  
Db 1 MDMSFL 6

RESULT 6  
US-10-347-470A-26  
Sequence 26, Application US/10347470A  
Publication No. US20040002054A1  
GENERAL INFORMATION:  
APPLICANT: Horvitz, H. Robert  
APPLICANT: Hwang, Ho Yon  
TITLE OF INVENTION: SOY NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 01997/542003  
CURRENT APPLICATION NUMBER: US/10/347,470A  
CURRENT FILING DATE: 2003-01-17  
PRIOR APPLICATION NUMBER: US 60/349,630  
PRIOR FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: US 60/390,930  
PRIOR FILING DATE: 2002-06-24  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 26  
LENGTH: 827  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-10-347-470A-26

Query Match 94.3%; Score 33; DB 12; Length 827;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
:|||||  
Db 370 LDMSFL 375

RESULT 7  
US-09-847-940B-15  
Sequence 15, Application US/09847940B  
Patent No. US20020156000A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J.  
APPLICANT: Ghosh, Sankar

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; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-15
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```
Query Match          91.4%; Score 32; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 LDMSPL 6
        |||||
Db      1 LDMSYL 6
```

```
RESULT 8
US-09-847-946A-15
; Sequence 15, Application US/09847946A
; Publication No. US2003054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-15
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```
Query Match          91.4%; Score 32; DB 11; Length 6;
Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 LDMSPL 6
        |||||
Db      1 LDMSYL 6
```

```
RESULT 9
US-09-764-877-1782
; Sequence 1782, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
```

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; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1782
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (51)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (56)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-877-1782
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```
Query Match          91.4%; Score 32; DB 10; Length 56;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 LDMSPL 6
        |||||
Db      27 LDWNFL 32
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RESULT 10
US-10-242-515-1782
; Sequence 1782, Application US/10242515
; Publication No. US2004000948A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005C1
; CURRENT APPLICATION NUMBER: US/10/242,515
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,877
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1782
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (51)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (56)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-242-515-1782
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Query Match          91.4%; Score 32; DB 12; Length 56;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
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Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSFL 6  
|||  
Db 27 LDMSFL 32

RESULT 11  
US-10-104-047-2340  
; Sequence 2340, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2340  
; LENGTH: 743  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-2340

Query Match 91.4%; Score 32; DB 12; Length 743;  
Best Local Similarity 83.3%; Pred. No. 1.5e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
|||  
Db 98 VDMSFL 103

RESULT 12  
US-09-925-302-460  
; Sequence 460, Application US/09925302  
; Patent No. US20020044941A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 460  
; LENGTH: 124  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (112)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (113)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (119)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (123)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-302-460

Query Match 88.6%; Score 31; DB 9; Length 124;  
Best Local Similarity 100.0%; Pred. No. 5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 DMSFL 6  
|||  
Db 50 DMSFL 54

RESULT 13  
US-09-738-626-4783  
; Sequence 4783, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIAI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAOKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738,626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7059  
; SOFTWARE: PatentIn ver. 3.0  
; SEQ ID NO 4783  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-738-626-4783

Query Match 88.6%; Score 31; DB 10; Length 157;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 5  
|||  
Db 72 LDMSFL 76

RESULT 14  
US-10-078-770-86  
; Sequence 86, Application US/10078770  
; Publication No. US20030003471A1  
; GENERAL INFORMATION:  
; APPLICANT: Famodu, Omojayo O.  
; APPLICANT: Forge, Charlie  
; APPLICANT: Miao, Guo-Hua  
; TITLE OF INVENTION: CDNAS Encoding Polypeptides  
; FILE REFERENCE: BB-1365 US NA  
; CURRENT APPLICATION NUMBER: US/10/078,770  
; CURRENT FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: 09/614,188  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: 60/143,400  
; PRIOR FILING DATE: 1999-07-12  
; PRIOR APPLICATION NUMBER: 60/153,534  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: 60/161,223  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/159,878  
; PRIOR FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: 60/157,401  
; PRIOR FILING DATE: 1999-10-01

;; PRIOR APPLICATION NUMBER: 60/143,419  
;; PRIOR FILING DATE: 1999-07-12  
;; PRIOR APPLICATION NUMBER: 60/143,409  
;; PRIOR FILING DATE: 1999-07-12  
;; NUMBER OF SEQ ID NOS: 196  
;; SOFTWARE: Microsoft Office 97  
;; SEQ ID NO 86  
;; LENGTH: 184  
;; TYPE: PRT  
;; ORGANISM: Zea mays  
;; FEATURE:  
;; NAME/KEY: UNSURE  
;; LOCATION: (98)  
;; NAME/KEY: UNSURE  
;; LOCATION: (104)..(105)  
;; NAME/KEY: UNSURE  
;; LOCATION: (115)  
;; NAME/KEY: UNSURE  
;; LOCATION: (117)  
;; NAME/KEY: UNSURE  
;; LOCATION: (123)  
;; NAME/KEY: UNSURE  
;; LOCATION: (126)..(127)  
;; NAME/KEY: UNSURE  
;; LOCATION: (136)  
;; NAME/KEY: UNSURE  
;; LOCATION: (159)  
;; NAME/KEY: UNSURE  
;; LOCATION: (174)..(175)  
US-10-078-770-86

Query Match 88.6%; Score 31; DB 15; Length 184;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSP 5  
Db 18 LDWSP 22

RESULT 15  
US-10-078-770-96  
;; Sequence 96, Application US/10078770  
;; Publication No. US20030003471A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Famodu, OmoIayo O.  
;; APPLICANT: Forge, Charlie  
;; APPLICANT: Miao, Guo-Hua  
;; TITLE OF INVENTION: CDMS Encoding Polypeptides  
;; FILE REFERENCE: BB-1365 US NA  
;; CURRENT APPLICATION NUMBER: US/10/078,770  
;; CURRENT FILING DATE: 2002-02-19  
;; PRIOR APPLICATION NUMBER: 09/614,188  
;; PRIOR FILING DATE: 2000-07-12  
;; PRIOR APPLICATION NUMBER: 60/143,400  
;; PRIOR FILING DATE: 1999-07-12  
;; PRIOR APPLICATION NUMBER: 60/153,534  
;; PRIOR FILING DATE: 1999-09-13  
;; PRIOR APPLICATION NUMBER: 60/161,223  
;; PRIOR FILING DATE: 1999-10-22  
;; PRIOR APPLICATION NUMBER: 60/159,878  
;; PRIOR FILING DATE: 1999-10-15  
;; PRIOR APPLICATION NUMBER: 60/157,401  
;; PRIOR FILING DATE: 1999-10-01  
;; PRIOR APPLICATION NUMBER: 60/143,419  
;; PRIOR FILING DATE: 1999-07-12  
;; PRIOR APPLICATION NUMBER: 60/143,409  
;; PRIOR FILING DATE: 1999-07-12  
;; NUMBER OF SEQ ID NOS: 196  
;; SOFTWARE: Microsoft Office 97  
;; SEQ ID NO 96  
;; LENGTH: 238  
;; TYPE: PRT

;; ORGANISM: Zea mays  
US-10-078-770-96

Query Match 88.6%; Score 31; DB 15; Length 238;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSP 5  
Db 26 LDWSP 30

Search completed: February 18, 2004, 15:42:00  
Job time : 17.7529 secs

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## OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds  
(without alignments)  
35.929 Million cell updates/sec

Title: US-09-643-260-14

Perfect score: 35

Sequence: 1 LDMSFL 6

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	91.4	829	4 US-09-252-991A-27150	Sequence 27150, A
2	31	88.6	86	4 US-09-107-532A-7054	Sequence 7054, Ap
3	31	88.6	277	1 US-08-118-270-68	Sequence 68, Appl
4	31	88.6	277	5 PCT-US93-08528-68	Sequence 68, Appl
5	31	88.6	382	2 US-08-360-606B-30	Sequence 30, Appl
6	30	85.7	177	4 US-09-328-352-5063	Sequence 5063, Ap
7	30	85.7	365	4 US-09-328-352-7147	Sequence 7147, Ap
8	30	85.7	397	4 US-09-107-532A-4918	Sequence 4918, Ap
9	30	85.7	413	4 US-09-328-352-7815	Sequence 7815, Ap
10	30	85.7	745	2 US-08-887-518-3	Sequence 3, Appl
11	30	85.7	745	2 US-09-023-321-3	Sequence 3, Appl
12	30	85.7	745	2 US-08-890-853-4	Sequence 4, Appl
13	30	85.7	745	2 US-09-032-475-3	Sequence 3, Appl
14	30	85.7	745	2 US-09-099-125A-4	Sequence 4, Appl
15	30	85.7	745	2 US-09-099-124A-4	Sequence 4, Appl
16	30	85.7	745	3 US-09-032-476-4	Sequence 4, Appl
17	30	85.7	745	3 US-08-890-854-4	Sequence 4, Appl
18	30	85.7	745	3 US-09-023-324-4	Sequence 4, Appl
19	30	85.7	745	3 US-09-168-629-2	Sequence 2, Appl
20	30	85.7	745	3 US-08-910-820-10	Sequence 10, Appl
21	30	85.7	745	3 US-08-810-131A-2	Sequence 2, Appl
22	30	85.7	745	4 US-09-109-986-4	Sequence 4, Appl
23	30	85.7	745	4 US-09-844-908-10	Sequence 10, Appl
24	30	85.7	745	4 US-09-868-758-3	Sequence 3, Appl
25	30	85.7	756	2 US-08-887-518-4	Sequence 4, Appl
26	30	85.7	756	2 US-09-023-321-4	Sequence 2, Appl
27	30	85.7	756	2 US-08-890-853-2	Sequence 2, Appl

28	30	85.7	756	2 US-09-032-475-4	Sequence 4, Appl
29	30	85.7	756	2 US-09-099-125A-2	Sequence 2, Appl
30	30	85.7	756	2 US-09-099-124A-2	Sequence 2, Appl
31	30	85.7	756	3 US-09-032-476-2	Sequence 2, Appl
32	30	85.7	756	3 US-08-890-854-2	Sequence 2, Appl
33	30	85.7	756	3 US-09-023-324-2	Sequence 2, Appl
34	30	85.7	756	3 US-09-168-629-15	Sequence 15, Appl
35	30	85.7	756	3 US-08-910-820-9	Sequence 9, Appl
36	30	85.7	756	4 US-09-109-986-2	Sequence 2, Appl
37	30	85.7	756	4 US-09-844-908-9	Sequence 9, Appl
38	30	85.7	756	4 US-09-868-758-4	Sequence 4, Appl
39	30	85.7	768	2 US-08-222-617A-5	Sequence 5, Appl
40	30	85.7	996	4 US-09-417-197-123	Sequence 123, App
41	30	85.7	997	4 US-09-417-197-121	Sequence 121, App
42	30	85.7	3666	2 US-08-222-617A-12	Sequence 12, Appl
43	30	85.7	3727	2 US-08-222-617A-27	Sequence 27, Appl
44	30	85.7	3778	2 US-08-222-617A-2	Sequence 2, Appl
45	29	82.9	70	3 US-09-242-050-4	Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-09-252-991A-27150  
Sequence 27150, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfeld et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 27150  
LENGTH: 829  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-27150

Query Match 91.4%; Score 32; DB 4; Length 829;  
Best Local Similarity 83.3%; Pred. No. 6.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
|||:  
Db 486 LDMSYL 491

RESULT 2  
US-09-107-532A-7054  
Sequence 7054, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDING ADDRESSES:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC

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OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/107.532A
  FILING DATE: 30-Jun-1998
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 60/085,598
    FILING DATE: 14 May 1998
    APPLICATION NUMBER: 60/051571
    FILING DATE: July 2, 1997
  ATTORNEY/AGENT INFORMATION:
    NAME: Arietello, Pamela Deneke
    REGISTRATION NUMBER: 40,489
    REFERENCE/DOCKET NUMBER: GTC-012
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (781)893-5007
    TELEFAX: (781)893-8277
  INFORMATION FOR SEQ ID NO: 7054:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 86 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      HYPOTHEICAL: YES
      ORIGINAL SOURCE:
        ORGANISM: Enterococcus faecium
      FEATURE:
        NAME/KEY: misc feature
        LOCATION: (B) LOCATION 1...86
      SEQUENCE DESCRIPTION: SEQ ID NO: 7054:
US-09-107-532A-7054

Query Match      88.6%; Score 31; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DWSF 5
DB 42 DWSF 46

RESULT 3
US-08-118-270-68
Sequence 68, Application US/08118270
General Information:
  PATENT NO. 5508384
  APPLICANT: Murphy, Randall B.
  TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
  NUMBER OF SEQUENCES: 348
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: BROWDY AND NEIMARK
    STREET: 419 Seventh Street, N.W., Suite 300
    CITY: Washington
    STATE: D.C.
    COUNTRY: USA
    ZIP: 20004
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/118,270
    FILING DATE: 09-SEP-1993
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/943,236
      FILING DATE: 10-SEP-1992
      ATTORNEY/AGENT INFORMATION:
        NAME: Townsend, Kevin G.
        REGISTRATION NUMBER: 34,033
        REFERENCE/DOCKET NUMBER: MURPHY-2A
        TELEPHONE: 202-737-3528
        TELEFAX: 202-737-3528
        TELEX: 248633
      INFORMATION FOR SEQ ID NO: 68:
        SEQUENCE CHARACTERISTICS:
          LENGTH: 277 amino acids
          TYPE: amino acid
          STRANDEDNESS: single
          TOPOLOGY: linear
          MOLECULE TYPE: peptide
PCT-US93-08528-68
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```
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 202-628-5197
  TELEFAX: 202-737-3528
  TELEX: 248633
  INFORMATION FOR SEQ ID NO: 68:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 277 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: peptide
US-08-118-270-68

Query Match      88.6%; Score 31; DB 1; Length 277;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6
DB 81 DWSFL 85

RESULT 4
PCT-US93-08528-68
Sequence 68, Application PC/TUS9308528
General Information:
  APPLICANT: New York University
  TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
  NUMBER OF SEQUENCES: 348
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: BROWDY AND NEIMARK
    STREET: 419 Seventh Street, N.W., Suite 300
    CITY: Washington
    STATE: D.C.
    COUNTRY: USA
    ZIP: 20004
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: PCT/US93/08528
    FILING DATE: 09-SEP-1993
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/943,236
      FILING DATE: 10-SEP-1992
      ATTORNEY/AGENT INFORMATION:
        NAME: Townsend, Kevin G.
        REGISTRATION NUMBER: 34,033
        REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
        TELECOMMUNICATION INFORMATION:
          TELEPHONE: 202-628-5197
          TELEFAX: 202-737-3528
          TELEX: 248633
        INFORMATION FOR SEQ ID NO: 68:
          SEQUENCE CHARACTERISTICS:
            LENGTH: 277 amino acids
            TYPE: amino acid
            STRANDEDNESS: single
            TOPOLOGY: linear
            MOLECULE TYPE: peptide
PCT-US93-08528-68

Query Match      88.6%; Score 31; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSFL 6
DB 81 DWSFL 85
```

RESULT 5  
US-08-360-606B-30  
Sequence 30, Application US/08360606B  
Patent No. 5919617  
GENERAL INFORMATION:  
APPLICANT: Jnanendra K. Bhattacharjee  
APPLICANT: Richard C. Garrad  
APPLICANT: Paul L. Skatrud  
APPLICANT: Robert P. Peery  
TITLE OF INVENTION: Methods and Reagents for  
TITLE OF INVENTION: Detecting Fungal Pathogens in a  
TITLE OF INVENTION: Biological Sample  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 S. Wacker Drive Suite 3200  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,606B  
FILING DATE: December 21, 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Berghoff, Paul H.  
REGISTRATION NUMBER: 30,243  
REFERENCE/DOCKET NUMBER: 94,319  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)913-0001  
TELEFAX: (312)913-0002  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 382 amino acid residues  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: yes  
HYPOTHETICAL: yes  
ORIGINAL SOURCE:  
ORGANISM: Candida albicans  
US-08-360-606B-30

Query Match 88.6%; Score 31, DB 2, Length 382,  
Best Local Similarity 100.0%; Pred. No. 4,3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSF 5  
DB 151 LDMSF 155

RESULT 6  
US-09-328-352-5063  
Sequence 5063, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
TITLE OF INVENTION: BAUMANNIT FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 5063  
LENGTH: 177  
TYPE: PRT

ORGANISM: Acinetobacter baumannii  
US-09-328-352-5063

Query Match 85.7%; Score 30; DB 4; Length 177;  
Best Local Similarity 66.7%; Pred. No. 2,9e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
DB 137 IDMTFL 142

RESULT 7  
US-09-328-352-7147  
Sequence 7147, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
TITLE OF INVENTION: BAUMANNIT FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 7147  
LENGTH: 365  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-7147

Query Match 85.7%; Score 30; DB 4; Length 365;  
Best Local Similarity 66.7%; Pred. No. 6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
DB 23 LDMSFL 28

RESULT 8  
US-09-107-532A-4918  
Sequence 4918, Application US/09107532A  
Patent No. 6563275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucetle-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Arinello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 4918:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 397 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (B) LOCATION 1...397  
SEQUENCE DESCRIPTION: SEQ ID NO: 4918:  
US-09-107-532A-4918

Query Match 85.7%; Score 30; DB 4; Length 397;  
Best Local Similarity 66.7%; Pred. No. 6.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
: : : :  
Db 233 IDMTFL 238

RESULT 9  
US-09-328-352-7815  
Sequence 7815, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-033PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 7815  
LENGTH: 413  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-7815

Query Match 85.7%; Score 30; DB 4; Length 413;  
Best Local Similarity 66.7%; Pred. No. 6.8e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
: : : :  
Db 183 IDMTFL 188

RESULT 10  
US-08-887-518-3  
Sequence 3, Application US/08887518  
Patent No. 5843721  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
APPLICANT: Wu, Lin  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-887-518-3

Query Match 85.7%; Score 30; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
: : : :  
Db 738 LDMSWL 743

RESULT 11  
US-09-023-321-3  
Sequence 3, Application US/09023321  
Patent No. 5844073  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
APPLICANT: Wu, Lin  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,321  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-321-3



Query Match 85.7%; Score 30; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
DB 738 LDMSWL 743

## RESULT 12

US-08-890-853-4  
Sequence 4, Application US/08890853  
Patent No. 5851812  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Moronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-853-4

Query Match 85.7%; Score 30; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
DB 738 LDMSWL 743

## RESULT 13

US-09-032-475-3  
Sequence 3, Application US/09032475  
Patent No. 5854003  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
APPLICANT: Wu, Lin  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO

STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,475  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/887,518  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-09-032-475-3

Query Match 85.7%; Score 30; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
DB 738 LDMSWL 743

## RESULT 14

US-09-099-125A-4  
Sequence 4, Application US/09099125A  
Patent No. 5916760  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Moronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,125A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:

Search completed: February 18, 2004, 14:41:50  
 Job time : 7.06579 secs.

TELEPHONE: (415) 343-4341  
 TELEFAX: (415) 343-4342  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 745 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-099-125A-4

Query Match 85.7%; Score 30; DB 2; Length 745;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
 |||||  
 DB 738 LDMSWL 743

RESULT 15  
 US-09-099-124A-4  
 Sequence 4, Application US/09099124A  
 Patent No. 5839302  
 GENERAL INFORMATION:  
 APPLICANT: Goedel, David V.  
 APPLICANT: Woronicz, John  
 TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
 STREET: 268 BUSH STREET, SUITE 3200  
 CITY: SAN FRANCISCO  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/099,124A  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/890,853  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OSMAN, RICHARD A  
 REGISTRATION NUMBER: 36,627  
 REFERENCE/DOCKET NUMBER: T97-006-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 343-4341  
 TELEFAX: (415) 343-4342  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 745 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-099-124A-4

Query Match 85.7%; Score 30; DB 2; Length 745;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
 |||||  
 DB 738 LDMSWL 743

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## OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds  
(without alignments)  
35.929 Million cell updates/sec

Title: US-09-643-260-13

Perfect score: 33

Sequence: 1 LDMSAL 6

Scoring table:

BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4231088 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgm2\_6/ptcdatc/1/1aa/5A.COMB.pep.\*
- 2: /cgm2\_6/ptcdatc/1/1aa/5B.COMB.pep.\*
- 3: /cgm2\_6/ptcdatc/1/1aa/6A.COMB.pep.\*
- 4: /cgm2\_6/ptcdatc/1/1aa/6B.COMB.pep.\*
- 5: /cgm2\_6/ptcdatc/1/1aa/PTCUS.COMB.pep.\*
- 6: /cgm2\_6/ptcdatc/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	93.9	502	4	US-09-635-872A-13
2	31	93.9	502	4	US-09-636-077A-13
3	30	90.9	118	4	US-08-311-731A-240
4	30	90.9	516	4	US-09-277-262-2
5	30	90.9	735	4	US-09-252-991A-32240
6	30	90.9	1891	2	US-08-804-198-6
7	30	90.9	1891	2	US-08-804-198-6
8	29	87.9	201	1	US-07-929-580B-5
9	29	87.9	223	1	US-07-708-885B-3
10	29	87.9	223	1	US-07-714-386-3
11	29	87.9	268	1	US-07-708-888A-3
12	29	87.9	268	1	US-07-252-991A-30879
13	29	87.9	297	4	US-09-172-952-10
14	29	87.9	345	3	US-08-858-003-14
15	29	87.9	345	3	US-08-858-003-14
16	29	87.9	345	3	US-08-997-467-34
17	29	87.9	352	3	US-09-198-452A-702
18	29	87.9	464	4	US-09-252-991A-29305
19	29	87.9	480	4	US-09-252-991A-17687
20	29	87.9	529	4	US-09-252-991A-29757
21	29	87.9	703	4	US-09-252-991A-17865
22	29	87.9	1580	2	US-08-804-227C-11
23	29	87.9	1580	2	US-08-804-198-5
24	29	87.9	3729	2	US-08-804-227C-4
25	28	84.8	208	1	US-08-631-607-3
26	28	84.8	208	1	US-09-098-358B-3
27	28	84.8	536	4	US-09-252-991A-31124

28	28	84.8	1151	4	US-09-252-991A-23596	Sequence 23596, A
29	28	84.8	1843	3	US-09-413-814-50	Sequence 50, Appl
30	28	84.8	2593	3	US-09-036-987A-2	Sequence 2, Appl
31	28	84.8	2593	3	US-09-370-700-2	Sequence 2, Appl
32	28	84.8	2593	4	US-09-603-207-2	Sequence 1, Appl
33	28	84.8	3248	1	US-08-353-700-1	Sequence 1, Appl
34	28	84.8	3248	5	PCT-US95-16216-1	Sequence 1, Appl
35	27	81.8	29	3	US-09-082-279B-1276	Sequence 1276, Ap
36	27	81.8	29	4	US-09-315-304B-1276	Sequence 1276, Ap
37	27	81.8	29	4	US-09-834-784-1276	Sequence 1276, Ap
38	27	81.8	35	3	US-09-082-279B-1427	Sequence 1427, Ap
39	27	81.8	35	4	US-09-315-304B-1427	Sequence 1427, Ap
40	27	81.8	35	4	US-09-834-784-1427	Sequence 1427, Ap
41	27	81.8	45	3	US-09-040-285A-9	Sequence 9, Appl
42	27	81.8	80	3	US-09-040-285A-3	Sequence 3, Appl
43	27	81.8	111	4	US-09-107-532A-5707	Sequence 5707, Ap
44	27	81.8	209	3	US-09-040-285A-8	Sequence 8, Appl
45	27	81.8	229	3	US-09-040-285A-7	Sequence 7, Appl

## ALIGNMENTS

RESULT 1  
US-09-635-872A-13  
; Sequence 13, Application US/09635872A  
; Patent No. 6534300  
; GENERAL INFORMATION:  
; APPLICANT: CANFIELD, WILLIAM  
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASE:  
; FILE REFERENCE: 195613US0  
; CURRENT APPLICATION NUMBER: US/09/635, 872A  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/153, 831  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 13  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-635-872A-13

Query Match 93.9%; Score 31; DB 4; Length 502;  
Best Local Similarity 83.3%; Pred. No. 4,8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 LDMSAL 6  
372 LDMSAM 377

RESULT 2  
US-09-636-077A-13  
; Sequence 13, Application US/09636077A  
; Patent No. 6537785  
; GENERAL INFORMATION:  
; APPLICANT: CANFIELD, WILLIAM  
; TITLE OF INVENTION: METHODS OF TREATING LYSOSOMAL STORAGE DISEASE  
; FILE REFERENCE: 195612US0  
; CURRENT APPLICATION NUMBER: US/09/636, 077A  
; CURRENT FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/153, 831  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 13  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-636-077A-13

Query Match 93.9%; Score 31; DB 4; Length 502;

Best Local Similarity 83.3%; Pred. No. 4.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
Db 372 LDMSAM 377

## RESULT 3

US-08-311-731A-240  
Sequence 240, Application US/08311731A  
Patent No. 6583266  
GENERAL INFORMATION:  
APPLICANT: SMITH, DOUGLAS  
APPLICANT: MAO, JEN-I  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 411  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,731A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: GATES, EDWARD R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: C0044/7125  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/720-3500  
TELEFAX: 617/720-2441  
INFORMATION FOR SEQ ID NO: 240:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Mycobacterium leprae  
US-08-311-731A-240

Query Match 90.9%; Score 30; DB 4; Length 118;  
Best Local Similarity 83.3%; Pred. No. 1.6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
Db 93 LDMSAV 98

## RESULT 4

US-09-277-262-2  
Sequence 2, Application US/09277262  
Patent No. 6395482  
GENERAL INFORMATION:  
APPLICANT: KAREYIORGOU, Maria  
APPLICANT: GOGOS, Joseph A  
TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE  
TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED  
FILE REFERENCE: 600-1-223 CIP

CURRENT APPLICATION NUMBER: US/09/277,262  
CURRENT FILING DATE: 1999-03-26  
EARLIER APPLICATION NUMBER: 09/229,530  
EARLIER FILING DATE: 1999-01-13  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 516  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-277-262-2

Query Match 90.9%; Score 30; DB 4; Length 516;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
Db 231 LDMSL 236

## RESULT 5

US-09-252-991A-32240  
Sequence 32240, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: MARC J. RUBENFIELD et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196,116  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 32240  
LENGTH: 735  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-32240

Query Match 90.9%; Score 30; DB 4; Length 735;  
Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
Db 379 VDMSAL 384

## RESULT 6

US-08-804-227C-12  
Sequence 12, Application US/08804227C  
Patent No. 5876991  
GENERAL INFORMATION:  
APPLICANT: Dehoff, Bradley S.  
APPLICANT: Kuhstoss, Stuart A.  
APPLICANT: Roestock, Paul R., Jr.  
APPLICANT: Sutton, Kimberly L.  
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: THOMAS G. PLANT 1501  
STREET: LILLY CORPORATE CENTER  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: USA  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS  
SOFTWARE: ASCII(DOS) Text only  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/804,227C  
FILING DATE: February 21, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Plant, Thomas, G.  
REGISTRATION NUMBER: 35,784  
REFERENCE/DOCKET NUMBER: X-8231  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 317-276-2459  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1891 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-804-227C-12

Query Match 90.9%; Score 30; DB 2; Length 1891;  
Best Local Similarity 83.3%; Pred. No. 2.8e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMVAL 6  
DB 904 LDMVAL 909

RESULT 7  
US-08-804-198-6  
Sequence 6, Application US/08804198  
Patent No. 5945320  
GENERAL INFORMATION:  
APPLICANT: Burett, Stanley G.  
APPLICANT: Kuhnroos, Stuart A.  
APPLICANT: Rao, Negaraja R.  
APPLICANT: Richardson, Mark A.  
APPLICANT: Roelbeck, Paul R., Jr.  
TITLE OF INVENTION: PLATENOIDE SYNTHASE GENE  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PAUL R. CANTRELL 1138  
STREET: LILLY CORPORATE CENTER  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: USA  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Macintosh 7.0  
SOFTWARE: Microsoft Word 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/804,198  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CANTRELL, PAUL R.  
REGISTRATION NUMBER: 36,470  
REFERENCE/DOCKET NUMBER: P9113  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 317-276-3885  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1891 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-804-198-6

Query Match 90.9%; Score 30; DB 2; Length 1891;  
Best Local Similarity 83.3%; Pred. No. 2.8e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMVAL 6  
DB 904 LDMVAL 909

RESULT 8  
US-07-929-580B-5  
Sequence 5, Application US/07929580B  
Patent No. 5426181  
GENERAL INFORMATION:  
APPLICANT: Lee, Tae Ho  
APPLICANT: Lee, Gene W.  
APPLICANT: Vilcek, Jan  
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-14,  
TITLE OF INVENTION: DNA Coding Therefor and Uses Thereof  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Broadway and Neilmark  
STREET: 419 Seventh Street, NW  
CITY: Washington  
STATE: DC  
COUNTRY: US  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/929,580B  
FILING DATE: 19920814  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/640,492  
FILING DATE: 14-JAN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Guy Kevin  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: LEE25\VLCEK-2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 201 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-929-580B-5

Query Match 87.9%; Score 29; DB 1; Length 201;  
Best Local Similarity 83.3%; Pred. No. 4.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMVAL 6  
DB 180 LDMVAL 185

RESULT 9  
US-07-708-885B-3  
Sequence 3, Application US/07708885B  
Patent No. 5245017  
GENERAL INFORMATION:  
APPLICANT: Maswoswe, Sibusiswe M.  
APPLICANT: Briggsman, Joseph V.  
APPLICANT: Toth, Carol A.  
APPLICANT: Thomas, Peter  
TITLE OF INVENTION: Method for Isolating  
TITLE OF INVENTION: CEA-Binding Protein

NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lahive & Cockfield  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 720kb storage  
COMPUTER: IBM XT  
OPERATING SYSTEM: DOS 3.30  
SOFTWARE: Word Perfect 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/708,8858  
FILING DATE: 19910531  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 223 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: C-reactive protein  
PUBLICATION INFORMATION:  
AUTHORS: Lei, Ke-Jian  
AUTHORS: Liu, Teresa  
AUTHORS: Zou, Gerald  
AUTHORS: Soravia, Emilia  
AUTHORS: Liu, Teh-Yung  
AUTHORS: Goldman, Neil D.  
TITLE: Genomic Sequence for Human  
JOURNAL: J. of Biological Chemistry  
VOLUME: 260  
ISSUE: 24  
PAGES: 13377-83  
DATE: 25 OCT 1985  
US-07-708-8858-3

Query Match 87.9%; Score 29; DB 1; Length 223;  
Best Local Similarity 83.3%; Pred. No. 4.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
DB 202 LDMSAL 207

RESULT 10  
US-07-714-386-3  
Sequence 3, Application US/07114386  
Patent No. 5278290  
GENERAL INFORMATION:  
APPLICANT: Thomas, Peter  
APPLICANT: Toth, Carol A.  
APPLICANT: Maswowe, Sibustsiwe M.  
APPLICANT: Brigman, Joseph V.  
TITLE OF INVENTION: Binding Protein for  
NUMBER OF SEQUENCES: 4  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lahive & Cockfield  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02109  
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 720kb storage  
COMPUTER: IBM XT  
OPERATING SYSTEM: DOS 3.30  
SOFTWARE: Word Perfect 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/714,386  
FILING DATE: 19910531  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 223 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: C-reactive protein  
PUBLICATION INFORMATION:  
AUTHORS: Lei, Ke-Jian  
AUTHORS: Liu, Teresa  
AUTHORS: Zou, Gerald  
AUTHORS: Soravia, Emilia  
AUTHORS: Liu, Teh-Yung  
AUTHORS: Goldman, Neil D.  
TITLE: Genomic Sequence for Human  
JOURNAL: J. of Biological Chemistry  
VOLUME: 260  
ISSUE: 24  
PAGES: 13377-83  
DATE: 25 OCT 1985  
US-07-714-386-3

Query Match 87.9%; Score 29; DB 1; Length 223;  
Best Local Similarity 83.3%; Pred. No. 4.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
DB 202 LDMSAL 207

RESULT 11  
US-07-708-888A-3  
Sequence 3, Application US/07708888A  
Patent No. 5281697  
GENERAL INFORMATION:  
APPLICANT: Toth, Carol A.  
APPLICANT: Maswowe, Sibustsiwe M.  
APPLICANT: Brigman, Joseph V.  
TITLE OF INVENTION: CEA-Binding Protein  
NUMBER OF SEQUENCES: 4  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lahive & Cockfield  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 720kb  
MEDIUM TYPE: storage  
COMPUTER: IBM XT  
OPERATING SYSTEM: DOS 3.30  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/708,888A  
FILING DATE: 19910531  
PRIOR APPLICATION DATA:



Query Match 87.9%; Score 29; DB 3; Length 345;  
 Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDM5AL 6  
 |||||  
 DB 43 LDM5VL 48

## RESULT 15

US-09-078-166-34

; Sequence 34, Application US/09078166

; Patent No. 6063561

; GENERAL INFORMATION:

; APPLICANT: Katz, Leonard

; APPLICANT: Staeg, Diane L.

; APPLICANT: Summers Jr., Richard G.

; APPLICANT: Ruan, Xiaolan

; APPLICANT: Pereda-Lopez, Ana

; TITLE OF INVENTION: NOVEL POLYPEPTIDE DERIVATIVES

; TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Abbott Laboratories

; STREET: 100 Abbott Park Rd.

; CITY: Abbott Park

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: PasteSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/078,166

; FILING DATE: 16-MAY-1979

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Dianne Casulo

; REGISTRATION NUMBER: P-40,943

; REFERENCE/DOCKET NUMBER: 4952.US.P2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (847)-938-3137

; TELEFAX: (847)-938-2623

; TELEX:

; INFORMATION FOR SEQ ID NO: 34:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 345 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 6063561e

; US-09-078-166-34

Query Match 87.9%; Score 29; DB 3; Length 345;  
 Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDM5AL 6  
 |||||  
 DB 43 LDM5VL 48

Search completed: February 18, 2004, 14:41:50  
 Job time : 8.06579 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3664 Seconds  
(without alignments)  
89.145 Million cell updates/sec

Title: US-09-643-260-12

Perfect score: 36  
Sequence: 1 LDYSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriopl:\*
- 17: sp\_archaeop:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	94.4	241	16 Q98D63	Q98D63 rhizobium 1
2	34	94.4	281	16 Q8NVL6	Q8NVL6 staphylococ
3	34	94.4	282	16 Q933C8	Q933C8 staphylococ
4	34	94.4	282	16 Q065S1	Q065S1 mycobacteri
5	33	91.7	195	11 Q8BR0	Q8BR0 mus musculu
6	33	91.7	237	11 Q9JMP2	Q9JMP2 mus musculu
7	33	91.7	263	11 Q9CRS3	Q9CRS3 mus musculu
8	33	91.7	392	11 Q99KPS	Q99KPS mus musculu
9	32	88.9	66	16 Q8CKO2	Q8CKO2 yerisina pe
10	32	88.9	93	12 Q70791	Q70791 rice yellow
11	32	88.9	107	2 Q684S5	Q684S5 ancylobacte
12	32	88.9	138	2 Q8GBK5	Q8GBK5 uncultured
13	32	88.9	138	2 Q8GBK0	Q8GBK0 uncultured
14	32	88.9	138	2 Q8GBJ4	Q8GBJ4 uncultured
15	32	88.9	153	16 Q8XBY6	Q8XBY6 escherichia
16	32	88.9	168	16 Q91265	Q91265 pseudomona

17	32	88.9	179	11 Q8BZU5	Q8BZU5 mus musculu
18	32	88.9	193	12 Q99FJ7	Q99FJ7 human echov
19	32	88.9	195	5 Q18653	Q18653 caenorhabd1
20	32	88.9	230	10 Q945X8	Q945X8 theobroma c
21	32	88.9	244	10 Q945Y3	Q945Y3 theobroma c
22	32	88.9	248	4 Q96T10	Q96T10 homo sapien
23	32	88.9	250	10 Q945X9	Q945X9 theobroma c
24	32	88.9	251	16 Q9K8S3	Q9K8S3 bacillus ha
25	32	88.9	255	10 Q945Y4	Q945Y4 theobroma c
26	32	88.9	255	10 Q945Z3	Q945Z3 theobroma c
27	32	88.9	255	10 Q945Y5	Q945Y5 theobroma c
28	32	88.9	259	16 Q826N5	Q826N5 salmone
29	32	88.9	271	17 Q978V7	Q978V7 thermoplas
30	32	88.9	278	6 Q9XTA8	Q9XTA8 oryctolagus
31	32	88.9	302	16 Q8X8Q1	Q8X8Q1 escherichia
32	32	88.9	312	10 Q9AYF3	Q9AYF3 oryza sativ
33	32	88.9	315	13 Q91838	Q91838 coturnix co
34	32	88.9	349	5 Q17692	Q17692 caenorhabd1
35	32	88.9	379	16 Q82935	Q82935 salmone
36	32	88.9	382	2 Q68661	Q68661 actinobacil
37	32	88.9	382	10 Q8H2C3	Q8H2C3 persea amer
38	32	88.9	383	16 Q8FKN0	Q8FKN0 escherichia
39	32	88.9	386	16 Q84474	Q84474 chlamydia t
40	32	88.9	391	16 P95247	P95247 mycobacteri
41	32	88.9	407	2 Q55047	Q55047 shigella so
42	32	88.9	414	2 Q950Y1	Q950Y1 pleiomonas
43	32	88.9	414	2 Q9F738	Q9F738 shigella so
44	32	88.9	414	11 Q9CXT6	Q9CXT6 mus musculu
45	32	88.9	415	16 Q8VJK7	Q8VJK7 mycobacteri

## ALIGNMENTS

## RESULT 1

Q98D63 PRELIMINARY; PRT; 241 AA.

AC Q98D63, PRELIMINARY; PRT; 241 AA.  
 DT 01-OCT-2001 (TREMBLrel. 18, Created)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Putative hydrolase, ripening-related protein-like.  
 GN MUR4841.  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 OX NCBI\_TaxID=381;  
 RN [1]  
 RP STRAIN=MAF303099;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Matanabe A., Idehara K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.,  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 Mesorhizobium loti."  
 RL DNA Res. 7:331-338(2000).  
 DR EMBL; AF003005; BAB51408.1; -;  
 DR InterPro; IPR006402; HAD-SF-IA-v3.  
 DR InterPro; IPR005834; Hydrolase.  
 DR Pfam; PF00702; Hydrolase; 1.  
 DR TIGRPFAM; TIGR01509; HAD-SF-IA-v3; 1.  
 KW Hydrolase; Complete proteome.  
 SQ SEQUENCE 241 AA; 27332 MW; 6AB5B55907CC27A CRC64;

Query Match 94.4%; Score 34; DB 16; Length 241;

Best Local Similarity 83.3%; Pred. No. 1.2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 90 LDYSWL 95

## RESULT 2

Q8NVL6 PRELIMINARY; PRT; 281 AA.  
 AC Q8NVL6; 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DE Hypothetical protein MW1944.  
 GN MW1944.  
 OS Staphylococcus aureus (strain MW2).  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=196620;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=23040717; PubMed=12044378;  
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,  
 RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,  
 RA Yamamoto K., Hiramatsu K.;  
 RT "Genome and virulence determinants of high virulence community-  
 acquired MRSA.";  
 RL Lancet 359:1819-1827(2002).  
 DR EMBL; AP004828; BAB5809.1;-  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 281 AA; 33223 MW; 824E3760C6698B42 CRC64;

Query Match 94.4%; Score 34; DB 16; Length 281;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6  
 DB 132 LDYSWL 137

## RESULT 3

Q932C8 PRELIMINARY; PRT; 282 AA.  
 AC Q932C8; 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DE Hypothetical protein SAV0804.  
 GN SAV0804.  
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=158878;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=21311952; PubMed=11418146;  
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,  
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Ilan J.-O., Ito T.,  
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,  
 RA Mizutani-U Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,  
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,  
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,  
 RA Hatori M., Ogasawara N., Hayashi H., Hiramatsu K.;  
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus  
 aureus.";  
 RL Lancet 357:1225-1240(2001).  
 DR EMBL; AP003360; BAB5696.1;-  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 282 AA; 33281 MW; 3529EEF85F1B1A6 CRC64;

Query Match 94.4%; Score 34; DB 16; Length 282;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6  
 DB 132 LDYSWL 137

RESULT 4  
 O06551 PRELIMINARY; PRT; 282 AA.  
 AC O06551; 01-JUL-1997 (TREMBlrel. 04, Created)  
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
 DE Hypothetical 30.9 kDa protein (O-methyltransferase, putative).  
 GN OMT OR RV1153C OR MTC165.20C OR MT1187.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37Rv;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Baaham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornby T., Jaffe K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sutcliffe J.E., Taylor K., Whitehead S., Barrett B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,  
 RA Kolony J.F., Nelson W.C., Umayam L.A., Smolaleva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikala A.,  
 RA Bhat W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains.";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z95584; CAB09012.1;-  
 DR EMBL; AR006966; AKK4544.1;-  
 DR TIGR; MT1187;-  
 DR TubercuList; RV1153C;-  
 DR InterPro; IPR003455; DUF142.  
 DR Pfam; PF02409; Omt N; 1.  
 KW Hypothetical protein; Transferase; Methyltransferase;  
 KW Complete proteome.  
 SQ SEQUENCE 282 AA; 30887 MW; 41760C508774154A CRC64;

Query Match 94.4%; Score 34; DB 16; Length 282;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6  
 DB 142 LDYSWL 147

RESULT 5  
 Q8BRB0 PRELIMINARY; PRT; 195 AA.  
 AC Q8BRB0; 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DE Hypothetical protein.  
 GN Mus musculus (Mouse).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]

Query Match 94.4%; Score 34; DB 16; Length 282;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; PubMed=12466851;
RA MEDLINE=22354683; PubMed=12466851;
RA the FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK045045; BAC32196.1; -.
KM Hypothetical protein.
SQ SEQUENCE 195 AA; 22669 MW; 6C33550846800762 CRC64;

Query Match 91.7%; Score 33; DB 11; Length 195;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDYSWL 6
Db 58 VDYSWL 63

RESULT 6
O9JMF2 PRELIMINARY; PRT: 237 AA.
AC O9JMF2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Unknown protein (Fragment).
GN 3322402L07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20145471; PubMed=10679242;
RA Inoue S., Sano H., Ohta M.;
RT "Growth suppression of Escherichia coli by induction of expression of
RT mammalian genes with transmembrane or Arpase domains.";
RL Biochem. Biophys. Res. Commun. 258:553-561(2000).
DR EMBL; AB030195; BAA92758.1; -.
DR MGI; MGI:1921273; 3322402L07RIK.
FT NON_TER
SQ SEQUENCE 237 AA; 26633 MW; B0928A9C7A41D377 CRC64;

Query Match 91.7%; Score 33; DB 11; Length 237;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDYSWL 6
Db 167 VDYSWL 172

RESULT 7
O9CRS3 PRELIMINARY; PRT: 263 AA.
AC O9CRS3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE 17 days embryo head cDNA, RIKEN full-length enriched library,
DE clone:3322402L07 product:hypothetical protein, full insert sequence
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;

```

```

RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carlini P., Fukuda S., Fukunishi Y., Furuno M.,
RA Haneagaki T., Hara A., Hayatsu N., Hiramoto K., Hirakata T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito K., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA the FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino Y., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami Y., Kaishiki M.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
DR EMBL; AK014383; BAB29312.2; -.
KM Hypothetical protein.
FT NON_TER
SQ SEQUENCE 263 AA; 30215 MW; 692304F88AD341AF CRC64;

Query Match 91.7%; Score 33; DB 11; Length 263;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDYSWL 6
Db 126 VDYSWL 131

RESULT 8

```

099KPS  
ID 099KPS PRELIMINARY; PRT; 392 AA.  
AC 099KPS;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Similar to cyclin 1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Straubeberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC004071; AA04071.1; -  
DR InterPro; IPR001680; WD40.  
DR Pfam; PF00400; WD40; 3.  
DR SMART; SM00320; WD40; 2.  
DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
KW Cyclin; Repeat; WD repeat.  
SQ SEQUENCE 392 AA; 44527 MW; 4B2E5CBAJA22075A CRC64;

Query Match 91.7%; Score 33; DB 11; Length 392;  
Best Local Similarity 83.3%; Pred. No. 3.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSWL 6  
DB 384 VDYSWL 389

RESULT 9  
08CKO2 PRELIMINARY; PRT; 66 AA.  
AC 08CKO2;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Hypothetical.  
GN Y3132.  
OS Yersinia pestis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Yersinia.  
OX NCBI\_TaxID=632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-KIMS / Bivovar Mediaeval18;  
RX MEDLINE=22137863; PubMed=1142430;  
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,  
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,  
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,  
RA Straley S.C., McDonough K.A., Nilles M.L., Mason J.S., Blattner F.R.,  
RA Perry R.D.;  
RT "Genome sequence of Yersinia pestis KIM";  
RL J. Bacteriol. 184:4601-4611(2002).  
DR EMBL; AE013914; AAM86682.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 66 AA; 7780 MW; EE5586B890246D8 CRC64;

Query Match 88.9%; Score 32; DB 16; Length 66;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DYSWL 6  
DB 46 DYSWL 50

RESULT 10  
070791 PRELIMINARY; PRT; 93 AA.  
AC 070791;

DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Hypothetical protein.  
GN 6.  
OS Rice yellow stunt virus.  
OC Viruses; ssRNA negative-strand viruses; Nonnegavirales;  
OC Rhabdoviridae; Nucleorhabdovirus.  
OX NCBI\_TaxID=59380;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pang R., Luo Z., Zhao H.;  
RT "Novel structure of the rice yellow stunt virus genome: a plant  
RT rhabdovirus encodes seven genes."  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB011257; BAA25159.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 93 AA; 10543 MW; A10CC3BD41F88305 CRC64;

Query Match 88.9%; Score 32; DB 12; Length 93;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSWL 6  
DB 63 IDYSWI 68

RESULT 11  
068455 PRELIMINARY; PRT; 107 AA.  
ID 068455;  
AC 068455;  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Halocid dehalogenase (Fragment).  
OS Ancylobacter aquaticus.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhodimicrobiaceae; Ancylobacter.  
OX NCBI\_TaxID=100;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CN13;  
RA Fortin N., Fulthorpe R.R., Allen D.G., Greer C.W.;  
RT "Molecular analysis of bacterial isolates and total community DNA from  
RT kraft pulp mill effluent treatment systems."  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF043240; AAC08952.1; -  
DR HSP; Q60099; IA06.  
DR InterPro; IPR005833; Hlgmase/hydrolase.  
DR InterPro; IPR005834; Hydrolase.  
DR Pfam; PF00702; Hydrolase; 1.  
DR PRINTS; PR00413; HADHALOGNASE.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 107 AA; 12177 MW; 2B77D4354B5D0C8 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 107;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSWL 6  
DB 6 LDYSWL 11

RESULT 12  
08GBKS PRELIMINARY; PRT; 138 AA.  
ID 08GBKS;  
AC 08GBKS;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

```

DE Putative halocarboxylic acid dehalogenase (Fragment).
GN DEHII.
OS uncultured bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP SEQUENCE FROM N.A.
RA Marchael J.R., Weightman A.J.;
RT "Relating the cultivable gene pool with the metagenome pool in activated
   sludge.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ511306; CAD54096.1; -.
FT NON TER 1
FT NON TER 138
SQ SEQUENCE 138 AA; 15508 MW; A10B803019693F53 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 138;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
DB 6 LEYSWL 11

RESULT 13
Q8GBKO PRELIMINARY; PRT; 138 AA.
AC Q8GBKO;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative halocarboxylic acid dehalogenase (Fragment).
GN DEHII.
OS uncultured bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP SEQUENCE FROM N.A.
RA Marchael J.R., Weightman A.J.;
RT "Relating the cultivable gene pool with the metagenome pool in activated
   sludge.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ511311; CAD54101.1; -.
FT NON TER 1
FT NON TER 138
SQ SEQUENCE 138 AA; 15643 MW; 3F31CE5C83979082 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 138;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
DB 6 LEYSWL 11

RESULT 14
Q8GBJ4 PRELIMINARY; PRT; 138 AA.
AC Q8GBJ4;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative halocarboxylic acid dehalogenase (Fragment).
GN DEHII.
OS uncultured bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP SEQUENCE FROM N.A.
RA Marchael J.R., Weightman A.J.;
RT "Relating the cultivable gene pool with the metagenome pool in activated

```

```

RT sludge.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ511319; CAD54109.1; -.
FT NON TER 1
FT NON TER 138
SQ SEQUENCE 138 AA; 15525 MW; 9C48CD30E1C42F40 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 138;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6
DB 6 LEYSWL 11

RESULT 15
Q8XBY6 PRELIMINARY; PRT; 153 AA.
AC Q8XBY6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein 20706.
GN 20706 OR EC30606.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Groetbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potomousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Okubo E., Nakayama K., Murata T., Tanaka M., Toke T.,
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shingawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
   O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22 (2001).
DR EMBL; AE005236; AAG54901.1; -.
DR EMBL; AP002552; BAB34029.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 153 AA; 17334 MW; 1AD056E0EAA29C65 CRC64;

Query Match 88.9%; Score 32; DB 16; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSW 5
DB 83 LDYSW 87

```

Search completed: February 18, 2004, 14:35:52  
 Job time : 19.3684 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds  
(without alignments)  
79.423 Million cell updates/sec

Title: US-09-643-260-12  
Perfect score: 36  
Sequence: 1 LDYSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

```
Searched: .127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863
```

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SW1BBProc\_41: \*

**Pred. No.** is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	33	91.7	404	1	ADMR_HUMAN	O15218 homo sapien
2	32	88.9	94	1	VLYS_BPAP5	Q9C117 bacteriophag
3	32	88.9	229	1	HAD2_P58P	P24070 pseudomonae
4	32	88.9	253	1	HAD_XANUV	O60099 xanthobacte
5	32	88.9	259	1	ABGR_SALTU	P67068 salmonella
6	32	88.9	302	1	ABGR_ECOLI	P77744 escherichia
7	32	88.9	313	1	TRF1_CHICK	Q90876 gallus gall
8	32	88.9	400	1	AAT_RHILP	O86459 rhizobium l
9	32	88.9	524	1	VGLG_RABAV	O08089 rabies viru
10	32	88.9	684	1	XYNA_CALSR	P40944 caldicellulu
11	32	88.9	735	1	PCT_BRWCH	O47162 erwinia chr
12	32	88.9	1039	1	GNNE_CALSA	P10474 c endoglucos
13	31	86.1	200	1	VE15_HAEIN	P44173 haemophilus
14	31	86.1	431	1	UL78_HCVNA	P16751 human cytom
15	31	86.1	745	1	IKKA_HUMAN	O15111 h inhibitory
16	31	86.1	745	1	IKKA_MOUSE	O60680 m inhibitory
17	31	86.1	756	1	IKKB_HUMAN	O14920 homo sapien
18	31	86.1	757	1	IKKB_MOUSE	O88351 mus muscul
19	31	86.1	757	1	IKKB_RAT	Q9qy78 rattus norv
20	30	83.3	225	1	YMBB_BACSU	P39585 bacillus su
21	30	83.3	394	1	MPGS_ABRPE	Q9ydm5 aeropyrum f
22	30	83.3	460	1	GNJC_CLOFO	P37701 clostridium
23	30	83.3	460	1	GNJC_CLOCE	P37699 clostridium
24	30	83.3	566	1	FOIM_COXHU	P45650 coxiella bi
25	30	83.3	670	1	ACLI_NEURU	O6X097 neurospora
26	30	83.3	674	1	ACLI_SORNA	O3J968 bordetia me
27	30	83.3	768	1	IVRC_STRCO	Q93512 streptomyces
28	30	83.3	868	1	NI80_YEAST	P33420 saccharomyces
29	30	83.3	1029	1	YFCS_YEAST	P43571 saccharomy
30	30	83.3	1091	1	ACYL_MOUSEB	O91592 mus muscul
31	30	83.3	1100	1	ACYL_RAT	P16638 rattus norv
32	30	83.3	1101	1	ACYL_HUMAN	P53356 homo sapien
33	29	80.6	167	1	YMH6_CAEBL	P34473 caenorhabdi

34	29	80.6	191	1	YCB1	ECOL1	P37904	escherichia
35	29	80.6	217	1	YVYE	BAC5	P32437	bacillus su
36	29	80.6	224	1	DEH2	MORSP	O01329	moxarella s
37	29	80.6	224	1	HAD2	PSEPU	O59128	pseudomonas
38	29	80.6	227	1	HAD1	PSEPU	O52087	pseudomonas
39	29	80.6	227	1	HAD	PSEFL	O59666	pseudomonas
40	29	80.6	232	1	HAD	PSESP	O53464	pseudomonas
41	29	80.6	233	1	MTGA	NRIMA	O54293	neisseria m
42	29	80.6	244	1	MOB2	SCHPO	O74558	schizosaccha
43	29	80.6	252	1	ARCPU		O28455	archaeoglob
44	29	80.6	261	1	YHRQ	ECOL1	P45543	escherichia
45	29	80.6	267	1	EBAG	PLASP	P80036	flavobacter

## ALIGNMENTS

ID	ADMR_HUMAN	STANDARD;	PRT;	404	AA.
AC	015219;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Adrenomedullin receptor (AM-R).				
GN	ADMR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98042541; PubMed=9367907;				
RA	Haenze J., Dittlich K., Dotisch J., Rascher W.;				
RT	"Molecular cloning of a novel human receptor gene with homology to the				
RT	rat adrenomedullin receptor and high expression in heart and immune				
RT	system.";				
RL	Biochem. Biophys. Res. Commun. 240:183-188(1997).				
CC	- FUNCTION: RECEPTOR FOR ADRENOMEDULLIN. THE ACTIVITY OF THIS				
CC	RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE				
CC	CYCLASE (BY SIMILARITY).				
CC	- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE,				
CC	IMMUNE SYSTEM, ADRENAL GLAND AND LIVER.				
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	HIGHEST RESEMBLANCE WITH THE RDC1 ORPHAN RECEPTOR.				
CC	-----				
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CC	or send an email to <a href="mailto:license@fdb-rib.ch">license@fdb-rib.ch</a> ).				
CC	-----				
DR	EMBL, Y13583; CA473910.1; -.				
DR	PIR, JCS784; JCS784.				
DR	GeneW; HGNC:13708; ADMR.				
DR	MIM; 605307; -.				
DR	GO; GO:0016021; C:Integral to membrane; TAS.				
DR	InterPro; IPR000276; GPCR_Rhodpsn.				
DR	Pfam; PF00001; 7tm.1.1.				
DR	PRINTS; PR00237; GPCRHHODPSN.				
DR	PROSITE; PS00237; G_PROTEIN_REC_P1.1; 1.				
DR	PROSITE; PS0262; G_PROTEIN_REC_P2.1; 1.				
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.				
FT	DOMAIN 1	57			
FT	TRANSMEM	58	79		
FT	DOMAIN	80	90		
FT	TRANSMEM	91	113		
FT	DOMAIN	114	127		
FT	TRANSMEM	128	149		
FT	DOMAIN	150	170		
FT	CYTOPLASMIC (POTENTIAL).				

```

FT TRANSNM 171 193 4 (POTENTIAL).
FT DOMAIN 194 217 EXTRACELLULAR (POTENTIAL).
FT TRANSNM 218 239 5 (POTENTIAL).
FT DOMAIN 240 258 CYTOPLASMIC (POTENTIAL).
FT TRANSNM 259 280 6 (POTENTIAL).
FT DOMAIN 281 299 EXTRACELLULAR (POTENTIAL).
FT TRANSNM 300 320 7 (POTENTIAL).
FT DOMAIN 321 404 CYTOPLASMIC (POTENTIAL).
FT DISULFID 126 202 BY SIMILARITY.
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 404 AA; 45323 MW; EP187ECDF2DC6C1 CRC64;

Query Match 91.7%; Score 33; DB 1; Length 404;
Best Local Similarity 83.3%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSWL 6
DB 115 LDYTWL 120

RESULT 2
VLVS BPAPS STANDARD; PRT; 94 AA.
AC Q9T17;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative lysate protein S (P11).
GN 11.
OS Bacteriophage ABSE-1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
OC NCBI_TaxID=106199;
RN [1]
RP MEDLINE=99420383; PubMed=10489345;
RA van der Wijk F., Dulleman A.M., Verbeek M., van den Heuvel J.F.J.M.;
RT "Isolation and characterization of ABSE-1, a bacteriophage infecting
the secondary endosymbiont of acrythosiphon pisum.";
RL Virology 262:104-113 (1999).
CC -1- PUNCTATION: ESSENTIAL FOR LYSIS OF THE BACTERIAL CELL WALL BY
DISRUPTING THE CELL MEMBRANE, THEREBY GIVING HYDROLYTIC ENZYMES
ACCESS TO THE CELL WALL (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LAMBDA PHAGE S PROTEIN FAMILY.
CC -----
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CC -----
EMBL: AF157835; AAF03954.1; -
DR InterPro: IPR006481; holin_lambda.
DR Pfam: PF05106; Phage_holin_3; 1.
DR TIGRfam: TIGR01594; holin_lambda; 1.
KW Phage lysate protein.
SQ SEQUENCE 94 AA; 10589 MW; C3E81A3181150120 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DYSWL 6
DB 66 DYSWL 70

RESULT 3
HAD2_PSESP STANDARD; PRT; 229 AA.
ID_HAD2_PSESP

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AC P24070;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 2-haloalkanoic acid dehalogenase II (EC 3.8.1.2) (L-2-haloacid
dehalogenase II) (Haloalkanoic acid halohydrilase II) (DHCHII).
OS Pseudomonas sp. (strain CBS3).
OC Bacteria; Proteobacteria.
OC NCBI_TaxID=306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139597; PubMed=1995594;
RA Schneider B., Mueller R., Frank R., Lingens F.;
RT "Complete nucleotide sequences and comparison of the structural genes
of two 2-haloalkanoic acid dehalogenases from Pseudomonas sp. strain
CBS3.";
RL J. Bacteriol. 173:1530-1535 (1991).
CC -1- CATALYTIC ACTIVITY: (S)-2-haloacid + H(2)O = (R)-2-hydroxyacid +
halide.
CC -1- SIMILARITY: BELONGS TO THE 2-HALOALKANOIC ACID DEHALOGENASE
FAMILY.
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CC -----
EMBL: M62909; AAA25833.1; -
DR PIR; B38452; B38452.
DR HSSP; Q53464; 12RN.
DR InterPro: IPR006328; HAD_II.
DR InterPro: IPR006388; HAD_SF_IA_V2.
DR InterPro: IPR005833; Hlgase/hydrilase.
DR InterPro: IPR005834; Hydrolase.
DR Pfam: PF00702; Hydrolase; 1.
DR PRINTS; PR00413; HADHALOGENASE.
DR TIGRfam: TIGR01493; HAD-SF-IA-V2; 1.
DR TIGRfam: TIGR01428; HAD_type_II; 1.
KW Hydrolase.
FT ACT SITE
SQ SEQUENCE 10 10 NUCLEOPHILE (BY SIMILARITY).
FT ACT SITE 229 AA; 25712 MW; A77AA63C97DD40AB CRC64;

Query Match 88.9%; Score 32; DB 1; Length 229;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSWL 6
DB 45 LDYSWL 50

RESULT 4
HAD_XANNU STANDARD; PRT; 253 AA.
ID_HAD_XANNU
AC Q60099; Q56757;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 2-haloalkanoic acid dehalogenase (EC 3.8.1.2) (L-2-haloacid
dehalogenase) (Haloalkanoic acid halohydrilase).
GN DHB.
OS Xanthobacter autotrophicus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hyphomicrobiaceae; Xanthobacter.
OC NCBI_TaxID=280;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-18.
RX STRAIN=GJ10;
RX MEDLINE=92078101; PubMed=1744048;
RA van der Ploeg J., van Hall G., Janssen D.B.;

```

RT "Characterization of the haloacid dehalogenase from Xanthobacter  
 RT autotrophicus GJ10 and sequencing of the dh1b gene.";  
 RL J. Bacteriol. 173:7925-7933(1991).  
 RN [2]  
 RP SEQUENCE OF 1-122 FROM N.A.  
 RC STRAIN=GJ10;  
 RX MEDLINE=9606306; PubMed=7580000;  
 RA van der Ploeg J., Janssen D.B.;  
 RT "Sequence analysis of the upstream region of dh1b, the gene encoding  
 RT haloalkanoic acid dehalogenase of Xanthobacter autotrophicus GJ10.";  
 RL Biodegradation 6:257-263(1995).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) AND REVISION TO 84.  
 RC STRAIN=GJ10;  
 RX MEDLINE=98070500; PubMed=9407083;  
 RA Ridder I.S., Rozeboom H.J., Kalk K.H., Janssen D.B., Dijkstra B.W.;  
 RT "Three-dimensional structure of L-2-haloacid dehalogenase from  
 RT Xanthobacter autotrophicus GJ10 complexed with the substrate-analogue  
 RT formate.";  
 RL J. Biol. Chem. 272:33015-33022(1997).  
 CC -1- FUNCTION: CATALYZES THE HYDROLYTIC DEHALOGENATION OF SMALL L-2-  
 CC HALOALKANOIC ACIDS TO YIELD THE CORRESPONDING D-2-HYDROXYALKANOIC  
 CC ACIDS. ACTIVE WITH 2-HALOGENATED CARBOXYLIC ACIDS AND CONVERTS  
 CC ONLY THE L-ISOMER OF 2-CHLOROPROPIONIC ACID WITH INVERSION OF  
 CC CONFIGURATION TO PRODUCE D-LACTATE. OPTIMAL ACTIVITY IS BETWEEN PH  
 CC 9-10, AND MAXIMAL ACTIVITY SEEN AT PH 9.5.  
 CC -1- CATALYTIC ACTIVITY: (S)-2-haloacid + H(2)O = (R)-2-hydroxyacid +  
 CC halide.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SIMILARITY: BELONGS TO THE 2-HALOALKANOIC ACID DEHALOGENASE  
 CC FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; M81691; AAA27590.1; -;  
 CC EMBL; X86084; CAA60039.1; -;  
 CC PIR; S52840; S52840.  
 CC DR PDB; 1A06; 28-JAN-98.  
 CC DR PDB; 1Q05; 29-NOV-99.  
 CC DR PDB; 1Q06; 20-DEC-00.  
 CC DR PDB; 1Q07; 20-DEC-00.  
 CC DR InterPro; IPR006328; HAD\_II.  
 CC DR InterPro; IPR006388; HAD\_SF\_1A\_V2.  
 CC DR InterPro; IPR005833; H1gnase/hydrlase.  
 CC DR Pfam; PF00702; Hydrolase; 1.  
 CC DR PRINTS; PR00413; HADHALOGENASE.  
 CC DR TIGRAME; TIGR01493; HAD-SF-1A-V2; 1.  
 CC DR TIGRAME; TIGR01428; HAD\_Type\_II; 1.  
 CC KM Hydrolyase; 3D-structure.  
 CC FT ACT\_SITE 8  
 CC FT ACT\_SITE 8  
 CC FT STRAND 4  
 CC FT STRAND 7  
 CC FT STRAND 10  
 CC FT STRAND 13  
 CC FT STRAND 14  
 CC FT STRAND 14  
 CC FT HELIX 16  
 CC FT HELIX 19  
 CC FT HELIX 20  
 CC FT HELIX 26  
 CC FT HELIX 29  
 CC FT HELIX 31  
 CC FT HELIX 31  
 CC FT HELIX 33  
 CC FT HELIX 35  
 CC FT HELIX 38  
 CC FT HELIX 52  
 CC FT HELIX 53  
 CC FT HELIX 72  
 CC FT HELIX 73  
 CC FT HELIX 74  
 CC FT HELIX 79  
 CC FT HELIX 86  
 CC FT STRAND 87  
 CC FT STRAND 94  
 CC FT STRAND 94  
 CC FT TURN 96  
 CC FT TURN 97

FT HELIX 98 105  
 FT TURN 106 107  
 FT STRAND 109 114  
 FT HELIX 118 127  
 FT TURN 126 129  
 FT HELIX 131 133  
 FT STRAND 136 139  
 FT HELIX 140 143  
 FT TURN 144 144  
 FT TURN 147 148  
 FT HELIX 150 160  
 FT HELIX 150 160  
 FT STRAND 167 171  
 FT HELIX 174 183  
 FT TURN 184 184  
 FT STRAND 186 190  
 FT HELIX 195 203  
 FT HELIX 209 217  
 FT TURN 222 223  
 FT STRAND 229 231  
 FT HELIX 234 236  
 FT HELIX 237 243  
 SQ SEQUENCE 253 AA; 27469 MW; E2AB9DEBD37A5716 CRC64;  
 QY 1 IDYSWL 6  
 Db 43 LKYSWL 48  
 Query Match 88.9%; Score 32; DB 1; Length 253;  
 Best Local Similarity 83.3%; Pred. No. 34;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 5  
 ID SSAT SALTY STANDARD; PRT; 259 AA.  
 AC P96068;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Secretion system apparatus protein ssat.  
 GN SSAT OR STM1421.  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2;  
 RX MEDLINE=97285756; PubMed=9140973;  
 RA Henzel M., Shea J.E., Raupach B., Monack D., Falkow S., Gleason C.,  
 RA Kubo T., Holden D.W.;  
 RT "Functional analysis of ssat and the ssat/U operon, 13 genes encoding  
 RT components of the type III secretion apparatus of Salmonella  
 RT pathogenicity island 2.";  
 RL Mol. Microbiol. 24:155-167(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2 / SGSC142 / ATCC 700720;  
 RX MEDLINE=2154948; PubMed=11677609;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvanev B.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
 RT LT2.";  
 RL Nature 413:852-856(2001).  
 CC -1- FUNCTION: PART OF A TYPE III SECRETION SYSTEM.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).  
 CC -1- SIMILARITY: BELONGS TO THE FLIR/MOPS/SPAR FAMILY.  
 CC -----  
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DR EMBL; X99944; CAA68201.1; -  
 DR EMBL; AE008761; AAL20345.1; -  
 DR SisyGene; SG10717; ssat.  
 DR InterPro; IPR002010; Bac\_export\_1.  
 DR InterPro; IPR006304; Spar\_yact.  
 DR Pfam; PF01311; Bac\_export\_1; 1.  
 DR PRINTS; PR00953; TYPE3IMRPROT.  
 DR TIGRPFam; TIGR01401; flir\_1like\_III; 1.  
 KM Transport; Protein transport; Transmembrane; Complete proteome.  
 FT TRANSMEM 9 POTENTIAL.  
 FT TRANSMEM 35 POTENTIAL.  
 FT TRANSMEM 78 POTENTIAL.  
 FT TRANSMEM 127 147 POTENTIAL.  
 FT TRANSMEM 185 205 POTENTIAL.  
 FT TRANSMEM 214 234 POTENTIAL.  
 SQ SEQUENCE 259 AA; 29218 MM; 855F0734991373DD CRC64;

Query Match 88.9%; Score 32; DB 1; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DYSWL 6  
 Db 67 DYSWL 71

RESULT 6  
 ABGR\_ECOLI STANDARD; PRT; 302 AA.  
 ID ABGR\_ECOLI  
 AC P77744;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Putative transcriptional regulator abgr.  
 DE ABGR OR B1339.  
 GN Escherichia coli.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OC NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RA MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. II, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12";  
 RL Science 277:1453-1474 (1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RA MEDLINE=97251357; PubMed=9097039;  
 RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  
 RA Kaezi H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,  
 RA Sempel G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,  
 RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horuchi T.;  
 RT "A 570-Kb DNA sequence of the Escherichia coli K-12 genome  
 RT corresponding to the 28.0-40.1 min region on the linkage map";  
 RL DNA Res. 3:363-377 (1996).  
 RN [3]  
 RP CHARACTERIZATION.  
 RC STRAIN=BN101;  
 RX MEDLINE=99047572; PubMed=9829935;

RA Hussein M.J., Green J.M., Nichols B.P.;  
 RT "Characterization of mutations that allow p-aminobenzoyl-glutamate  
 RT utilization by Escherichia coli.";  
 RL J. Bacteriol. 180:6260-6268 (1998).  
 CC -1- FUNCTION: COULD BE THE REGULATOR OF THE ABG OPERON  
 CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL  
 CC REGULATORS.

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DR EMBL; AE000232; AAC74421.1; -  
 DR EMBL; D90772; BAA14941.1; -  
 DR EMBL; D90773; BAA14944.1; -  
 DR PIR; F64883; F64883.  
 DR EcoGene; EG13353; abgr.  
 DR InterPro; IPR000847; HTH\_LYSR.  
 DR InterPro; IPR005119; LysR\_subsc.  
 DR Pfam; PF00126; HTH\_1; 1.  
 DR Pfam; PF03466; LysR\_substrate; 1.  
 DR PRINTS; PR00039; HTH\_LYSR.  
 DR PROSITE; PS00044; HTH\_LYSR\_FAMILY; 1.  
 KM Transcription regulation; DNA-binding; Complete proteome.  
 FT DNA\_BIND 22 41058 MM; 57C83FA6D8BA66 CRC64;  
 SQ SEQUENCE 302 AA; 34058 MM; 57C83FA6D8BA66 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 302;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSW 5  
 Db 191 LDYSW 195

RESULT 7  
 IRF1\_CHICK STANDARD; PRT; 313 AA.  
 ID IRF1\_CHICK  
 AC Q90876;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Interferon regulatory factor 1 (IRF-1).  
 DE IRF1.  
 GN Gallus gallus (Chicken).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;  
 OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95241453; PubMed=7536924;  
 RA Jungwirth C., Rebber M., Ozato K., Degen H.J., Schultze U.,  
 RA David I.B.;  
 RT "Chicken interferon consensus sequence-binding protein (ICSBP) and  
 RT interferon regulatory factor (IRF) 1 genes reveal evolutionary  
 RT conservation in the IRF gene family.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:3105-3109 (1995).  
 CC -1- FUNCTION: SPECIFICALLY BINDS TO THE UPSTREAM REGULATORY REGION OF  
 CC TYPE I IFN AND IFN-INDUCIBLE MHC CLASS I GENES (THE INTERFERON  
 CC CONSENSUS SEQUENCE (ICS) AND ACTIVATES THOSE GENES (BY  
 CC SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: Belongs to the IRF family.

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DR EMBL; L39766; AAA62160.1; -  
 DR HSR; P15314; IIR1.  
 DR InterPro; IPR001346; IIR.  
 DR Pfam; PF00605; IIR; 1.  
 DR PRINTS; PR00267; INTERNEGCT.  
 DR PRODOM; PD002355; IIR; 1.  
 DR SMART; SM00348; IIR; 1.  
 DR PROSITE; PS00601; IIR; 1.  
 KW Transcription regulation; DNA-binding; Activator; Nuclear protein.  
 FT DNA BIND 7 109 TRYPTOPHAN PENTAD REPEAT.  
 SQ SEQUENCE 313 AA; 36009 MW; 0895FA736FA7463 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 313;  
 Best Local Similarity 83.3%; Pred. No. 43;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSWL 6  
 |||  
 DB 295 LDYSWL 300

RESULT 8  
 ID AAT\_RHLP STANDARD; PRT; 400 AA.  
 AC 086459;  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Aspartate aminotransferase (EC 2.6.1.1) (Transaminase A) (ASPART).  
 GN ASPC OR AATA.  
 OS Rhizobium leguminosarum (biovar phaseol1).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.  
 OX NCBI\_TaxID=385;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=8002;  
 RA Allway D;  
 RT "Sequence of an aspartate aminotransferase from Rhizobium  
 RL leguminosarum."  
 CC Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +  
 CC L-glutamate.  
 CC -1- SIMILARITY: BELONGS TO CLASS-1 OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
 CC AMINOTRANSFERASES.

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DR EMBL; AJ006709; CA07198.1; -  
 DR HSR; O56232; IBKG.  
 DR InterPro; IPR001176; ACC\_synthase.  
 DR InterPro; IPR004839; Nhttransf1/2.  
 DR Pfam; PF00155; aminotran\_1\_2; 1.  
 DR PRINTS; PR00753; ACCSYNTHASE.  
 DR PROSITE; PS00105; AA\_TRANSFR\_CLASS\_1; 1.  
 KW Transferrase; Aminotransferase; Pyridoxal phosphate.  
 FT BINDING 239 239 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 SQ SEQUENCE 400 AA; 43752 MW; 1375BE0A72934304 CRC64;

Query Match 88.9%; Score 32; DB 1; Length 400;

Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDYSW 5  
 |||  
 DB 87 LDYSW 91

RESULT 9  
 ID VGLG\_RABVV STANDARD; PRT; 524 AA.  
 AC 008089;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Spike glycoprotein precursor.  
 GN G.  
 OS Rabies virus (strain Vnukovo-32).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Rhabdoviridae; Lyssavirus.  
 OX NCBI\_TaxID=45418;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95070778; PubMed=7979981;  
 RA Fodor I., Grabko V.I., Khozinaki V.V., Selimov M.A.;  
 RT "Nucleotide and deduced amino acid sequences of the glycoprotein gene  
 of rabies virus vaccine strain Vnukovo-32."  
 Arch. Virol. 135:451-459(1994).  
 CC -1- FUNCTION: THIS PROTEIN FORMS SPIKES ON THE SURFACE OF THE VIRION.  
 CC IT IS RESPONSIBLE BOTH FOR THE BINDING OF THE VIRUS TO SUSCEPTIBLE  
 CC HOST CELLS AND FOR INDUCING THE UPTAKE OF THE VIRUS BY THE CELL.  
 CC THE INTERACTION BETWEEN THE INTERNAL COMPONENTS OF THE VIRION AND  
 CC THE PORTION OF THE GLYCOPROTEIN EXPOSED ON THE CYTOPLASMIC FACE OF  
 CC THE PLASMA MEMBRANE PROBABLY DIRECTS ENVELOPMENT AND VIRUS  
 CC BUDDING.  
 CC -1- SUBUNIT: Homotrimer.

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DR EMBL; X71879; CA50713.1; -  
 DR PIR; S33419; S33419.  
 DR InterPro; IPR01903; Rhabd\_glycop.  
 DR Pfam; PF00974; Rhabdo\_glycop.1.  
 KW Transmembrane; Envelope protein; Glycoprotein; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 524  
 FT TRANSMEM 20 524 BY SIMILARITY.  
 FT CARBOHYD 56 476 SPIKE GLYCOPROTEIN.  
 FT CARBOHYD 56 476 BY SIMILARITY.  
 FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 484 484 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 524 AA; 58692 MW; 6DB36E50406CC16D CRC64;

Query Match 88.9%; Score 32; DB 1; Length 524;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DYSWL 6  
 |||  
 DB 137 DYSWL 141

RESULT 10  
 ID XYNA\_CALSR STANDARD; PRT; 684 AA.  
 AC P40944;  
 DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, last sequence update)  
 DT 28-FEB-2003 (Rel. 41, last annotation update)  
 DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)  
 GN (1,4-beta-D-xylan xylanohydrolase A).  
 OS Caldicellulositriptor sp. (strain R8B.4).  
 OC Bacteriella; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;  
 CC Caldicellulositriptor.  
 CX NCBI\_TaxID=28238;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97077616; PubMed=8920183;  
 RA Dvalveit P.P., Glibbs M.D., Saul D.J., Bergquist P.L.;  
 RT "Cloning, sequencing and overexpression in *Escherichia coli* of a  
 RT xylanase gene, xyna from the thermophilic bacterium R8B.4 genus  
 RT Caldicellulositriptor";  
 RL Appl. Microbiol. Biotechnol. 45:86-93(1996).  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -1- PATHWAY: Xylan degradation.  
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL  
 CC HYDROLASES).  
 CC -----  
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 CC -----  
 CC EMBL; L18965; AAB42044.1; -.  
 CC DR PIR; S41788; S41788.  
 CC DR HSSP; P10478; S41788.  
 CC DR InterPro: IPR003305; CBM\_Cenc.  
 CC DR InterPro: IPR001000; Glyco\_hydro\_10.  
 CC DR Pfam; PF02018; CBM\_4\_9; 2.  
 CC DR SMART; SM00633; Glyco\_10; 1.  
 CC DR PROSITE; PS00591; GLYCOSYL\_HYDROL\_F10; 1.  
 CC DR Xylan degradation; Hydrolase; Glycosidase; Signal; Repeat.  
 CC FT SIGNAL 1 34 POTENTIAL.  
 CC FT CHAIN 35 684 ENDO-1,4-BETA-XYLANASE A.  
 CC FT ACT\_SITE 490 490 PROTON DONOR (BY SIMILARITY).  
 CC FT ACT\_SITE 598 598 NUCLEOPHILE (BY SIMILARITY).  
 CC SQ SEQUENCE 684 AA; 78353 MW; 0AE575FAFB4B5B6 CRC64;  
 CC -----  
 CC Query Match 88.9%; Score 32; DB 1; Length 684;  
 CC Best Local Similarity 100.0%; Pred. No. 99;  
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC -----  
 CC QY 2 DYSWL 6  
 CC DB 650 DYSWL 654  
 CC -----  
 CC RESULT 11  
 CC FCT ERMCH STANDARD; PRT; 735 AA.  
 CC ID Q47162;  
 CC DT 01-NOV-1997 (Rel. 35, Created)  
 CC DT 01-NOV-1997 (Rel. 35, last sequence update)  
 CC DT 01-NOV-1997 (Rel. 35, last annotation update)  
 CC DE Ferrichrysobactin receptor precursor.  
 CC GN FCT.  
 CC OS *Erythra chrysanthemum*.  
 CC OC Bacteriella; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Pectobacterium.  
 CC CX NCBI\_TaxID=556;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC STRAIN=3937;  
 CC FT MEDLINE=96165286; PubMed=8576065;  
 CC -----

RA Sauvage C., Franza T., Expert D.;  
 RT "Analysis of the *Erythra chrysanthemum* ferrichrysobactin receptor  
 RT gene: resemblance to the *Bacteriella coli* fcpA-fes bidirectional  
 RT promoter region and homology with hydroxamate receptors";  
 GN Bacteriol. 178:1227-1231(1996).  
 CC -1- FUNCTION: INVOLVED IN THE INITIAL STEP OF IRON UPTAKE BY BINDING  
 CC CHRYSOBACTIN, AN IRON CHELATIN SIDEROPHORE THAT ALLOWS THE  
 CC BACTERIA TO EXTRACT IRON FROM THE ENVIRONMENT.  
 CC -1- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.  
 CC -----  
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 CC or send an email to [license@1sb-sib.ch](mailto:license@1sb-sib.ch)).  
 CC -----  
 CC EMBL; X87967; CAA61205.1; -.  
 CC DR PIR; S57486; S57486.  
 CC DR HSSP; P06971; 2FCP.  
 CC DR InterPro: IPR000531; TonB\_boxC.  
 CC DR Pfam; PF00593; TonB\_dep\_Rec\_1; FALSE\_NEG.  
 CC DR PROSITE; PS01156; TONB\_DEPENDENT\_REC\_1; 1.  
 CC DR PROSITE; PS00430; TONB\_DEPENDENT\_REC\_1; 1.  
 CC DR Signal; Receptor; Transmembrane; Outer membrane; Iron transport;  
 CC Transporth; TonB box.  
 CC FT SIGNAL 1 38 POTENTIAL.  
 CC FT CHAIN 39 735 PERICHRYSOBACTIN RECEPTOR.  
 CC FT SITE 45 52 TONB BOX.  
 CC FT SITE 718 735 TONB C-TERMINAL BOX.  
 CC FT TRANSMEM 39 54 PERIPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 46 45 POTENTIAL.  
 CC FT TRANSMEM 55 82 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 83 91 POTENTIAL.  
 CC FT TRANSMEM 92 107 PERIPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 108 116 POTENTIAL.  
 CC FT TRANSMEM 117 124 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 125 133 POTENTIAL.  
 CC FT TRANSMEM 134 169 PERIPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 170 178 POTENTIAL.  
 CC FT TRANSMEM 179 179 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 180 188 POTENTIAL.  
 CC FT TRANSMEM 189 194 PERIPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 195 203 POTENTIAL.  
 CC FT TRANSMEM 204 222 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 223 231 POTENTIAL.  
 CC FT TRANSMEM 232 251 PERIPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 262 270 POTENTIAL.  
 CC FT TRANSMEM 271 286 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 287 295 POTENTIAL.  
 CC FT TRANSMEM 296 312 PERIPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 313 321 POTENTIAL.  
 CC FT TRANSMEM 322 326 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 329 337 POTENTIAL.  
 CC FT TRANSMEM 338 343 PERIPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 344 352 POTENTIAL.  
 CC FT TRANSMEM 353 378 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 379 387 POTENTIAL.  
 CC FT TRANSMEM 388 392 PERIPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 393 401 POTENTIAL.  
 CC FT TRANSMEM 402 403 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 413 424 PERIPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 425 433 POTENTIAL.  
 CC FT TRANSMEM 434 448 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 449 457 POTENTIAL.  
 CC FT TRANSMEM 458 461 PERIPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 462 470 POTENTIAL.  
 CC FT TRANSMEM 471 495 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 496 504 POTENTIAL.  
 CC FT TRANSMEM 505 509 PERIPLASMIC (POTENTIAL).  
 CC -----

FT TRANSMEM 510 518 POTENTIAL.  
 FT DOMAIN 519 538 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 539 547 POTENTIAL.  
 FT DOMAIN 548 552 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 553 561 POTENTIAL.  
 FT DOMAIN 562 568 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 569 577 POTENTIAL.  
 FT DOMAIN 578 599 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 600 608 POTENTIAL.  
 FT DOMAIN 609 649 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 650 658 POTENTIAL.  
 FT DOMAIN 659 674 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 675 683 POTENTIAL.  
 FT DOMAIN 684 695 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 696 704 POTENTIAL.  
 FT DOMAIN 705 706 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 707 715 POTENTIAL.  
 FT DOMAIN 716 726 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 727 735 POTENTIAL.  
 SQ SEQUENCE 735 AA; 81055 MW; 3C37073B4538DC3C CRC64;

Query Match 88.9%; Score 32; DB 1; Length 735;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDYSWL 6  
 DB 399 LDYKWL 404

## RESULT 12

ID GUNB\_CALSA STANDARD; PRT; 1039 AA.  
 AC P10474;

DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endoglucanase/exoglucanase B precursor [Includes: Endoglucanase  
 DE (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)  
 DE (Cellulohydrolyase); Exoglucanase (EC 3.2.1.91) (Exocellulohydrolyase)]  
 DE (1,4-beta-cellulohydrolyase)].  
 GN CELB.  
 OS Caldocellum saccharolyticum (Caldicellulosiruptor saccharolyticus).  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;  
 OC Caldicellulosiruptor.  
 OK NCBI\_TaxId=44001;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8908398; PubMed=2769517;  
 RA Saul D.J., Williams L.C., Love D.R., Chanley I.W., Bergquist P.I.;  
 RT "Nucleotide sequence of a gene from Caldocellum saccharolyticum  
 RT encoding for exocellulase and endocellulase activity."  
 RL Nucleic Acids Res. 17:439-439(1989).  
 CC -1- FUNCTION: THIS PROTEIN IS MADE UP OF TWO DOMAINS: THE N-TERMINAL  
 CC DOMAIN HAS EXOGLUCANASE ACTIVITY WHILE THE C-TERMINAL DOMAIN IS  
 CC AN ENDOGLUCANASE  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic  
 CC linkages in cellulose, lichenin and cereal beta-D-glucans.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages  
 CC in cellulose and cellotetraose, releasing cellobiose from the non-  
 CC reducing ends of the chains.  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO CELLULOSE FAMILY  
 CC P (FAMILY 10 OF GLYCOSYL HYDROLASES).  
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO CELLULOSE FAMILY  
 CC A (FAMILY 5 OF GLYCOSYL HYDROLASES).  
 CC -----  
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CC EMBL: X13602; CA31936.1; -  
 DR PIR; S02711; S02711.  
 DR HSSP; Q06851; INBC.  
 DR InterPro; IPR001956; CBD 3.  
 DR InterPro; IPR001000; Glyco\_hydro\_10.  
 DR InterPro; IPR001547; Glyco\_hydro\_5.  
 DR Pfam; PF00942; CBM 3.1.  
 DR Pfam; PF00150; cellulase; 1.  
 DR Pfam; PF00331; Glyco\_hydro\_10; 1.  
 DR PRINTS; PR00134; GLYHRLASE10.  
 DR ProDom; PD001947; CBD 3.1.  
 DR SMART; SM00633; Glyco\_10; 1.  
 DR PROSITE; PS00591; GLYCOSYL\_HYDROL\_F10; 1.  
 DR PROSITE; PS00659; GLYCOSYL\_HYDROL\_F5; 1.  
 KW Cellulose degradation; Hydrolyase; Glycosidase; Repeat;  
 KW Multifunctional enzyme; Signal.  
 FT SIGNAL 1 28  
 FT CHAIN 29 1039  
 FT DOMAIN 376 416  
 FT DOMAIN 417 570  
 FT DOMAIN 571 618  
 FT ACT SITE 177 177  
 FT ACT SITE 285 285  
 FT ACT SITE 792 792  
 FT ACT SITE 1039 117641 MW; 0E0378171594DDAE CRC64;  
 SQ SEQUENCE 1039 AA; 117641 MW; 0E0378171594DDAE CRC64;

Query Match 88.9%; Score 32; DB 1; Length 1039;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYKSWL 6  
 DB 339 DYKSWL 343

## RESULT 13

ID YE15\_HABIN STANDARD; PRT; 200 AA.  
 AC P44187;

DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical protein H11415.  
 DE H11415.  
 GN H11415.  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Haemophilus.  
 OK NCBI\_TaxId=727;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=RD / KW20 / ATCC 51907;  
 RX MEDLINE=95350630; PubMed=7542800;  
 RA Fleisemann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
 RA Scott J.D., Shetty R., Liu L.-I., Glodex A., Kelley J.M.,  
 RA Weisman J.F., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D.,  
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,  
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
 RA Venter J.C.;  
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae  
 RT Rd."  
 RL Science 269:496-512(1995).  
 CC -1- SIMILARITY: SOME, TO MYCOBACTERIOPHAGES D29 AND L5 GP10.  
 CC -----  
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 -----  
 CC EMBL; U32821; AAC23066.1; -.  
 DR PIR; H64028; H64028.  
 DR HSSP; P23951; 2BAA.  
 DR TIGR; H11415; -.  
 KM Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 200 AA; 22895 MW; 42199FDNA4859FBB CRC64;  
 Query March 86.1%; Score 31; DB 1; Length 200;  
 Best Local Similarity 83.3%; Pred. No. 42;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDYSWL 6  
 DB 61 LNYSWL 66  
 RESULT 14  
 UL78\_HCMVA STANDARD; PRT; 431 AA.  
 AC P16751;  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein UL78.  
 GN UL78.  
 OS Human cytomegalovirus (strain AD169).  
 OC Viruses; dsDNA viruses, not RNA stage; Herpesviridae;  
 OC Betaherpesvirinae; Cytomegalovirus.  
 NC NCBI\_TaxID=10360;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90269039; PubMed=2161319;  
 RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,  
 RA Horenell T., Hutchison C.A. III, Kourzides T., Martignetti J.A.,  
 RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;  
 RT "Analysis of the protein-coding content of the sequence of human  
 RT cytomegalovirus strain AD169."  
 RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -----  
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 CC -----  
 CC EMBL; X17403; CA35351.1; -.  
 DR PIR; S09841; S09841.  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECIP\_F1\_2; UNKNOWN\_1.  
 KM Hypothetical protein; Transmembrane.  
 FT TRANSMEM 42 62 POTENTIAL.  
 FT TRANSMEM 74 94 POTENTIAL.  
 FT TRANSMEM 111 131 POTENTIAL.  
 FT TRANSMEM 153 173 POTENTIAL.  
 FT TRANSMEM 202 222 POTENTIAL.  
 FT TRANSMEM 236 256 POTENTIAL.  
 FT TRANSMEM 279 299 POTENTIAL.  
 FT CARBOHYD 105 105 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 431 AA; 47357 MW; 34668FE7F908C657 CRC64;  
 Query March 86.1%; Score 31; DB 1; Length 431;  
 Best Local Similarity 83.3%; Pred. No. 94;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LDYSWL 6  
 DB 180 LDYRWL 185

RESULT 15  
 IKKA HUMAN STANDARD; PRT; 745 AA.  
 ID IKKA HUMAN  
 AC O1511; O14666; Q13132; O92467;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (IC 2.7.1.-)  
 DE (I kappa-B kinase alpha) (IKBA) (IKK- $\alpha$ ) (Ikkappa kinase)  
 DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous  
 DE kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIA).  
 GN CHUK OR IKKA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.  
 RC TISSUE=T-cell;  
 RX MEDLINE=97386461; PubMed=9244310;  
 RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Roche M.;  
 RT "Identification and characterization of an Ikkappa kinase."  
 RL Cell 90:373-383(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=97394468; PubMed=9252186;  
 RA Didonato J.A., Hayakawa M., Rothenberg D.M., Zandi E., Karin M.;  
 RT "A cytokine-responsive Ikkappa kinase that activates the transcription  
 RT factor NF-kappaB."  
 RL Nature 388:548-554(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND  
 RP SER-176.  
 RC TISSUE=Cervical carcinoma;  
 RX MEDLINE=98008813; PubMed=9346484;  
 RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,  
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;  
 RT "IKK-1 and IKK-2: cytokine-activated Ikkappa kinases essential for  
 RT NF-kappaB activation."  
 RL Science 278:860-866(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RX MEDLINE=95032998; PubMed=9813230;  
 RA Hu M.C.-T., Wang Y.-P.;  
 RT "Ikkappa kinase-alpha and -beta genes are coexpressed in adult and  
 RT embryonic tissues but localized to different human chromosomes."  
 RL Gene 222:31-40(1998).  
 RN [5]  
 RP SEQUENCE OF 32-745 FROM N.A.  
 RC TISSUE=Cervical carcinoma;  
 RX MEDLINE=96258427; PubMed=8777433;  
 RA Connolly M.A., Marcu K.B.;  
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper  
 RT families of interacting proteins, contains a serine-threonine kinase  
 RT catalytic domain."  
 RL Cell. Mol. Biol. Res. 41:537-549(1995).  
 RN [6]  
 RP PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179  
 RP AND SER-180.  
 RX MEDLINE=98188283; PubMed=9520446;  
 RA Ling L., Cao Z., Goeddel D.V.;  
 RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of  
 RT Ser-176."  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).  
 RN [7]  
 RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.  
 RX MEDLINE=99413720; PubMed=10465710; Pfeiffer S.R., Pfeiffer L.M.,  
 RA Ozes O.N., Mayo L.D., Guetin J.A., Pfeiffer S.R., Pfeiffer L.M.,  
 RA Donner D.B.;  
 RT "NF-kappaB activation by tumour necrosis factor requires the Akt  
 RT serine-threonine kinase.";

RL Nature 401:82-85(1999).  
 RN [8]  
 RP IKK- $\alpha$  BINDING.  
 RX MEDLINE=99212141; PubMed=10195894;  
 RA Delhase M., Hayekawa M., Chen Y., Karin M.;  
 RT "Positive and negative regulation of I $\kappa$ B kinase activity through  
 RL IKK $\alpha$  subunit phosphorylation.";  
 Science 284:305-313(1999).  
 RN [9]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., DiDonato J.A., Lin A.;  
 RT "Coordinate regulation of I $\kappa$ B kinase by mitogen-activated protein  
 RL kinase kinase kinase 1 and NF- $\kappa$ B-inducing kinase.";  
 Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [10]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712223;  
 RA Jobin C., Sartor R.B.;  
 RT "The I $\kappa$ B kinase B/NF- $\kappa$ B system: a key determinant of mucosal  
 RL inflammation and protection.";  
 Am. J. Physiol. 278:C451-C462(2000).  
 RN [11]  
 RP SUBUNIT OF A COMPLEX CONTAINING CREBBP, NCOA2, NCOA3, IKK $\alpha$  AND IKK $\beta$ .  
 RX MEDLINE=21968797; PubMed=11971985;  
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,  
 RT "Regulation of SRC-3 (PCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator  
 RL activity by I $\kappa$ B kinase.";  
 Mol. Cell. Biol. 22:3549-3561(2002).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF- $\kappa$ B thus leading to  
 the dissociation of the inhibitor/NF- $\kappa$ B complex and  
 ultimately the degradation of the inhibitor. Also phosphorylates  
 NCOA3.  
 CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated  
 when dephosphorylated.  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK- $\beta$  but  
 also as an homodimer. Directly interacts with IKK- $\gamma$ /NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 also bind to MAP3K14/NIK, MEK1, IKAP and IKK- $\alpha$ -P65-P50  
 complex. A weak interaction with TRAF2 cannot be excluded. Part of  
 a complex composed of NCOA2, NCOA3, IKK $\alpha$ , IKK $\beta$  and CREBBP.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Widely expressed.  
 CC -1- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by  
 MEK1, and dephosphorylated by PP2A. Autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPAB KINASE SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL, AF012890; AAC51662.1; -;  
 DR EMBL, AF009225; AAC51671.1; -;  
 DR EMBL, AF080157; AAD08996.1; -;  
 DR EMBL, U22512; AAC50713.1; -;  
 DR HSSP, Q63450; 1A06.  
 DR GeneW, HGNC:1974; CHUK.  
 DR MIM, 600664; -;  
 DR GO, GO:0005737; C:cytoplasm; TAS.  
 DR GO, GO:0008384; P:IkappaB kinase activity; TAS.  
 DR GO, GO:0007345; P:embryogenesis and morphogenesis; TAS.  
 DR GO, GO:0007252; P:I-kappaB phosphorylation; TAS.  
 DR GO, GO:0006955; P:immune response; TAS.  
 DR InterPro, IPR000719; Prot\_kinase.  
 DR InterPro, IPR002290; Ser\_thr\_kinase.  
 DR InterPro, IPR001245; Tyr\_kinase; I.  
 DR Pfam, PF00069; kinase; I.

DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 KW transferase; Serine/threonine-protein kinase; ATP-binding;  
 KW phosphorylation.  
 FT DOMAIN 15 302  
 FT 455 476  
 FT DOMAIN 738 743  
 FT NP\_BIND 21 29  
 FT BINDING 44 44  
 FT ACT\_SITE 144 144  
 FT MOD\_RES 23 23  
 FT MOD\_RES 176 176  
 FT MUTAGEN 23 23  
 FT MUTAGEN 44 44  
 FT MUTAGEN 44 44  
 FT MUTAGEN 176 176  
 FT MUTAGEN 176 176  
 FT MUTAGEN 176 176  
 FT MUTAGEN 179 179  
 FT MUTAGEN 180 180  
 FT CONFLICT 543 543  
 FT CONFLICT 604 604  
 FT CONFLICT 679 680  
 FT CONFLICT 684 684  
 FT CONFLICT 686 687  
 SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;  
 Query Match 86.1%; Score 31; DB 1; Length 745;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDYSWL 6  
 DB 738 LDMSWL 743  
 Search completed: February 18, 2004, 14:28:10  
 Job time : 4.55263 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds  
(without alignments)  
87.531 Million cell updates/sec

Title: US-09-643-260-12

Perfect score: 36

Sequence: 1 LDYSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	94.7	282	2 B70555	probable omt prote
2	33	91.4	404	2 JC5784	adrenomedullin rec
3	32	88.9	122	2 S52840	haloalkanoic acid
4	32	88.9	153	2 P90704	hypothetical prote
5	32	88.9	153	2 A85555	hypothetical prote
6	32	88.9	168	2 A83390	hypothetical prote
7	32	88.9	195	2 T29815	hypothetical prote
8	32	88.9	229	2 B38452	2-haloacid dehalog
9	32	88.9	251	2 B84016	hypothetical prote
10	32	88.9	259	2 AG0696	probable type III
11	32	88.9	302	2 C90869	probable transcrip
12	32	88.9	302	2 F85749	probable transcrip
13	32	88.9	302	2 F64883	probable transcrip
14	32	88.9	349	2 T15422	hypothetical prote
15	32	88.9	379	2 AH0542	conserved hypotet
16	32	88.9	386	2 H71511	probable 2-compo
17	32	88.9	391	2 A70663	probable PEP prote
18	32	88.9	414	2 T44513	hypothetical prote
19	32	88.9	440	2 T32190	hypothetical prote
20	32	88.9	524	2 S33419	glycoprotein G - r
21	32	88.9	684	2 S41788	anti-1,4-beta-xyla
22	32	88.9	694	2 A95251	antigen, cell wall
23	32	88.9	694	2 P98115	conserved hypotet
24	32	88.9	700	2 T30910	xylnase (BC 3.2.1
25	32	88.9	735	2 T34531	hypothetical prote
26	32	88.9	705	2 S57486	ferrichrysoactin
27	32	88.9	872	2 B75073	ATP-dependent RNA
28	32	88.9	915	2 A43802	cellulase (BC 3.2.
29	32	88.9	1039	2 S02711	cellulase (BC 3.2.

30	32	88.9	1209	2 T16663	hypothetical prote
31	32	88.9	1232	2 D64413	cobalamn biosynth
32	32	88.9	1319	2 S75705	hypothetical prote
33	32	88.9	1779	2 T31085	xylnase - Caldice
34	31	86.1	200	2 H64028	hypothetical prote
35	31	86.1	234	2 A63543	phosphoglycolate p
36	31	86.1	262	2 T20203	hypothetical prote
37	31	86.1	431	2 S09841	hypothetical prote
38	31	86.1	618	2 D71055	probable indolepyr
39	31	86.1	745	2 T49101	conserved helix-10
40	31	86.1	837	2 H82970	hypothetical prote
41	31	86.1	1010	2 D72203	hypothetical prote
42	30	83.3	61	2 D82732	hypothetical prote
43	30	83.3	144	2 A10698	probable pathogen
44	30	83.3	154	2 F90195	conserved hypotet
45	30	83.3	225	2 S38672	ywbB protein - Bac

#### ALIGNMENTS

Result 1  
B70555  
probable omt protein - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
C:Accession: B70555  
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, J.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellon, S.; Squares, S.  
Mature 393, 537-544, 1998  
A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295887; PMID:9634230  
A:Accession: B70555  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-282 <COL>  
A:Cross-references: GB:Z95584; GB:AL123456; NID:G3261774; PID:CA809012.1; PID:6317129;  
A:Experimental source: strain H37RV  
C:Genes: omt  
Query Match 94.4%; Score 34; DB 2; Length 282;  
Best Local Similarity 83.3%; Pred. No. 36;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDYSWL 6  
DB 142 LDYSWL 147  
RESULT 2  
JC5784  
adrenomedullin receptor - human  
C:Species: Homo sapiens (man)  
C>Date: 24-Jan-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jul-2000  
C:Accession: JC5784  
R:Haenze, J.; Dietrich, K.; Doetsch, J.; Raecher, W.  
Biochem. Biophys. Res. Commun. 240, 183-188, 1997  
A>Title: Molecular cloning of a novel human receptor gene with homology to the rat adre  
A:Reference number: JC5784; MUID:98042541; PMID:9367907  
A:Accession: JC5784  
A:Molecule type: mRNA  
A:Residues: 1-404 <HAE>  
A:Cross-references: GB:Y13583; NID:G2652933; PID:CAA73910.1; PID:G2652934  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: glycoprotein; receptor; transmembrane protein  
F:58-79/Domain: transmembrane #status predicted <TM1>  
F:91-113/Domain: transmembrane #status predicted <TM2>  
F:128-149/Domain: transmembrane #status predicted <TM3>  
F:171-199/Domain: transmembrane #status predicted <TM4>  
F:218-239/Domain: transmembrane #status predicted <TM5>

F:260-280/Domain: transmembrane #status predicted <TM6>  
 F:301-320/Domain: transmembrane #status predicted <TM7>  
 F:28,37/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 91.7% Score 33; DB 2; Length 404;  
 Best Local Similarity 83.3%; Pred. No. 82;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6  
 |||||  
 DB 115 LDYTWL 120

## RESULT 3

S52840

haloalkanoic acid dehalogenase - Xanthobacter autotrophicus (fragment)

C/Species: Xanthobacter autotrophicus

C/Date: 19-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 11-Jan-2000

C/Accession: S52840

R:van der Ploeg, J.; Janssen, D.B.

submitted to the EMBL Data Library, April 1995

A/Description: Sequence analysis of the upstream region of dhb, the gene encoding halo

A/Reference number: S52838

A/Accession: S52840

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-122 <VAN>

A/Cross-references: EMBL:X66084; NID:G763396; PIDN:CA60039.1; PID:G763399

C/superfamily: Alkaligenes eutrophus phosphoglycolate phosphatase

Query Match 88.9% Score 32; DB 2; Length 122;  
 Best Local Similarity 83.3%; Pred. No. 36;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6  
 |||||  
 DB 43 LDYSWL 48

## RESULT 4

P90704

hypothetical protein Eca606 (imported) - Escherichia coli (strain O157:H7, substrain R1

C/Species: Escherichia coli

C/Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001

C/Accession: P90704

R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hartford, M.; Shingawa, H.

DNA Res. 8, 11-22, 2001

A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene

A/Reference number: A9629; MUID:21156231; PMID:11258796

A/Accession: P90704

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-153 <NAV>

A/Cross-references: GB:BA000007; PIDN:BA034029.1; PID:G13360064; GSPDB:GN00154

A/Experimental source: strain O157:H7, substrain R1MD 050952

C/Genetics:

A/Gene: Eca606

Query Match 88.9% Score 32; DB 2; Length 153;  
 Best Local Similarity 100.0%; Pred. No. 45;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 5  
 |||||  
 DB 83 LDYSWL 87

## RESULT 5

A85555

hypothetical protein Z0706 (imported) - Escherichia coli (strain O157:H7, substrain EDL9

C/Species: Escherichia coli

C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001

C/Accession: A85555  
 R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh

iller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Diallanta, E.; Petamousta, K.; Apodect

Nature 409, 529-533, 2001

A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A/Reference number: A85480; MUID:21074935; PMID:11206551

A/Accession: A85555

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-153 <STO>

A/Cross-references: GB:AE005174; NID:G12513450; PIDN:AA054901.1; GSPDB:GN00145; UNGP:Z

A/Experimental source: strain O157:H7, substrain EDL933

C/Genetics:

A/Gene: Z0706

Query Match 88.9% Score 32; DB 2; Length 153;  
 Best Local Similarity 100.0%; Pred. No. 45;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 5  
 |||||  
 DB 83 LDYSWL 87

## RESULT 6

A83390

probable sigma-70 factor, ECF subfamily PA2050 (imported) - Pseudomonas aeruginosa (str

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C/Accession: A83390

R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; I

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lardig, K.; Lin

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: A83390

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-168 <STO>

A/Cross-references: GB:AE004631; GB:AE004091; NID:G9948050; PIDN:AA05438.1; GSPDB:GN00

A/Experimental source: strain PA01

C/Genetics:

A/Gene: PA2050

Query Match 88.9% Score 32; DB 2; Length 168;  
 Best Local Similarity 100.0%; Pred. No. 50;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6  
 |||||  
 DB 18 DYSWL 22

## RESULT 7

T29815

hypothetical protein C46A5.8 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C/Accession: T29815

R/Johnson, D.; Stellyes, L.

submitted to the EMBL Data Library, June 1996

A/Description: The sequence of C. elegans cosmid C46A5.

A/Reference number: Z20690

A/Accession: T29815

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-195 <JOH>

A/Cross-references: EMBL:U61948; PIDN:AA03148.1; GSPDB:GN00022; CESP:C46A5.8

A/Experimental source: strain Bristol N2; clone C46A5

C/Genetics:

A/Gene: CESP:C46A5.8

A/Map position: 4



A:introns: 93/3; 122/3

## Query Match

Best Local Similarity 88.9%; Score 32; DB 2; Length 195;  
C/Species: *Pseudomonas* sp.  
C/Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #text\_change 24-Nov-1999  
C/Accession: B38452  
R/Schneider, B.; Mueller, R.; Frank, R.; Langens, F.  
J. Bacteriol. 173, 1530-1535, 1991  
A>Title: Complete nucleotide sequences and comparison of the structural genes of two 2-h  
A/Reference number: A38452; MUID:91139597; PMID:1995594  
A/Accession: B38452  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-229 <SCH>  
A/Cross-references: GB:M62909; GB:M37619; NID:9151249; PIDN:AAA25833.1; PID:9151250  
C/Keyword: hydrolase

QY 2 DYSLW 6  
|||  
DB 74 DYSLW 78

## RESULT 8

B38452  
2-haloesid dehalogenase (EC 3.8.1.2) II - *Pseudomonas* sp.

C/Species: *Pseudomonas* sp.  
C/Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #text\_change 24-Nov-1999  
C/Accession: B38452  
R/Schneider, B.; Mueller, R.; Frank, R.; Langens, F.  
J. Bacteriol. 173, 1530-1535, 1991  
A>Title: Complete nucleotide sequences and comparison of the structural genes of two 2-h  
A/Reference number: A38452; MUID:91139597; PMID:1995594  
A/Accession: B38452  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-229 <SCH>  
A/Cross-references: GB:M62909; GB:M37619; NID:9151249; PIDN:AAA25833.1; PID:9151250  
C/Keyword: hydrolase

## Query Match

Best Local Similarity 88.9%; Score 32; DB 2; Length 229;  
C/Species: *Bacillus halodurans*  
C/Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C/Accession: B84016  
R/Takami, H.; Nakagawa, K.; Takai, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai  
Nucleic Acids Res. 28, 4317-4331, 2000  
A>Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and  
A/Reference number: A83650; MUID:20512582; PMID:11058132  
A/Accession: B84016  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-251 <STO>  
A/Cross-references: GB:AP001517; GB:BA000004; NID:910175500; PIDN:BA06649.1; GSPDB:GN00  
A/Experimental source: strain C-125  
C/Genetics:

QY 1 LDYSW 6  
|||  
DB 45 LDYSW 50

## RESULT 9

B84016  
hypothetical protein BH2930 [imported] - *Bacillus halodurans* (strain C-125)

C/Species: *Bacillus halodurans*  
C/Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C/Accession: B84016  
R/Takami, H.; Nakagawa, K.; Takai, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai  
Nucleic Acids Res. 28, 4317-4331, 2000  
A>Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and  
A/Reference number: A83650; MUID:20512582; PMID:11058132  
A/Accession: B84016  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-251 <STO>  
A/Cross-references: GB:AP001517; GB:BA000004; NID:910175500; PIDN:BA06649.1; GSPDB:GN00  
A/Experimental source: strain C-125  
C/Genetics:

Query Match 88.9%; Score 32; DB 2; Length 251;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDYSW 5  
|||  
DB 153 LDYSW 157

## RESULT 10

AG0696  
probable type III secretion protein *sear* [imported] - *Salmonella enterica* subsp. *enteric*

C/Species: *Salmonella enterica* subsp. *enterica* serovar *Typh*  
A/Note: this species has also been called *Salmonella typh*  
C/Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C/Accession: AG0696

R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Cawston, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
, S.; Moile, S.; O'Garra, P.  
Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K  
A>Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* ser  
A/Reference number: AB0502; MUID:21534947; PMID:11677608  
A/Accession: AG0696  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-259 <PAR>  
A/Cross-references: GB:AL513382; PIDN:CAD01944.1; PID:916502786; GSPDB:GN00176  
C/Genetics:

Query Match 88.9%; Score 32; DB 2; Length 259;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 DYSLW 6  
|||  
DB 67 DYSLW 71

## RESULT 11

C90869  
probable transcription regulator *lysr*-type [imported] - *Escherichia coli* (strain O157:H

C/Species: *Escherichia coli*  
C/Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 24-Aug-2001  
C/Accession: C90869  
R/Hayashi, T.; Makino, K.; Onishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.;  
gaawara, N.; Yasunaga, T.; Kuwara, S.; Shibata, T.; Hattori, M.; Shingawa, H.  
DNA Res. 8, 11-22, 2001  
A>Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen  
A/Reference number: A96239; MUID:21156231; PMID:11258796  
A/Accession: C90869  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-302 <HAY>  
A/Cross-references: GB:BA000007; PIDN:BA035346.1; PID:913361388; GSPDB:GN00154  
A/Experimental source: strain O157:H7, substrain RMD 0509952  
C/Genetics:

C/Suprafamily: regulatory protein *lysr*

Query Match 88.9%; Score 32; DB 2; Length 302;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSW 5  
|||  
DB 191 LDYSW 195

## RESULT 12

F85749  
probable transcription regulator *lysr*-type *ydaK* [imported] - *Escherichia coli* (strain C

C/Species: *Escherichia coli*  
C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C/Accession: F85749  
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh  
iller, L.; Grobeck, B.J.; Davis, N.W.; Llam, A.; Dialante, E.; Potamousta, K.; Apodaca  
Nure 409, 529-533, 2001  
A>Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
A/Reference number: AB5480; MUID:21074935; PMID:11206551  
A/Accession: F85749  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-302 <STO>  
A/Cross-references: GB:AB005174; NID:912515416; PIDN:AA056458.1; GSPDB:GN00145; UNCP:22  
A/Experimental source: strain O157:H7, substrain EDJ933  
C/Genetics:

A/Gene: *ydaK*

C:Superfamily: regulatory protein 1lv

Query Match 88.9%; Score 32; DB 2; Length 302;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSW 5  
DB 191 LDYSW 195

# RESULT 13

P64883  
Probable transcription regulator ydak - Escherichia coli (strain K-12)

C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
C:Accession: F64883  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617; PMID:9278503  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-302 <BLAT>  
A:Cross-references: GB:AE000232; GB:U00096; NID:g1787600; PIND:AACT4421.1; PID:g1787601;  
A:Experimental source: strain K-12, substrain M61655  
C:Genetics:  
A:Gene: ydak  
C:Superfamily: regulatory protein 1lv  
C:Keywords: DNA binding; transcription regulation  
F:21-51/Region: regulatory protein lyx motif

Query Match 88.9%; Score 32; DB 2; Length 302;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDYSW 5  
DB 191 LDYSW 195

# RESULT 14

T15422  
hypothetical protein C06A8.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 31-Jan-2000  
C:Accession: T15422  
R:Leimach, D.  
submitted to the EMBL Data Library, November 1995  
A:Description: The sequence of C. elegans cosmid C06A8.  
A:Reference number: Z18348  
A:Accession: T15422  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-349 <LEI>  
A:Cross-references: EMBL:U39849; NID:g1055041; PID:AAA81047.1; CESP:C06A8

C:Gene: CESP:C06A8.6  
A:Introns: 29/3; 202/3; 263/3; 316/3  
C:Superfamily: decorin, leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan

Query Match 88.9%; Score 32; DB 2; Length 349;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DYSWL 6  
DB 49 DYSWL 53

# RESULT 15

AH0542

conserved hypothetical protein STY0359 (imported) - Salmonella enterica subsp. enteric  
C:Species: Salmonella enterica subsp. enterica serovar typh  
A>Note: this species has also been called Salmonella typh

C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AH0542

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher;  
th, T.; Connor, R.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar;  
, S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K  
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica ser  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AH0542

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-379 <PAR>  
A:Cross-references: GB:AL513382; PIND:CAD08784.1; PID:g16501600; GSPDB:GN00176

C:Gene: STY0359  
C:Superfamily: Streptomyces coelicolor hypothetical protein SCR15.16c

Query Match 88.9%; Score 32; DB 2; Length 379;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DYSWL 6  
DB 275 DYSWL 279

Search completed: February 18, 2004, 14:38:48  
Job time : 8.5921 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds  
(without alignments)  
35.929 Million cell updates/sec

Title: US-09-643-260-12

Perfect score: 36  
Sequence: 1 LDYSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgm2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
2: /cgm2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgm2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgm2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgm2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgm2\_6/prodata/1/1aa/backfillseq.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	91.7	404	1	US-08-696-770-2
2	33	91.7	404	2	US-09-015-557-2
3	32	88.9	217	4	US-09-107-532A-4133
4	32	88.9	228	4	US-09-552-991A-24998
5	32	88.9	230	2	US-08-637-759B-457
6	32	88.9	230	3	US-08-871-355A-457
7	32	88.9	230	4	US-09-301-945-457
8	32	88.9	351	3	US-08-591-685-7
9	32	88.9	375	3	US-08-591-685-11
10	32	88.9	404	2	US-08-882-197C-62
11	32	88.9	438	2	US-08-282-197C-59
12	32	88.9	1426	3	US-09-136-574A-43
13	31	86.1	745	2	US-08-887-518-3
14	31	86.1	745	2	US-09-023-321-3
15	31	86.1	745	2	US-08-890-853-4
16	31	86.1	745	2	US-09-032-475-3
17	31	86.1	745	2	US-09-099-125A-4
18	31	86.1	745	2	US-09-099-124A-4
19	31	86.1	745	2	US-09-032-476-4
20	31	86.1	745	3	US-08-890-854-4
21	31	86.1	745	3	US-09-023-324-4
22	31	86.1	745	3	US-09-168-629-2
23	31	86.1	745	3	US-08-910-820-10
24	31	86.1	745	3	US-08-810-131A-2
25	31	86.1	745	4	US-09-109-986-4
26	31	86.1	745	4	US-09-844-908-10
27	31	86.1	745	4	US-09-668-758-3

28	31	86.1	756	2	US-08-887-518-4	Sequence 4, App11
29	31	86.1	756	2	US-09-023-321-4	Sequence 4, App11
30	31	86.1	756	2	US-08-890-853-2	Sequence 2, App11
31	31	86.1	756	2	US-09-032-475-4	Sequence 4, App11
32	31	86.1	756	2	US-09-099-125A-2	Sequence 2, App11
33	31	86.1	756	2	US-09-099-124A-2	Sequence 2, App11
34	31	86.1	756	3	US-09-032-476-2	Sequence 2, App11
35	31	86.1	756	3	US-08-890-854-2	Sequence 2, App11
36	31	86.1	756	3	US-09-023-324-2	Sequence 2, App11
37	31	86.1	756	3	US-09-168-629-15	Sequence 15, App1
38	31	86.1	756	3	US-08-910-820-9	Sequence 9, App11
39	31	86.1	756	4	US-09-109-986-2	Sequence 2, App11
40	31	86.1	756	4	US-09-844-908-9	Sequence 9, App11
41	31	86.1	756	4	US-09-868-758-4	Sequence 4, App11
42	31	86.1	996	4	US-09-417-197-123	Sequence 123, App
43	31	86.1	997	4	US-09-417-197-121	Sequence 121, App
44	31	86.1	1709	4	US-09-392-812A-6	Sequence 6, App11
45	30	83.3	112	4	US-09-328-352-7614	Sequence 7614, Ap

#### ALIGNMENTS

RESULT 1  
US-08-696-770-2  
; Sequence 2, Application US/08696770  
; Patent No. 5763218  
; GENERAL INFORMATION:  
; APPLICANT: Fujii, Ryo  
; APPLICANT: Hinuma, Shuji  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven  
; APPLICANT: Soppet, Daniel  
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: Pasteo Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/696,770  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Han, William T  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: TAKS0001-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5219  
; TELEFAX: 610-270-5090  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 404 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLBUCE TYPE: Peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:

US-08-696-770-2

Query Match 91.7%; Score 33; DB 1; Length 404;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6  
Db 115 LDYTWL 120

RESULT 2

US-09-015-557-2  
; Sequence 2, Application US/09015557  
; Patent No. 5932702  
; GENERAL INFORMATION:  
; APPLICANT: Fujii, Ryo  
; APPLICANT: Hinuma, Shuji  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven  
; APPLICANT: Soppet, Daniel  
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/015,557  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/696,770  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Han, William T  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: TAK50001-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5219  
; TELEFAX: 610-270-5090  
; TEXAS:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 404 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; US-09-015-557-2

Query Match 91.7%; Score 33; DB 2; Length 404;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6  
Db 115 LDYTWL 120

RESULT 3

US-09-107-532A-4133

; Sequence 4133, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354

COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneka  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 4133:

SEQUENCE CHARACTERISTICS:  
LENGTH: 217 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...217  
SEQUENCE DESCRIPTION: SEQ ID NO: 4133:  
US-09-107-532A-4133

Query Match 88.9%; Score 32; DB 4; Length 217;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSW 5  
Db 89 LDYSW 93

RESULT 4

US-09-252-991A-24998  
; Sequence 24998, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfeld et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196,136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 24998  
; LENGTH: 228  
; TYPE: PRF  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-24998

Query Match 88.9%; Score 32; DB 4; Length 228;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6  
| | | | |  
DB 78 DYSWL 82

RESULT 5  
US-08-637-759B-457  
; Sequence 457, Application US/08637759B  
; Patent No. 5876931  
; GENERAL INFORMATION:  
; APPLICANT: David William Holden  
; TITLE OF INVENTION: Identification of Genes  
; NUMBER OF SEQUENCES: 501  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; STREET: 1201 West Peachtree Street  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/637,759B  
; FILING DATE: 03-MAY-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB95/02875  
; FILING DATE: 11-DEC-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: RPMS 101  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 873-8794  
; TELEFAX: (404) 873-8795  
; INFORMATION FOR SEQ ID NO: 457:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 230 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-637-759B-457

Query Match 88.9%; Score 32; DB 2; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6  
| | | | |  
DB 67 DYSWL 71

RESULT 6

US-08-871-355A-457  
; Sequence 457, Application US/08871355A  
; Patent No. 6015669  
; GENERAL INFORMATION:  
; APPLICANT: David William Holden  
; TITLE OF INVENTION: Identification of Genes  
; NUMBER OF SEQUENCES: 501  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; STREET: 1201 West Peachtree Street  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/871,355A  
; FILING DATE: 09-JUN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB95/02875  
; FILING DATE: 11-DEC-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: RPMS 101 CON  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 873-8794  
; TELEFAX: (404) 873-8795  
; INFORMATION FOR SEQ ID NO: 457:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 230 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-871-355A-457

Query Match 88.9%; Score 32; DB 3; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6  
| | | | |  
DB 67 DYSWL 71

RESULT 7  
US-09-201-945-457  
; Sequence 457, Application US/09201945  
; Patent No. 6342215  
; GENERAL INFORMATION:  
; APPLICANT: David William Holden  
; TITLE OF INVENTION: Identification of Genes  
; NUMBER OF SEQUENCES: 501  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; STREET: 1201 West Peachtree Street  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/201,945  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/637,759  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabec, Patricia L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: RPS 101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 457:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 230 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-09-201-945-457

Query Match 88.9%; Score 32; DB 4; Length 230;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6  
Db 67 DYSWL 71

RESULT 8  
US-08-591-685-7  
Sequence 7, Application US/08591685  
Patent No. 6083733  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Thermostable xylanases  
NUMBER OF SEQUENCES: 13  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/591,685  
FILING DATE:  
CLASSIFICATION: 435  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 351 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-591-685-7

Query Match 88.9%; Score 32; DB 3; Length 351;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6  
Db 317 DYSWL 321

RESULT 9  
US-08-591-685-11  
Sequence 11, Application US/08591685

Patent No. 6083733  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Thermostable xylanases  
NUMBER OF SEQUENCES: 13  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/591,685  
FILING DATE:  
CLASSIFICATION: 435  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 375 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-591-685-11

Query Match 88.9%; Score 32; DB 3; Length 375;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6  
Db 328 DYSWL 332

RESULT 10  
US-08-282-197C-62  
Sequence 62, Application US/08282197C  
Patent No. 5871730  
GENERAL INFORMATION:  
APPLICANT: Brzezinski, Ryszard  
APPLICANT: Dery, Claude V  
TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and  
METHOD OF INVENTION: Methods of Use  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Ave., NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,197C  
FILING DATE: 29-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbal, Michele A  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 1050.0410000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 404 amino acids  
TYPE: amino acid  
TOPOLOGY: both  
US-08-282-197C-62

Query Match 88.9%; Score 32; DB 2; Length 404;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6  
|||||

DB 328 DYSWL 332

## RESULT 11

US-08-282-197C-59  
; Sequence 59, Application US/08282197C  
; Patent No. 5871730  
; GENERAL INFORMATION:  
; APPLICANT: Brzezinski, Ryszard  
; APPLICANT: Dery, Claude V  
; TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and  
; TITLE OF INVENTION: Methods of Use  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Keagler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Ave., NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,197C  
FILING DATE: 29-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Clumbala, Michele A  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 1050.0410000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 438 amino acids  
TYPE: amino acid  
TOPOLOGY: both

US-08-282-197C-59

Query Match 88.9%; Score 32; DB 2; Length 438;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6  
|||||

DB 339 DYSWL 343

RESULT 12  
US-09-136-574A-43  
; Sequence 43, Application US/09136574A  
; Patent No. 6294366  
; GENERAL INFORMATION:  
; APPLICANT: Farrington, Graham K.  
; ANDERSON, Paige  
; GIBBS, Moreland  
; BERQUIST, Peter  
; DANIELS, Roy  
; MORGAN, Hugh W.  
; WILLIAMS, Diane P.

TITLE OF INVENTION: Compositions and Methods for  
Treating Cellulose Containing Fabrics Using Truncated  
Cellulase Enzyme Compositions

NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Center, P.O. Box 457  
CITY: Spring House  
STATE: PA  
COUNTRY: USA  
ZIP: 19477

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/136,574A  
FILING DATE: 19-Aug-1998  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/992,571  
FILING DATE: September 19, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: 1997US001/CIP

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1426 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6294366e  
SEQUENCE DESCRIPTION: SEQ ID NO: 43:  
US-09-136-574A-43

Query Match 88.9%; Score 32; DB 3; Length 1426;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DYSWL 6  
|||||

DB 339 DYSWL 343

## RESULT 13

US-08-887-518-3  
; Sequence 3, Application US/08887518  
; Patent No. 5843721  
; GENERAL INFORMATION:  
; APPLICANT: Roche, Mike  
; APPLICANT: Wu, Lin  
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-887-518-3

Query Match 86.1%; Score 31; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6  
||:||||  
DB 738 LDMSWL 743

RESULT 14  
US-09-023-321-3  
Sequence 3, Application US/09023321  
Patent No. 5844073  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Wu, Lin  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023.321  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/887.518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-321-3

Query Match 86.1%; Score 31; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDYSWL 6  
||:||||

DB 738 LDMSWL 743

RESULT 15  
US-08-890-853-4  
Sequence 4, Application US/08890853  
Patent No. 5851812  
GENERAL INFORMATION:  
APPLICANT: Goedel, David V.  
APPLICANT: Moronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890.853  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-853-4

Query Match 86.1%; Score 31; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDYSWL 6  
||:||||  
DB 738 LDMSWL 743

Search completed: February 18, 2004, 14:41:49  
Job time : 7.06579 secs



GenCore version 5.1.6  
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OM protein - protein search, using ew model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds  
(without alignments)  
35.929 Million cell updates/sec

Title: US-09-643-260-11

Perfect score: 35

Sequence: 1 LDFSML 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	91.4	452	4 US-09-252-991A-31360	Sequence 31360, A
2	31	88.6	21	1 US-08-798-897-13	Sequence 13, Appl
3	31	88.6	21	2 US-08-978-523-13	Sequence 13, Appl
4	31	88.6	23	2 US-08-337-646A-23	Sequence 23, Appl
5	31	88.6	23	3 US-08-927-326-23	Sequence 23, Appl
6	31	88.6	25	2 US-08-337-646A-29	Sequence 29, Appl
7	31	88.6	25	3 US-08-927-326-29	Sequence 29, Appl
8	31	88.6	154	3 US-08-077-848A-3	Sequence 3, Appl1
9	31	88.6	154	3 US-09-211-640-3	Sequence 3, Appl1
10	31	88.6	154	4 US-09-378-536-3	Sequence 3, Appl1
11	31	88.6	229	2 US-08-687-260-3	Sequence 19, Appl
12	31	88.6	232	2 US-08-408-095-19	Sequence 17, Appl
13	31	88.6	232	2 US-08-408-095-17	Sequence 18, Appl
14	31	88.6	232	1 US-08-408-095-18	Sequence 18, Appl
15	31	88.6	236	1 US-08-112-208C-11	Sequence 11, Appl
16	31	88.6	236	1 US-08-248-819A-11	Sequence 11, Appl
17	31	88.6	236	1 US-08-607-269-21	Sequence 21, Appl
18	31	88.6	236	1 US-08-607-269-22	Sequence 22, Appl
19	31	88.6	236	2 US-08-337-646A-11	Sequence 11, Appl
20	31	88.6	236	2 US-08-856-531-11	Sequence 11, Appl
21	31	88.6	236	2 US-08-856-034-11	Sequence 11, Appl
22	31	88.6	236	2 US-09-127-048-9	Sequence 9, Appl1
23	31	88.6	236	4 US-08-927-326-11	Sequence 11, Appl
24	31	88.6	236	4 US-09-379-820A-11	Sequence 21, Appl
25	31	88.6	236	5 PCT-US95-04600-21	Sequence 21, Appl
26	31	88.6	236	5 PCT-US95-04600-22	Sequence 22, Appl
27	31	88.6	239	1 US-08-333-565-51	Sequence 51, Appl

28	31	88.6	239	1 US-08-112-208C-10	Sequence 10, Appl
29	31	88.6	239	1 US-08-248-819A-10	Sequence 10, Appl
30	31	88.6	239	1 US-08-248-819A-12	Sequence 12, Appl
31	31	88.6	239	1 US-08-607-269-20	Sequence 20, Appl
32	31	88.6	239	1 US-08-471-058-12	Sequence 12, Appl
33	31	88.6	239	1 US-08-405-702A-12	Sequence 12, Appl
34	31	88.6	239	1 US-08-690-095-4	Sequence 4, Appl1
35	31	88.6	239	2 US-08-465-485A-21	Sequence 21, Appl
36	31	88.6	239	2 US-08-661-479-51	Sequence 51, Appl
37	31	88.6	239	2 US-08-365-466A-15	Sequence 15, Appl
38	31	88.6	239	2 US-08-365-466A-17	Sequence 17, Appl
39	31	88.6	239	2 US-08-337-646A-10	Sequence 10, Appl
40	31	88.6	239	2 US-08-337-646A-12	Sequence 12, Appl
41	31	88.6	239	2 US-08-408-095-16	Sequence 16, Appl
42	31	88.6	239	2 US-08-856-531-10	Sequence 10, Appl
43	31	88.6	239	2 US-08-856-034-10	Sequence 10, Appl
44	31	88.6	239	3 US-08-471-057-12	Sequence 12, Appl
45	31	88.6	239	3 US-09-113-789-4	Sequence 4, Appl1

#### ALIGNMENTS

```

RESULT 1
US-09-252-991A-31360
Sequence 31360, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31360
LENGTH: 452
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31360

Query Match      91.4% Score 32; DB 4; Length 452;
Best Local Similarity 83.3% Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDFSML 6
Db      410 LDFSML 415

RESULT 2
US-08-798-897-13
Sequence 13, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Gaestel, John
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Emond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
US-08-798-897-13

Query Match 88.6%; Score 31; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6  
Db 7 DFSWL 11

RESULT 3  
US-08-978-523-13  
Sequence 13, Application US/08978523  
Patent No. 5883229  
GENERAL INFORMATION:  
APPLICANT: Guastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
TITLE OF INVENTION: Homologue  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,523  
FILING DATE: herewith  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Emond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
US-08-978-523-13

Query Match 88.6%; Score 31; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6  
Db 7 DFSWL 11

RESULT 4  
US-08-337-646A-23  
Sequence 23, Application US/08337646A  
Patent No. 5856171  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: CELL DEATH REGULATORS  
NUMBER OF SEQUENCES: 78  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourile and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/337,646A  
FILING DATE: 10-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,819  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/112,208  
FILING DATE: 26-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000620  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-337-646A-23

Query Match 88.6%; Score 31; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6  
Db 16 DFSWL 20

RESULT 5  
US-08-927-326-23  
Sequence 23, Application US/08927326  
Patent No. 6184202  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.

TITLE OF INVENTION: CELL DEATH REGULATORS  
NUMBER OF SEQUENCES: 78  
CORRESPONDENCE ADDRESS:  
ADDRESSSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/927,326  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/337,646  
FILING DATE: 10-NOV-1994  
APPLICATION NUMBER: US 08/248,819  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/112,208  
FILING DATE: 26-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000620  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-927-326-23

Query Match 88.6%; Score 31; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DFSWL 6  
Db 16 DFSWL 20

RESULT 6  
US-08-337-646A-29  
Sequence 29, Application US/08337646A  
Patent No. 5856171  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: CELL DEATH REGULATORS  
NUMBER OF SEQUENCES: 78  
CORRESPONDENCE ADDRESS:  
ADDRESSSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/337,646A

FILING DATE: 10-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,819  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/112,208  
FILING DATE: 26-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000620  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-337-646A-29

Query Match 88.6%; Score 31; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DFSWL 6  
Db 16 DFSWL 20

RESULT 7  
US-08-927-326-29  
Sequence 29, Application US/08927326  
Patent No. 6184202  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: CELL DEATH REGULATORS  
NUMBER OF SEQUENCES: 78  
CORRESPONDENCE ADDRESS:  
ADDRESSSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/927,326  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/337,646  
FILING DATE: 10-NOV-1994  
APPLICATION NUMBER: US 08/248,819  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/112,208  
FILING DATE: 26-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000620  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-927-326-29

Query Match 88.6%; Score 31; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6  
|||  
Db 16 DFSWL 20

RESULT 8  
US-08-077-848A-3  
Sequence 3, Application US/08077848A  
Patent No. 5470955  
GENERAL INFORMATION:  
APPLICANT: Craig, Ruth W.  
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1  
TITLE OF INVENTION: POLYPEPTIDE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Judas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/077,848A  
FILING DATE: 16-JUN-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: PD-2845  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 154 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: bcl-2alpha  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..154  
US-08-077-848A-3

Query Match 88.6%; Score 31; DB 1; Length 154;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6  
|||  
Db 126 DFSWL 130

RESULT 9

US-09-211-640-3  
Sequence 3, Application US/09211640  
Patent No. 6020466  
GENERAL INFORMATION:

APPLICANT: Craig, Ruth W.  
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1  
TITLE OF INVENTION: POLYPEPTIDE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Judas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/211,640  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/441,375  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: PD-2845  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 154 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: bcl-2alpha  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..154  
US-09-211-640-3

Query Match 88.6%; Score 31; DB 3; Length 154;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6  
|||  
Db 126 DFSWL 130

RESULT 10  
US-09-378-536-3  
Sequence 3, Application US/09378536  
Patent No. 6200763  
GENERAL INFORMATION:  
APPLICANT: Craig, Ruth W.  
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1  
TITLE OF INVENTION: POLYPEPTIDE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Judas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,536  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/077,848  
FILING DATE: 16-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Halle, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: PD-2845  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 154 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: bcl-2alpha  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..154  
US-09-378-536-3

Query Match 88.6%; Score 31; DB 3; Length 154;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DPSWL 6  
DB 126 DPSWL 130

RESULT 11  
US-09-687-260-3  
Sequence 3, Application US/09687260  
Patent No. 6528263  
GENERAL INFORMATION:  
APPLICANT: Craigs, Ruth W.  
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1  
POLYPEPTIDE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/687,260  
FILING DATE: 12-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,536  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Halle, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: PD-2845  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 154 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: bcl-2alpha  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..154  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-687-260-3

Query Match 88.6%; Score 31; DB 4; Length 154;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DPSWL 6  
DB 126 DPSWL 130

RESULT 12  
US-08-408-095-19  
Sequence 19, Application US/08408095  
Patent No. 5858678  
GENERAL INFORMATION:  
APPLICANT: Chinadural, Govindasamy  
TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SUGRUE, MION, ZINN, MACPEAK & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/408,095  
FILING DATE: 21-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mack, Susan J.  
REGISTRATION NUMBER: 30,951  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7860  
TELEFAX: (202)293-7060  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 229 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-408-095-19

Query Match 88.6%; Score 31; DB 2; Length 229;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DPSWL 6  
DB 126 DPSWL 130

Db 201 DFSWL 205

RESULT 13  
US-08-408-095-17  
Sequence 17, Application US/08408095  
Patent No. 5858678  
GENERAL INFORMATION:  
APPLICANT: Chinadurai, Govindaswamy  
TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/408,095  
FILING DATE: 21-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mack, Susan J.  
REGISTRATION NUMBER: 30,951  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-408-095-17

Query Match 88.6%; Score 31; DB 2; Length 232;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6  
Db 204 DFSWL 208

RESULT 14  
US-08-408-095-18  
Sequence 18, Application US/08408095  
Patent No. 5858678  
GENERAL INFORMATION:  
APPLICANT: Chinadurai, Govindaswamy  
TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/408,095

FILING DATE: 21-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mack, Susan J.  
REGISTRATION NUMBER: 30,951  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-408-095-18

Query Match 88.6%; Score 31; DB 2; Length 232;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6  
Db 204 DFSWL 208

RESULT 15  
US-08-112-208C-11  
Sequence 11, Application US/08112208C  
Patent No. 5691179  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: CELL DEATH REGULATORS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourile and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/112,208C  
FILING DATE: 26-AUG-1993  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 236 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-112-208C-11

Query Match 88.6%; Score 31; DB 1; Length 236;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DFSWL 6  
Db 208 DFSWL 212

• Wed Feb 18 17:21:03 2004

us-09-643-260-11.ra1

Page 7

Search completed: February 18, 2004, 14:41:49  
Job time : 8.06579 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds  
(without alignments)  
79.423 Million cell updates/sec

Title: US-09-643-260-10

Perfect score: 33

Sequence: 1 LDASWL 6

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched:

127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	90.9	290	1	BLAI_XANMA
2	30	90.9	648	1	Y084_HUMAN
3	30	90.9	918	1	CARP_CORGL
4	30	90.9	919	1	CARP_CORCT
5	29	87.9	177	1	CYCL_PARDE
6	29	87.9	245	1	HIS4_SHEON
7	29	87.9	277	1	THTI_CABEL
8	29	87.9	286	1	YD8C_ECOLI
9	29	87.9	289	1	THTR_CHICK
10	29	87.9	295	1	THTR_RAT
11	29	87.9	296	1	RECO_NANSP
12	29	87.9	296	1	THTM_HUMAN
13	29	87.9	296	1	THTR_RAT
14	29	87.9	296	1	THTR_BOVIN
15	29	87.9	296	1	THTR_CHICK
16	29	87.9	296	1	THTR_HUMAN
17	29	87.9	296	1	THTR_MOUSE
18	29	87.9	359	1	RFBG_SALTY
19	29	87.9	360	1	NMT2_CABEL
20	29	87.9	424	1	Y826_METTH
21	29	87.9	430	1	PUCK_BACSU
22	29	87.9	459	1	NU4M_WGUSL
23	29	87.9	464	1	Y113_CABEL
24	29	87.9	477	1	RP54_ECOLI
25	29	87.9	477	1	RP54_KLEPN
26	29	87.9	477	1	RP54_SALTY
27	29	87.9	481	1	CHPS_EMENT
28	29	87.9	491	1	XYIE_ECOLI
29	29	87.9	509	1	TDT_HUMAN
30	29	87.9	510	1	G6PD_ASPNG
31	29	87.9	511	1	G6PD_EMENT
32	29	87.9	511	1	DKC1_HUMAN
33	29	87.9	520	1	TDT_BOVIN

34	29	87.9	854	1	DIS1_HUMAN	Q9ar15 homo sapien
35	29	87.9	1034	1	BGAL_BACME	O52847 bacillus me
36	29	87.9	1043	1	RPO_NODAY	O91mm4 nodamura vi
37	29	87.9	3770	1	ACVS_EMENT	P27742 emericella
38	28	84.8	225	1	ALKD_PSEPU	P00885 pseudomonas
39	28	84.8	230	1	GPR4_BUCAP	O8x9n1 buchnera ap
40	28	84.8	325	1	IRF1_HUMAN	P10914 homo sapien
41	28	84.8	401	1	HIS2_SYNY3	P74592 synchocyst
42	28	84.8	494	1	DROM_HUMAN	O9np87 homo sapien
43	28	84.8	502	1	NU2C_MESVI	O9mug6 mesocriceta
44	28	84.8	506	1	TDT_CHICK	P36195 gallus gall
45	28	84.8	508	1	NO60_DROME	O44081 drosophila

## ALIGNMENTS

RESULT 1  
BLAI\_XANMA STANDARD; PRT; 290 AA.  
AC P52700;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Metallo-beta-lactamase LI precursor (Beta-lactamase, type II)  
DS (EC 3.5.2.6) (Penicillinase).  
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
OC Xanthomonadaceae; Stenotrophomonas.  
OX NCBI\_TaxID=40324;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IID 1275;  
RX MEDLINE=94289479; PubMed=8018721;  
RA Walsh T.R., Hall L., Asensio S.J., Nichols W.W., Cartwright S.J.,  
RA Macgowan A.P., Bennett P.W.;  
RT "Sequence analysis of the LI metallo-beta-lactamase from Xanthomonas maltophilia."  
RT Biochem. Biophys. Acta 1218:199-201(1994).  
RN [2]  
RP SEQUENCE OF 34-65.  
RC STRAIN=IID 1275;  
RX MEDLINE=86025393; PubMed=3931629;  
RA Bicknell R., Emanuel E.L., Gagnon J., Waley S.G.;  
RT "The production and molecular properties of the zinc beta-lactamase of Pseudomonas maltophilia IID 1275."  
RT Biochem. J. 229:791-797(1985).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).  
RX MEDLINE=99030465; PubMed=9611546;  
RA Ullah J.H., Walsh T.R., Taylor I.A., Emery D.C., Verma C.S.,  
RA Gambin S.J., Spencer J.;  
RT "The crystal structure of the LI metallo-beta-lactamase from Stenotrophomonas maltophilia at 1.7 A resolution."  
RT J. Mol. Biol. 284:125-136(1998).  
CC -1- FUNCTION: HAS A HIGH ACTIVITY AGAINST IMPENEM. UNSTABLE BELOW PH 8, UNLESS ZINC IS PRESENT.  
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-amino acid.  
CC -1- COFACTOR: BINDS TWO ZINC IONS PER MOLECULE.  
CC -1- ENZYME REGULATION: Inhibited by Hg(2+) or Cu(2+). Reduced enzymatic activity in presence of Co(2+), Ni(2+), Cd(2+), and Mn(2+).  
CC -1- SUBUNIT: Homotrimer.  
CC -1- SUBCELLULAR LOCATION: Periplasmic (potential).  
CC -1- SIMILARITY: Belongs to the class-B beta-lactamase family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial



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-----

DR EMBL; X75074; CAA52968.1; -  
 DR PIR; S45349; S45349.  
 DR PDB; 1SML; 20-SEP-99.  
 DR InterPro; IPR001018; Beta\_lactamase\_B.  
 DR InterPro; IPR001279; Bactamase-like.  
 DR Pfam; PF00753; lactamase\_B.1.  
 DR PROSITE; PS00743; BETA\_LACTAMASE\_B\_1.1.  
 DR PROSITE; PS00744; BETA\_LACTAMASE\_B\_2. FALSE NEG.  
 KW Hydrolyase; Zinc; Antibiotic resistance; Periplasmic; Signal;  
 3D-structure.

KM SIGNAL 1  
 FT PROPEP 22  
 FT CHAIN 34  
 FT DISULFID 239  
 FT METAL 105  
 FT METAL 107  
 FT METAL 109  
 FT METAL 181  
 FT METAL 205  
 FT METAL 217  
 FT CONFLICT 36  
 FT CONFLICT 40  
 FT CONFLICT 56  
 FT CONFLICT 63  
 FT CONFLICT 63  
 FT HELIX 36  
 FT STRAND 41  
 FT STRAND 45  
 FT TURN 49  
 FT STRAND 51  
 FT STRAND 56  
 FT TURN 57  
 FT STRAND 59  
 FT STRAND 62  
 FT TURN 67  
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 FT STRAND 76  
 FT HELIX 78  
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 FT HELIX 108  
 FT TURN 112  
 FT HELIX 114  
 FT STRAND 124  
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 FT TURN 143  
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 FT TURN 169  
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 FT TURN 218  
 FT TURN 221  
 FT HELIX 223  
 FT TURN 236  
 FT STRAND 241  
 FT HELIX 247  
 FT TURN 251  
 FT HELIX 254  
 FT TURN 260

POTENTIAL.  
 METALLO-BETA-LACTAMASE L1.  
 ZINC 1.  
 ZINC 1.  
 ZINC 2.  
 ZINC 1.  
 ZINC 2.  
 ZINC 2.  
 AS -> OR (IN REF. 2).  
 Q -> A (IN REF. 2).  
 TED -> ROH (IN REF. 2).  
 L -> H (IN REF. 2).

FT HELIX 267 287  
 SQ SEQUENCE 290 AA; 30801 MW; 0B34CAB54518BC1E CRC64;  
 Query Match 90.9%; Score 30; DB 1; Length 290;  
 Best Local Similarity 83.3%; Pred. No. 73;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
 DB 34 VDAASWL 39

RESULT 2  
 Y084 HUMAN STANDARD; PRT; 648 AA.  
 ID Y084 HUMAN  
 AC 014639;  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical protein KIAA0084 (HA2022) (Fragment).  
 GN KIAA0084.  
 OS Homo sapiens (Human).  
 OC Burkarya; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=95308325; PubMed=7788527;  
 RA Nagase T., Miyajima K., Tanaka A., Saruka T., Seki N., Sato S.,  
 RA Tabata S., Ishikawa K.-I., Kawabayashi Y., Kotani H., Nomura N.,  
 RT "Prediction of the coding sequences of unidentified human genes. III.  
 RT The coding sequences of 40 new genes (KIAA081-KIAA0120) deduced by  
 RT analysis of cDNA clones from human cell line KG-1.";  
 RL DNA Res. 2:37-43(1995).

-----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 DR EMBL; D42043; BAA0764.1; -  
 KM Hypothetical protein.  
 SQ SEQUENCE 648 AA; 70463 MW; 88F68A62D6C1CDA1 CRC64;  
 NON TER 1  
 SQ

Query Match 90.9%; Score 30; DB 1; Length 648;  
 Best Local Similarity 83.3%; Pred. No. 1,6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
 DB 384 LDASWL 389

RESULT 3  
 CAP CORGL STANDARD; PRT; 918 AA.  
 ID CAP CORGL  
 AC P12860;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase) (PEPC).  
 GN PEP OR CGL1585.  
 OS Corynebacterium glutamicum (Brevibacterium flavum).  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
 OX NCBI\_TaxID=1718;  
 RN [1]  
 RP SEQUENCE FROM N.A.

```

RC STRAIN-ATCC 13059 / AS019;
RA MEDLINE=89384460; PubMed=279518;
RA Eikmanns B.J., Follett M.T., Griot M.U., Sinskey A.J.;
RT "The phosphoenolpyruvate carboxylase gene of Corynebacterium
RT glutamicum: molecular cloning, nucleotide sequence, and expression.";
RL Mol. Genet. 218:330-339(1989).
RN (2)
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.
RC STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
RX MEDLINE=89326141; PubMed=2666264;
RA O'Regan M., Thierbach G., Bachmann B., Valleau D., Lepage P.,
RA Viret J.F., Lemoine Y.;
RT "Cloning and nucleotide sequence of the phosphoenolpyruvate
RT carboxylase-coding gene of Corynebacterium glutamicum ATCC13032.";
RL Gene 77:237-251(1989).
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
RX Nakagawa S.;
RL "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RT Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Through the carboxylation of phosphoenolpyruvate (PEP)
CC it forms oxaloacetate, a four-carbon dicarboxylic acid source for
CC the tricarboxylic acid cycle.
CC -1- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
CC phosphoenolpyruvate + CO(2).
CC -1- ENZYME REGULATION: ACTIVITY NOT STIMULATED BY ACETYL-COA IN THE
CC ABSENCE OF ANY ALLOSTERIC INHIBITOR, WHILE THE CORRESPONDING
CC PROTEIN FROM E. COLI IS STRONGLY STIMULATED.
CC -1- PATHWAY: Tricarboxylic acid cycle.
CC -1- SIMILARITY: BELONGS TO THE PEPCase FAMILY.
-----
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CC or send an email to license@isb-sdb.ch).
-----
CC EMBL; X14234; CNA32450.1; -
CC DR EMBL; M25819; AAB3537.1; -
CC DR EMBL; A09073; CAA0837.1; -
CC DR EMBL; AP05279; BAB98978.1; -
CC DR PIR; S05512; QYFKG.
CC DR HSSP; P00864; IFYI.
CC DR HAMAP; MF_00595; -; 1.
CC DR InterPro; IPR001449; PEPCase.
CC DR Pfam; PF00311; PEPCase; 1.
CC DR PRINTS; PR00150; PEPCaseX1.
CC DR PROSITE; PS00393; PEPCase_2; 1.
CC DR PROSITE; PS00781; PEPCase_1; 1.
CC KW Lyase; Carbon dioxide fixation; Tricarboxylic acid cycle;
CC Complete proteome.
CC FT INIT MET 0
CC FT ACT_SITE 137 137 BY SIMILARITY.
CC FT ACT_SITE 578 578 BY SIMILARITY.
CC FT ACT_SITE 606 607 KL -> NV (IN REF. 1).
CC FT CONFLICT 799 800 FT -> LP (IN REF. 1).
CC FT CONFLICT 914 914 L -> V (IN REF. 1).
CC FT CONFLICT 914 914 L -> V (IN REF. 1).
CC SQ SEQUENCE 918 AA; 103066 MW; A56C2703169D0698 CRC64;

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Query Match 90.9%; Score 30; DB 1; Length 918;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
 DB 104 LDATWL 109

RESULT 4  
 CAPT\_CORCT

```

ID CAPT CORCT STANDARD; PRT; 919 AA.
AC Q93MR3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase) (PEPC).
GN PEP.
OS Corynebacterium crenatum.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=168810;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CD945;
RA Liu Y., Ding J., Wang Y.;
RT "Cloning and expression of phosphoenolpyruvate carboxylase-coding gene
RT in Corynebacterium crenatum CD945.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Through the carboxylation of phosphoenolpyruvate (PEP)
CC it forms oxaloacetate, a four-carbon dicarboxylic acid source for
CC the tricarboxylic acid cycle.
CC -1- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
CC phosphoenolpyruvate + CO(2).
CC -1- PATHWAY: Tricarboxylic acid cycle.
CC -1- SIMILARITY: BELONGS TO THE PEPCase FAMILY.
-----
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-----
CC DR EMBL; AF406314; AAK92540.1; -
CC DR HAMAP; MF_00595; -; 1.
CC DR InterPro; IPR001449; PEPCase.
CC DR Pfam; PF00311; PEPCase; 1.
CC DR PRINTS; PR00150; PEPCaseX1.
CC DR PROSITE; PS00781; PEPCase_1; 1.
CC DR PROSITE; PS00393; PEPCase_2; 1.
CC KW Lyase; Carbon dioxide fixation; Tricarboxylic acid cycle.
CC FT ACT_SITE 138 138 BY SIMILARITY.
CC FT ACT_SITE 579 579 BY SIMILARITY.
CC SQ SEQUENCE 919 AA; 103331 MW; 10A3F364A4FPE604 CRC64;

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Query Match 90.9%; Score 30; DB 1; Length 919;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
 DB 105 LDATWL 110

RESULT 5  
 ID CYCL\_PARDR STANDARD; PRT; 177 AA.  
 AC P29899;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c-h precursor (Cytochrome C5511) (C552).  
 GN MOX.  
 OS *Paracoccus denitrificans*.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;  
 OC Rhodobacteraceae; *Paracoccus*.  
 OX NCBI\_TaxID=266;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Pd 1222;  
 RX MEDLINE=92041581; PubMed=1657871;  
 van Spanning R.J.M., Wansell C.W., de Boer T., Hazelaar M.J.,

RA Anazawa H., Harms N., Oltmann L.F., Stouthamer A.H.:  
 RT "Isolation and characterization of the *moxX*, *moxY*, and *moxR*  
 RT genes of *Paracoccus denitrificans*: inactivation of *moxX*, *moxY*, and  
 RT *moxR* and the resultant effect on methylothrophic growth." ;  
 RL J. Bacteriol. 173:6948-6961(1991).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).  
 RX MEDLINE=9418715; PubMed=810419;  
 RA Chen L., Durley R., Mathews F.S., Davidson V.L.:  
 RT "Structure of an electron transfer complex: methylamine  
 RT dehydrogenase, amicyanin, and cytochrome c551." ;  
 RL Science 264:86-90(1994).  
 CC -1- FUNCTION: ELECTRON ACCEPTOR FOR MDH. ACTS IN METHANOL OXIDATION.  
 CC THIS CYTOCHROME HAS A REDOX POTENTIAL OF ABOUT +190 MV.  
 CC -1- SUBCELLULAR LOCATION: Periplasmic (Potential).  
 CC -1- INDUCTION: DURING GROWTH ON METHANOL.  
 CC -----  
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 CC -----  
 CC EMBL, M57684; AAA25583.1; -.  
 DR PIR; B41377; B41377.  
 DR PDB; 2MTA; 31-JAN-94.  
 DR InterPro; IPR000345; Cytc heme bind.  
 DR PROSITE; PS00190; CYTOCHROME C/ 1.  
 KM Electron transport; Heme; Signal; Methanol utilization; Periplasmic;  
 KW 3D-structure. 1  
 FT SIGNAL 1 22 POTENTIAL.  
 FT CHAIN 23 177 CYTOCHROME C-L. (BY SIMILARITY).  
 FT BINDING 79 79 HEME (COVALENT) (BY SIMILARITY).  
 FT BINDING 82 82 HEME (COVALENT) (BY SIMILARITY).  
 FT METAL 83 83 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
 FT STRAND 27 27  
 FT STRAND 34 34  
 FT STRAND 37 39  
 FT HELIX 42 44  
 FT HELIX 48 56  
 FT HELIX 60 63  
 FT TURN 65 67  
 FT HELIX 68 78  
 FT TURN 79 79  
 FT HELIX 80 83  
 FT TURN 85 86  
 FT HELIX 103 106  
 FT HELIX 108 117  
 FT TURN 121 122  
 FT TURN 127 129  
 FT HELIX 132 144  
 FT TURN 145 145  
 FT TURN 150 151  
 FT TURN 154 155  
 FT HELIX 158 162  
 FT TURN 163 163  
 SQ SEQUENCE 177 AA; 19396 MW; 6949FBC8B2C056E CRC64;  
 Query Match 87.9%; Score 29; DB 1; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 69;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DASWL 6  
 DB 152 DASWL 156  
 RESULT 6  
 HIS4\_SHEON STANDARD; PRT; 245 AA.  
 AC Q8EFB5;

DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) methylideneamino]  
 DE imidazole-4-carboxamide isomerase (EC 5.3.1.16)  
 DE (phosphoribosylformimino-5-aminoimidazole carboxamide ribotide  
 DE isomerase)  
 GN HIS4 OR SO2069.  
 OS Shewanella oneidensis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
 OC Alteromonadaceae; Shewanella.  
 OX NCBI\_Taxid=70863;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NR-1;  
 RX MEDLINE=22297686; PubMed=12368813;  
 RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,  
 RA Read T.D., Eisen J.A., Seshadri R., Ward N., Meehe B., Clayton R.A.,  
 RA Meyer T., Tsapin A., Scott J., Beaman M., Brinkac L., Daugherty S.,  
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Helt D.H., Kolonay J.F.,  
 RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,  
 RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,  
 RA Mueller J., Khouir H., Gill J., Uterback T.R., McDonald L.A.,  
 RA Fiedlyum T.V., Smith H.O., Venter J.C., Neilson K.H., Fraser C.M.;  
 RT "Genome sequence of the dissimilatory metal ion-reducing bacterium  
 RT *Shewanella oneidensis*." ;  
 RL Nat. Biotechnol. 20:1118-1123(2002).  
 CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-5-[(5-  
 CC phosphoribosylamino) methylideneamino] imidazole-4-carboxamide = 5-  
 CC [(5-phospho-1-deoxyribosyl)-1-ylamino] methylideneamino-1-(5-  
 CC phosphoribosyl)imidazole-4-carboxamide.  
 CC -1- PATHWAY: Histidine biosynthesis; fourth step.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE HIS4 / HISP FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL, AE015648; AAN55116.1; -.  
 DR TIGR; SO2069; -.  
 DR HAMAP; MF\_01014; -; 1.  
 DR InterPro; IPR006063; His4.  
 DR InterPro; IPR006062; His biosynth.  
 DR Pfam; PR00977; His biosynth; 1.  
 DR TIGRPFAM; TIGR00007; TIGR00007; 1.  
 KW Isomerase; Histidine biosynthesis; Complete proteome.  
 SQ SEQUENCE 245 AA; 26017 MW; 6D40B1B3604527DA CRC64;  
 Query Match 87.9%; Score 29; DB 1; Length 245;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DASWL 6  
 DB 42 DASWL 46  
 RESULT 7  
 THY1\_CABEL STANDARD; PRT; 277 AA.  
 AC P91247;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Putative thiosulfate sulfurtransferase Flig11.9 (EC 2.8.1.1).  
 GN Flig11.9.  
 OS *Caenorhabditis elegans*.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhoditidae; Peloderinae; Caenorhabditis.  
 OK NCBI\_TaxID=6239;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Brictol N2;  
 RA Latreille P., Deadman R.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.  
 CC -1- SIMILARITY: Contains 2 rhodanese domains.  
 CC -----  
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 CC -----  
 CC EMBL: U80451; AAB37840.1; --  
 CC DR PIR: T29797; T29797.  
 CC DR HSSP: P00586; IRHS.  
 CC DR WormPep: F11G1.9; CE09351.  
 CC DR InterPro: IPR001763; Rhodanese-like.  
 CC DR InterPro: IPR001307; Rhodanese.  
 CC DR Pfam: PF00581; Rhodanese; 1.  
 CC DR SMART: SM00450; RHOD; 1.  
 CC DR PROSITE: PS00683; RHODANES2; FALSE\_NEG.  
 CC DR PROSITE: PS50206; RHODANES3; 2.  
 CC KW Hypothetical protein; Transferrase; Repeat.  
 CC FT DOMAIN 15 153 RHODANES2 1.  
 CC FT ACT\_SITE 258 258 RHODANES2 2.  
 CC FT ACT\_SITE 258 258 BY SIMILARITY.  
 CC SQ SEQUENCE 277 AA; 30699 MW; 25BDP666CE12824C CRC64;  
 CC  
 CC Query Match 87.9%; Score 29; DB 1; Length 277;  
 CC Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 LDASW 5  
 CC DB 22 LDASW 26  
 CC  
 CC RESULT 8  
 CC YDBC\_ECOLI STANDARD; PRT; 286 AA.  
 CC AC P25906;  
 CC DT 01-MAY-1992 (Rel. 22, Created)  
 CC DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 CC DE Hypothetical oxidoreductase ydbc (EC 1.-.-.-).  
 CC YDBC OR B1406.  
 CC OS Escherichia coli.  
 CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Escherichia.  
 CC NCBI\_TaxID=562;  
 CC RN (1)  
 CC RP SEQUENCE FROM N.A.  
 CC RC STRAIN=K12;  
 CC RX MEDLINE=92190338; PubMed=1665988;  
 CC RA Moszer I., Glaser P., Danchin A.;  
 CC RT "Multiple 18 insertion sequences near the replication terminus in  
 CC Escherichia coli K-12.";  
 CC RL Biochimie 73:1361-1374(1991).  
 CC RN (2)  
 CC RP SEQUENCE FROM N.A.  
 CC RC STRAIN=K12 / MG1655;  
 CC RX MEDLINE=97426677; PubMed=9278503;  
 CC RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 CC Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 CC Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 CC Mau B., Shao Y.;  
 CC RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).  
 RN (3)  
 RN RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=97251357; PubMed=9097039;  
 RA Alba H., Baba T., Fujita K., Hayaishi K., Inada T., Isono K.,  
 RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,  
 RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,  
 RA Motomura K., Nakase S., Nakamura Y., Nishimoto H., Nishio Y.,  
 RA Oshima T., Saito N., Samped G., Seki Y., Sivasubram S.,  
 RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,  
 RA Yamamoto Y., Horuchi T.;  
 RT "A 570-Kb DNA sequence of the Escherichia coli K-12 genome  
 RT corresponding to the 28.0-40.1 min region on the linkage map.";  
 RL DNA Res. 3:363-377(1996).  
 CC [4]  
 CC RP SEQUENCE OF 1-69 FROM N.A.  
 CC RC STRAIN=M / ATCC 11105;  
 CC RX MEDLINE=98421522; PubMed=9748275;  
 CC RA Ferrandez A., Minambres B., Garcia B., Olivera E.R., Luengo J.M.,  
 CC RA Garcia J.L., Diaz E.;  
 CC RT "Carbonylism of phenylacetic acid in Escherichia coli. Characterization  
 CC of a new aerobic hybrid pathway".  
 CC J. Biol. Chem. 273:25974-25986(1998).  
 CC -1- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.  
 CC -----  
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 CC -----  
 CC DR EMBL: X62680; AAC44553.1; --  
 CC DR EMBL: AE000238; CAAC74488.1; --  
 CC DR EMBL: D90779; BAA15021.1; --  
 CC DR EMBL: X97452; CAA6103.1; --  
 CC DR PIR: A48399; A48399.  
 CC DR HSSP: P06632; 1HW6.  
 CC DR Ecogene; EG11309; ydbc.  
 CC DR InterPro: IPR001395; Aldo/Ket\_red.  
 CC DR Pfam; PF00248; Aldo\_ket\_red.  
 CC DR PRINTS; PR00069; ALDKETREDTASE.  
 CC DR ProDom; PD000288; Aldo/ket\_red; 1.  
 CC KW Hypothetical protein; Oxidoreductase; Complete proteome.  
 CC SQ SEQUENCE 286 AA; 30706 MW; 82B587AEA9115EP9 CRC64;  
 CC  
 CC Query Match 87.9%; Score 29; DB 1; Length 286;  
 CC Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 2 DASWL 6  
 CC DB 92 DASWL 96  
 CC  
 CC RESULT 9  
 CC THTR\_CHICK STANDARD; PRT; 289 AA.  
 CC AC P25324;  
 CC DT 01-MAY-1992 (Rel. 22, Created)  
 CC DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 CC DE Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese).  
 CC GN TST  
 CC OS Gallus gallus (Chicken).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC OC Gallus.  
 CC NCBI\_TaxID=9031;  
 CC RN (1)  
 CC RP SEQUENCE.

RC TISSUE=Liver;  
 RX MEDLINE=91113289; PubMed=2275748;  
 RA Kohanski R.A., Heinrichson R.L.;  
 RT "Primary structure of avian hepatic rhodanese.";  
 RL J. Protein Chem. 9:369-377(1990).  
 CC -1- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE  
 DETOXIFICATION.  
 CC -1- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -1- TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.  
 CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR  
 CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,  
 THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.  
 CC -1- SIMILARITY: Contains 2 rhodanese domains.  
 DR PIR; A37209; A37209.  
 DR HSSP; P00586; 1RHS.  
 DR InterPro; IPR001763; Rhodanese-like.  
 DR InterPro; IPR001307; Rhodanese.  
 DR Pfam; PF00581; Rhodanese; 2.  
 DR SMART; SM00450; RHOD; 2.  
 DR PROSITE; PS00380; RHODANES\_1; 1.  
 DR PROSITE; PS00683; RHODANES\_2; 1.  
 DR PROSITE; PS50206; RHODANES\_3; 2.  
 KM Transferrase; Mitochondrion; Repeat.  
 FT DOMAIN 24 142 RHODANES\_1.  
 FT DOMAIN 143 158 HINGE.  
 FT DOMAIN 172 284 RHODANES\_2.  
 FT ACT\_SITE 186 166 MAY PLAY A ROLE IN SUBSTRATE BINDING (BY  
 SIMILARITY).  
 FT ACT\_SITE 244 244 BY SIMILARITY.  
 FT ACT\_SITE 245 245 SUBSTRATE (THIOSULFATE) BINDING  
 (BY SIMILARITY).  
 FT ACT\_SITE 246 246 SUBSTRATE (THIOSULFATE) BINDING  
 (BY SIMILARITY).  
 SQ SEQUENCE 289 AA; 32286 MW; 8BFCF71DE0B2BA4 CRC64;  
 Query Match 87.9%; Score 29; DB 1; Length 289;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDASW 5  
 DB 31 LDASW 35  
 RESULT 10  
 THTR RAT STANDARD; PRT; 295 AA.  
 AC P24379;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Thiosulfate sulfotransferase (EC 2.8.1.1) (Rhodanese) (Fragment).  
 GN TST.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RX MEDLINE=91207296; PubMed=2018478;  
 RA Weiland K.L., Dooley T.P.;  
 RT Molecular cloning, sequencing and characterization of cDNA to rat  
 liver rhodanese, a thiosulphate sulphurtransferase.";  
 RL Biochem. J. 275:227-231(1991).  
 RN [2]  
 RP MUTAGENESIS.  
 RC TISSUE=Liver;  
 RX MEDLINE=95332330; PubMed=7608189;  
 RA Nagahara N., Okazaki T., Nishino T.;  
 RT "Cytosolic mercaptopropylate sulfotransferase is evolutionarily

RT related to mitochondrial rhodanese. Striking similarity in active site  
 RT amino acid sequence and the increase in the mercaptopropylate  
 RT sulfotransferase activity of rhodanese by site-directed  
 RT mutagenesis.";  
 RL J. Biol. Chem. 270:16230-16235(1995).  
 CC -1- FUNCTION: INVOLVED IN THE FORMATION OF IRON-SULFUR COMPLEXES,  
 CYANIDE DETOXIFICATION OR MODIFICATION OF SULFUR-CONTAINING  
 ENZYMES. OTHER THIOL COMPOUNDS, BESIDES CYANIDE, CAN ACT AS SULFUR  
 ION ACCEPTORS. ALSO HAS WEAK MERCAPTOPROPYLATE SULFOTRANSFERASE  
 (MST) ACTIVITY.  
 CC -1- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -1- TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.  
 CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR  
 CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,  
 THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.  
 CC -1- SIMILARITY: Contains 2 rhodanese domains.  
 CC -----  
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 CC -----  
 DR EMBL; X56228; CA93677.1; -.  
 DR PIR; S15081; S15081.  
 DR HSSP; P00586; 1RHS.  
 DR InterPro; IPR001763; Rhodanese-like.  
 DR InterPro; IPR001307; Rhodanese.  
 DR Pfam; PF00581; Rhodanese; 2.  
 DR SMART; SM00450; RHOD; 2.  
 DR PROSITE; PS00380; RHODANES\_1; 1.  
 DR PROSITE; PS00683; RHODANES\_2; 1.  
 DR PROSITE; PS50206; RHODANES\_3; 2.  
 KM Transferrase; Mitochondrion; Repeat.  
 FT NON\_TER 1 1  
 FT DOMAIN 23 141 RHODANES\_1.  
 FT DOMAIN 142 157 HINGE.  
 FT DOMAIN 171 286 RHODANES\_2.  
 FT ACT\_SITE 185 165 MAY PLAY A ROLE IN SUBSTRATE BINDING (BY  
 SIMILARITY).  
 FT ACT\_SITE 246 246 BY SIMILARITY.  
 FT ACT\_SITE 247 247 SUBSTRATE (THIOSULFATE) BINDING.  
 FT ACT\_SITE 248 248 SUBSTRATE (THIOSULFATE) BINDING.  
 FT MUTAGEN R->G; UNALTERED RHODANES ACTIVITY;  
 FT MUTAGEN K->S; DECREASED RHODANES ACTIVITY;  
 FT MUTAGEN UNALTERED MST ACTIVITY.  
 SQ SEQUENCE 295 AA; 33176 MW; 24C55B35690934E1 CRC64;  
 Query Match 87.9%; Score 29; DB 1; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDASW 5  
 DB 30 LDASW 34  
 RESULT 11  
 RECO ANASP STANDARD; PRT; 296 AA.  
 AC Q8YPL9;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE DNA repair protein reco (Recombination protein O).  
 GN RECO OR ALR4175.  
 OS Anabaena sp. (strain PCC 7120).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.

OX NCBI\_TaxID=103690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21595285; PubMed=11759840;  
 RA Kaneko T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,  
 RA Matnabe A., Iriuch M., Ichikawa A., Kawasumi K., Kimura T.,  
 RA Kishida Y., Kohara M., Matsumoto M., Matsumoto A., Muraki A.,  
 RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,  
 RA Yasuda M., Tabata S.,  
 RT "Complete genomic sequence of the filamentous nitrogen-fixing  
 RT cyanobacterium *Anabaena* sp. strain PCC 7120.";  
 RL DNA Res. 8:205-213 (2001).  
 CC -1- FUNCTION: Involved in DNA repair and recombination  
 CC -1- SIMILARITY: BELONGS TO THE RECO FAMILY.  
 CC -1- SIMILARITY: BELONGS TO THE RECO FAMILY.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AP003595; BAB75874.1; -.  
 DR PIR: AH2327; AH2327.  
 DR HAMAP: MF\_00201; -; 1.  
 DR InterPro: IPR003717; RECO.  
 DR Pfam: PF02565; RECO; 1.  
 DR DNA repair: DNA recombination; Complete proteome.  
 KW SEQUENCE 296 AA; 32728 MW; A5B3D540F162BB72 CR664;  
 SQ  
 Query Match 87.9%; Score 29; DB 1; Length 296;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DASWL 6  
 DB 256 DASWL 260  
 RESULT 12  
 THRM\_HUMAN STANDARD; PRT; 296 AA.  
 ID THRM\_HUMAN  
 AC P25325; 075750;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE 3-mercaptoacetyltransferase (EC 2.8.1.2) (MST).  
 GN MST OR TST2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=92062122; PubMed=1953758;  
 RA Pallini R., Guazzi G.C., Cannela C., Cacace M.G.,  
 RT "Cloning and sequence analysis of the human liver rhodanese:  
 RT comparison with the bovine and chicken enzymes.";  
 RL Biochem. Biophys. Res. Commun. 180:887-893 (1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20057165; PubMed=10591208;  
 RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,  
 RA Clamp M., Smith L.J., Alnecough R., Almeida J.P., Babbage A.K.,  
 RA Bagguley C., Bailey J., Bartow K.F., Bates K.N., Beasley O.P.,  
 RA Bird C.P., Blakey S.B., Bridgeman A.M., Buck D., Burgess J.,  
 RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,  
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,  
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,  
 RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,

RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,  
 RA Gilbert J.G.R., Goward M.E., Grafton D.V., Griffiths M.N.D., Hall C.,  
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,  
 RA Hunt S.E., Jones M.C., Kerhaw J., Kimberley A.M., King A.,  
 RA Laird G.K., Langford C.F., Leverhulme M.A., Lloyd C., Lloyd D.M.,  
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,  
 RA McElay J., McLaren S., McMurtry A.A., Milne S.A., Mortimore B.J.C.T.,  
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,  
 RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L.,  
 RA Scott C.E., Sehra H.K., Skuse C.D., Smalley S., Smith M.L.,  
 RA Soderlund C., Spraggon L., Steward C.A., Sulston J.E., Swann R.M.,  
 RA Vandin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,  
 RA Williams L., Williams S.A., Williamson H., Wilner T.E., Wilming L.,  
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,  
 RA Winochima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,  
 RA Shitani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,  
 RA Roe B.A., Chen P., Chu L., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,  
 RA Dorman A., Fang P., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,  
 RA Lewis J., Lewis S., Lin S.-P., Lon P., Malat B., Nguyen T., Pan H.,  
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,  
 RA Zhan Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,  
 RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Mux P.,  
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,  
 RA Cortes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,  
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,  
 RA Scheet P., Walker C., Wamsley A., Wohlmann P., Popin K., Nelson J.,  
 RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,  
 RA Emanual H.S., Shaikh T., Kurahashi H., Saito S., Budarf M.L.,  
 RA Mcdermid B.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,  
 RA Kim U.J., Shizuya H., Simon M.I., Dunham J.P., Beyard M., Kedra D.,  
 RA Seroussi E., Franssen I., Tapia I., Bruder C.B., O'Brien K.P.,  
 RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,  
 RA Tilahun Y., Wright H.,  
 RT "The DNA sequence of human chromosome 22.";  
 RL Nature 402:469-495 (1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Bone marrow, Muscle, and Pancreas;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen G.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang Y., Hsieh P.,  
 RA Diatchenko L., Marulita K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Uvedin T.B., Toshlyuk S., Carantini P., Prange C.,  
 RA Rabe S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Boak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalsky U., Smalios D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC -1- FUNCTION: TRANSFER OF A SULFUR ION TO CYANIDE OR TO OTHER THIOL  
 CC COMPOUNDS. ALSO HAS WEAK RHODANASE ACTIVITY. MAY HAVE A ROLE IN  
 CC CYANIDE DEGRADATION OR IN THIOL-SULFATE BIOSYNTHESIS.  
 CC -1- CATALYTIC ACTIVITY: 3-mercaptoacetyltransferase + pyruvate +  
 CC thioacetate.  
 CC -1- SUBUNIT: MONOMER OR DISULFIDE-LINKED HOMODIMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR  
 CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,  
 CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.  
 CC -1- SIMILARITY: Contains 2 rhodanese domains.  
 CC -1- CAUTION: Was originally (Ref.1) thought to be rhodanese.  
 CC -----  
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DT 01-AUG-1992 (Rel. 23, last sequence update)  
 DT 15-SEP-2003 (Rel. 42, last annotation update)  
 DE Thiolate sulfotransferase (EC 2.8.1.1) (Rhodanese).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovine; Bos.  
 NC NCBI\_TaxID=9913;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91161544; PubMed=2002017;  
 RT Miller D.M., Delgado R., Chirgwin J.M., Hardies S.C., Horowitz P.M.;  
 RL "Expression of cloned bovine adrenal rhodanese.";  
 RL J. Biol. Chem. 266:4686-4691(1991).  
 RN (2)  
 RP SEQUENCE OF 1-294.  
 RC TISSUE=Liver;  
 RX MEDLINE=79048424; PubMed=711737;  
 RT Ruseell J., Weng L., Kelm P.S., Heinrichson R.L.;  
 RL "The covalent structure of bovine liver rhodanese. Isolation and  
 partial structural analysis of cyanogen bromide fragments and the  
 complete sequence of the enzyme.";  
 RL J. Biol. Chem. 253:8102-8108(1978).  
 RN (3)  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=79007483; PubMed=691057;  
 RA Plogman J.H., Drent G., Kalk K.H., Hol W.G.J.;  
 RT "Structure of bovine liver rhodanese. 1. Structure determination at  
 2.5-A resolution and a comparison of the conformation and sequence of  
 its two domains.";  
 RL J. Mol. Biol. 123:557-594(1978).  
 RN (4)  
 RP X-RAY CRYSTALLOGRAPHY (1.36 ANGSTROMS).  
 RX MEDLINE=98437562; PubMed=9761843;  
 RA Gliubich F., Berni R., Colapietro M., Barba L., Zanotti G.;  
 RT "Structure of sulfur-substituted rhodanese at 1.36-A resolution.";  
 RL Acta Crystallogr. D 54:481-486(1998).  
 RN (5)  
 RP ACTIVE SITE.  
 RX MEDLINE=79048425; PubMed=711738;  
 RA Weng L., Heinrichson R.L., Westley J.;  
 RT "Active site cysteinyl and arginyl residues of rhodanese. A novel  
 formation of disulfide bonds in the active site promoted by  
 phenylglyoxal.";  
 RL J. Biol. Chem. 253:8109-8119(1978).  
 RN (6)  
 RP MUTAGENESIS OF ARG-186 AND LYS-249.  
 RX MEDLINE=94179198; PubMed=8132546;  
 RA Luo G.-X., Horowitz P.M.;  
 RT "The sulfotransferase activity and structure of rhodanese are  
 affected by site-directed replacement of Arg-186 or Lys-249.";  
 RL J. Biol. Chem. 269:8220-8225(1994).  
 CC -1- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE  
 DETOXIFICATION. BINDS MOLECULAR OXYGEN AND SULFUR.  
 CC -1- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -1- TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.  
 CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR  
 CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,  
 THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.  
 CC -1- SIMILARITY: Contains 2 rhodanese domains.  
 CC -----  
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 CC -----  
 CC EMBL; M58561; AAA30753.1; -

DR PIR; A23704; ROBO.  
 DR PDB; 1RHD; 27-JAN-84.  
 DR PDB; 1RHS; 21-JAN-98.  
 DR PDB; 2ORA; 01-AUG-96.  
 DR PDB; 1ORB; 15-OCT-95.  
 DR PDB; 1BOH; 27-APR-99.  
 DR PDB; 1BOI; 27-APR-99.  
 DR PDB; 1DP2; 13-DEC-00.  
 DR InterPro; IPR001763; Rhodanese-like.  
 DR InterPro; IPR001307; Rhodanese.  
 DR Pfam; PF00581; Rhodanese; 2.  
 DR SMART; SM00450; RHOD; 2.  
 DR PROSITE; PS00280; RHODANSE\_1; 1.  
 DR PROSITE; PS00683; RHODANSE\_2; 1.  
 DR PROSITE; PS50206; RHODANSE\_3; 2.  
 DR TRANSFERASE; Mitochondrion; 3d-structure; Repeat.  
 KW INIT MET  
 FT DOMAIN 0 24 142 0  
 FT FT 143 158  
 FT DOMAIN 172 287  
 FT ACT SITE 186 186  
 FT ACT SITE 247 247  
 FT ACT\_SITE 248 248  
 FT ACT\_SITE 249 249  
 FT ACT\_SITE 249 249  
 FT VARIANT 1 2  
 FT MUTAGEN 186 186  
 FT MUTAGEN 249 249  
 FT CONFLICT 99 99  
 FT CONFLICT 214 214  
 FT CONFLICT 219 219  
 FT STRAND 9 10  
 FT HELIX 12 20  
 FT TURN 21 22  
 FT STRAND 25 25  
 FT STRAND 26 27  
 FT TURN 28 32  
 FT TURN 38 39  
 FT TURN 43 49  
 FT HELIX 51 51  
 FT STRAND 53 54  
 FT STRAND 56 57  
 FT TURN 60 62  
 FT TURN 66 67  
 FT HELIX 77 86  
 FT TURN 87 88  
 FT TURN 91 92  
 FT STRAND 94 98  
 FT HELIX 108 117  
 FT TURN 118 119  
 FT STRAND 123 126  
 FT TURN 127 128  
 FT HELIX 129 135  
 FT TURN 136 137  
 FT STRAND 141 141  
 FT HELIX 158 160  
 FT STRAND 161 162  
 FT HELIX 164 173  
 FT STRAND 177 180  
 FT HELIX 184 188  
 FT TURN 189 189  
 FT STRAND 203 204  
 FT TURN 205 206  
 FT STRAND 208 209  
 FT HELIX 212 215  
 FT STRAND 216 216  
 FT TURN 218 219  
 FT STRAND 222 222  
 FT HELIX 225 234  
 FT TURN 235 236  
 FT TURN 239 240

RHODANSE 1.  
 HINGE.  
 RHODANSE 2.  
 MAY PLAY A ROLE IN SUBSTRATE BINDING.  
 SUBSTRATE (THIOSULFATE) BINDING  
 (BY SIMILARITY).  
 SUBSTRATE (THIOSULFATE) BINDING  
 (BY SIMILARITY).  
 MISSING (IN SOME PREPARATIONS, BUT THESE  
 STILL EXHIBIT COMPLETE ENZYME ACTIVITY).  
 R->A; NO RHODANSE ACTIVITY.  
 D -> N (IN REF. 2).  
 N -> D (IN REF. 2).  
 D -> N (IN REF. 2).



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FT STRAND 243 246
FT TURN 252 252
FT HELIX 253 262
FT TURN 263 264
FT STRAND 269 271
FT HELIX 274 281
FT HELIX 284 286
FT STRAND 287 289
FT TURN 290 291
FT STRAND 292 292
SQ SEQUENCE 296 AA; 33164 MW; C8769696FA6AC11 CRC64;

Query Match
Best Local Similarity 87.9%; Score 29; DB 1; Length 296;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASW 5
Db 31 LDASW 35

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RESULT 15
ID THTR CRIGR STANDARD; PRT; 296 AA.
AC P46635;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese).
GN TST.
OS Citreellus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=96106946; PubMed=8535164;
RA Trevino R.J., Hunt J., Horowitz P.M., Chirgwin J.M.;
RT "Chinese hamster rhodanese cDNA: activity of the expressed protein is
RT not blocked by a C-terminal extension.";
RL Protein Expr. Purif. 6:693-699 (1995).
CC -1- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE
CC DETOXIFICATION. BINDS MOLECULAR OXYGEN AND SULFUR.
CC -1- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.
CC -1- SUBUNIT: Monomer (by similarity).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR
CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,
CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
CC -1- SIMILARITY: Contains 2 rhodanese domains.
CC -----
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CC -----
DR EMBL; U23943; AAB84305.1; -.
DR HSSP; P00586; IRHS.
DR InterPro; IPR001763; Rhodanese-like.
DR InterPro; IPR001307; Rhodanese.
DR Pfam; PF00581; Rhodanese; 2.
DR SMART; SM00450; RHOD; 2.
DR PROSITE; PS00380; RHODANES_1; 1.
DR PROSITE; PS00683; RHODANES_2; 1.
DR PROSITE; PS50206; RHODANES_3; 2.
KW Transferase; Mitochondrion; Repeat.
FT INIT MET 0 0
FT DOMAIN 24 142 BY SIMILARITY.
FT RHODANES 1.

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FT DOMAIN 143 158 HINGE.
FT DOMAIN 172 287 RHODANES 2.
FT ACT_SITE 186 186 MAY PLAY A ROLE IN SUBSTRATE BINDING (BY
FT ACT_SITE 247 247 SIMILARITY).
FT ACT_SITE 248 248 BY SIMILARITY.
FT ACT_SITE 249 249 SUBSTRATE (THIOSULFATE) BINDING
FT ACT_SITE 249 249 (BY SIMILARITY).
FT ACT_SITE 249 249 SUBSTRATE (THIOSULFATE) BINDING
FT ACT_SITE 249 249 (BY SIMILARITY).
SQ SEQUENCE 296 AA; 33205 MW; 8811022BF9BAD666 CRC64;

Query Match
Best Local Similarity 87.9%; Score 29; DB 1; Length 296;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASW 5
Db 31 LDASW 35

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Search completed: February 18, 2004, 14:28:08  
Job time : 4.55263 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds  
(without alignments)  
35,929 Million cell updates/sec

Title: US-09-643-260-10  
Perfect score: 33  
Sequence: 1 LDASWL 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/Backfile1.pep:\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	90.9	919	3	US-08-985-916-16
2	30	90.9	935	4	US-09-271-438A-3
3	30	90.9	935	4	US-09-271-438A-8
4	29	87.9	118	4	US-09-634-238-354
5	29	87.9	136	4	US-09-370-838-123
6	29	87.9	194	4	US-09-252-991A-22578
7	29	87.9	277	4	US-09-252-991A-26048
8	29	87.9	438	4	US-09-252-991A-16758
9	29	87.9	661	4	US-09-252-991A-18225
10	29	87.9	834	4	US-09-252-991A-17616
11	28	84.8	128	4	US-09-205-258-254
12	28	84.8	210	3	US-08-611-587-4
13	28	84.8	219	3	US-09-247-373B-52
14	28	84.8	323	3	US-09-029-213B-25
15	28	84.8	402	4	US-09-328-352-5861
16	28	84.8	442	4	US-09-252-991A-26529
17	28	84.8	511	4	US-09-252-991A-27306
18	28	84.8	523	4	US-09-323-195A-17
19	28	84.8	588	4	US-09-252-991A-18861
20	27	81.8	36	5	US-08-118-270-244
21	27	81.8	36	5	PCT-US93-08528-244
22	27	81.8	134	4	US-09-732-210-395
23	27	81.8	144	4	US-09-732-210-629
24	27	81.8	167	4	US-09-252-991A-27865
25	27	81.8	233	4	US-09-252-991A-27758
26	27	81.8	263	2	US-08-790-137-4
27	27	81.8	263	2	US-08-824-874-5

28	27	81.8	263	3	US-08-807-151-5	Sequence 5, Appl1
29	27	81.8	263	3	US-09-210-084-5	Sequence 5, Appl1
30	27	81.8	263	4	US-09-478-957-5	Sequence 5, Appl1
31	27	81.8	263	4	US-09-764-762-5	Sequence 5, Appl1
32	27	81.8	272	4	US-09-252-991A-22260	Sequence 22260, A
33	27	81.8	316	4	US-09-252-991A-18153	Sequence 18153, A
34	27	81.8	385	2	US-08-694-915-2	Sequence 2, Appl1
35	27	81.8	413	2	US-08-960-756-2	Sequence 2, Appl1
36	27	81.8	416	2	US-08-694-915-4	Sequence 4, Appl1
37	27	81.8	423	1	US-08-844-064-7	Sequence 7, Appl1
38	27	81.8	423	4	US-09-009-433-7	Sequence 2, Appl1
39	27	81.8	423	4	US-08-850-348A-2	Sequence 295, App
40	27	81.8	464	4	US-09-634-238-295	Sequence 248, App
41	27	81.8	479	4	US-09-634-238-248	Sequence 2, Appl1
42	27	81.8	561	2	US-08-532-795-2	Sequence 2, Appl1
43	27	81.8	562	2	US-08-851-567B-30	Sequence 30, Appl1
44	27	81.8	569	2	US-08-532-795-23	Sequence 23, Appl1
45	27	81.8	569	2	US-08-532-795-29	Sequence 29, Appl1

## ALIGNMENTS

RESULT 1  
US-08-985-916-16  
; Sequence 16, Application US/08985916  
; Patent No. 6221636  
; GENERAL INFORMATION:  
; APPLICANT: ATSUSHI HAYAKAWA, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI  
; TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; COUNTRY: VA  
; ZIP: 22152  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/985, 916  
; FILING DATE: 05-DEC-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 8-325658  
; FILING DATE: 05-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: NORMAN F. OBLON  
; REGISTRATION NUMBER: 24,618  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 919 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-985-916-16

Query Match 90.9%; Score 30; DB 3; Length 919;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
DB 105 LDATWL 110

RESULT 2

US-09-271-438A-3  
; Sequence 3, Application US/09271438A  
; Patent No. 6331419  
; GENERAL INFORMATION:  
; APPLICANT: IZUI, Hiroshi  
; APPLICANT: ONO, Eiichi  
; APPLICANT: MATSUI, Kazuhiko  
; APPLICANT: MORIYA, Mika  
; APPLICANT: ITO, Hisao  
; APPLICANT: HARA, Yoshihiko  
; TITLE OF INVENTION: L-GUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GLUTAMIC ACID  
; FILE REFERENCE: 0010-0989-0  
; CURRENT APPLICATION NUMBER: US/09/271,438A  
; CURRENT FILING DATE: 1999-03-18  
; PRIOR APPLICATION NUMBER: JP10-69068  
; PRIOR FILING DATE: 1998-03-18  
; PRIOR APPLICATION NUMBER: JP10-297129  
; PRIOR FILING DATE: 1998-10-19  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 935  
; TYPE: PRT  
; ORGANISM: Enterobacter agglomerans  
US-09-271-438A-3

Query Match 90.9%; Score 30; DB 4; Length 935;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
||:||||  
Db 10 LDSSWL 15

RESULT 3  
US-09-271-438A-8  
; Sequence 8, Application US/09271438A  
; Patent No. 6331419  
; GENERAL INFORMATION:  
; APPLICANT: IZUI, Hiroshi  
; APPLICANT: ONO, Eiichi  
; APPLICANT: MATSUI, Kazuhiko  
; APPLICANT: MORIYA, Mika  
; APPLICANT: ITO, Hisao  
; APPLICANT: HARA, Yoshihiko  
; TITLE OF INVENTION: L-GUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GLUTAMIC ACID  
; FILE REFERENCE: 0010-0989-0  
; CURRENT APPLICATION NUMBER: US/09/271,438A  
; CURRENT FILING DATE: 1999-03-18  
; PRIOR APPLICATION NUMBER: JP10-69068  
; PRIOR FILING DATE: 1998-03-18  
; PRIOR APPLICATION NUMBER: JP10-297129  
; PRIOR FILING DATE: 1998-10-19  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 935  
; TYPE: PRT  
; ORGANISM: Enterobacter agglomerans  
US-09-271-438A-8

Query Match 90.9%; Score 30; DB 4; Length 935;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
||:||||  
Db 10 LDSSWL 15

RESULT 4  
US-09-634-238-354  
; Sequence 354, Application US/09634238  
; Patent No. 6544772  
; GENERAL INFORMATION:  
; APPLICANT: Glenn, Matthew  
; APPLICANT: Havukale, Ilkka J.  
; APPLICANT: Bloksberg, Leonard, N.  
; APPLICANT: Lubbers, Mark W.  
; APPLICANT: Dekker, James  
; APPLICANT: Christensen, Anna C.  
; APPLICANT: Holland, Ross  
; APPLICANT: O'Toole, Paul W.  
; APPLICANT: Reid, Julian R.  
; APPLICANT: Coolbear, Timothy  
; TITLE OF INVENTION: Polynucleotides, materials incorporating  
; FILE REFERENCE: 11000.1043U1  
; CURRENT APPLICATION NUMBER: US/09/634,238  
; CURRENT FILING DATE: 2000-08-08  
; NUMBER OF SEQ ID NOS: 422  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 354  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Lactobacillus rhamnosus  
US-09-634-238-354

Query Match 87.9%; Score 29; DB 4; Length 118;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5  
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Db 52 LDASW 56

RESULT 5  
US-09-370-838-123  
; Sequence 123, Application US/09370838  
; Patent No. 6444425  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Mohamath, Roadoh  
; APPLICANT: Seciet, Heather  
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF  
; FILE REFERENCE: 210121.475C1  
; CURRENT APPLICATION NUMBER: US/09/370,838  
; CURRENT FILING DATE: 1999-08-09  
; EARLIER APPLICATION NUMBER: US 09/265,323  
; EARLIER FILING DATE: 1999-04-02  
; NUMBER OF SEQ ID NOS: 289  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 123  
; LENGTH: 136  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-370-838-123

Query Match 87.9%; Score 29; DB 4; Length 136;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5  
|||||  
Db 32 LDASW 36

RESULT 6  
US-09-252-991A-22578  
; Sequence 22578, Application US/09252991A

Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 22578  
; LENGTH: 194  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-22578

Query Match 87.9%; Score 29; DB 4; Length 194;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DASWL 6  
Db 161 LDASWL 165

RESULT 7  
US-09-252-991A-26048  
; Sequence 26048, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 26048  
; LENGTH: 277  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-26048

Query Match 87.9%; Score 29; DB 4; Length 277;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDASWL 6  
Db 89 LDADWL 94

RESULT 8  
US-09-252-991A-16758  
; Sequence 16758, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 16758  
; LENGTH: 438  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-16758

Query Match 87.9%; Score 29; DB 4; Length 438;  
Best Local Similarity 83.3%; Pred. No. 9e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDASWL 6  
Db 142 LDTSWL 147

RESULT 9  
US-09-252-991A-18225  
; Sequence 18225, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 18225  
; LENGTH: 661  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18225

Query Match 87.9%; Score 29; DB 4; Length 661;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDASWL 6  
Db 546 LDGSLW 551

RESULT 10  
US-09-252-991A-17616  
; Sequence 17616, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 17616  
; LENGTH: 834  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-17616

Query Match 87.9%; Score 29; DB 4; Length 834;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LDASW 5
Db      474 LDASW 478

RESULT 11
US-09-205-258-254
; Sequence 254, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; FILE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949

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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patencin Ver. 2.0
; SEQ ID NO 254
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (12)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (128)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-254

Query Match      84.8%; Score 28; DB 4; Length 128;
Best Local Similarity 83.3%; Pred. No. 4e+02; 1; Indels 0; Gaps 0;
Matches 5; Conservative

QY      1 LDASW 6
Db      14 LDASW 19

RESULT 12
US-08-611-587-4
; Sequence 4, Application US/08611587
; Patent No. 6150931
; GENERAL INFORMATION:
; APPLICANT: PANDOLFO, MASSIMO
; APPLICANT: MONTERMINI, LAURA
; APPLICANT: MOLTO, MARIA D.
; APPLICANT: KOENIG, MICHAEL
; APPLICANT: CAMPUSANO, VICTORIA
; APPLICANT: COBBE, MIREILLE
; TITLE OF INVENTION: Direct Diagnosis of Friedreich Ataxia
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P. Patent Dept.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77010
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/611,587  
FILING DATE: 03-MAR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brashers-Macatee, Sarah J.  
REGISTRATION NUMBER: 38,087  
REFERENCE/DOCKET NUMBER: D-5901  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-651-5620  
TELEFAX: 713-651-5246  
TELEX: 76-2829  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 210 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
POSITION IN GENOME:  
UNITS: Dp  
US-08-611-587-4

Query Match 84.8%; Score 28; DB 3; Length 210;  
Best Local Similarity 83.3%; Pred. No. 6.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDASWL 6  
DB 198 LDLSWL 203

RESULT 13  
US-09-247-373B-52  
Sequence 52, Application US/09247373B  
Patent No. 6168954  
GENERAL INFORMATION:  
APPLICANT: MCGONIGLE, BRIAN  
APPLICANT: O'KEEFE, DANIEL  
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES  
FILE REFERENCE: CL-1108-A  
CURRENT APPLICATION NUMBER: US/09/247,373B  
CURRENT FILING DATE: 1999-02-10  
PRIOR APPLICATION NUMBER: 08/924,747  
PRIOR FILING DATE: 1997-09-05  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 52  
LENGTH: 219  
TYPE: PRT  
ORGANISM: SOYBEAN  
US-09-247-373B-52

Query Match 84.8%; Score 28; DB 3; Length 219;  
Best Local Similarity 66.7%; Pred. No. 6.7e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
DB 102 LDAMI 107

RESULT 14  
US-09-029-213B-25  
Sequence 25, Application US/09029213B  
Patent No. 6180098  
GENERAL INFORMATION:

APPLICANT: CHRISTIAN, Peter D.  
TITLE OF INVENTION: RECOMBINANT HELICOVERPA BACULOVIRUSES  
TITLE OF INVENTION: EXPRESSING HETEROLOGOUS DNA  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDermott, Wall & Emery  
STREET: 600 13th Street, NW  
CITY: Washington  
STATE: District of Columbia  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/029,213B  
FILING DATE: 31-AUG-1998  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph Hyosuk Kim  
REGISTRATION NUMBER: 41,425  
REFERENCE/DOCKET NUMBER: 50179-048  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-756-8000  
TELEFAX: 202-756-8087  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 323 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-09-029-213B-25

Query Match 84.8%; Score 28; DB 3; Length 323;  
Best Local Similarity 66.7%; Pred. No. 9.9e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
DB 191 LDSPWL 196

RESULT 15  
US-09-328-352-5861  
Sequence 5861, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 5861  
LENGTH: 342  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-5861

Query Match 84.8%; Score 28; DB 4; Length 342;  
Best Local Similarity 83.3%; Pred. No. 1e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDASWL 6  
DB 307 LDSPWL 312

Search completed: February 18, 2004, 14:41:48  
Job time: 7.06579 secs

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# OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 / Search time 17.3684 Seconds  
(without alignment)  
89.145 Million cell updates/sec

Title: US-09-643-260-9

Perfect score: 40  
Sequence: 1 LNMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL.23.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	95.0	526	8 Q9B964	Q9B964 ceratopsolen
2	38	95.0	3103	5 Q9GV77	Q9GV77 lycechinus
3	37	92.5	204	16 Q9KER2	Q9KER2 bacillus ha
4	37	92.5	311	16 Q9ZM07	Q9ZM07 rhizobium m
5	37	92.5	337	16 Q8UB44	Q8UB44 agrobacteri
6	37	92.5	464	12 Q9WR50	Q9WR50 macaca mula
7	36	90.0	207	16 Q8RI33	Q8RI33 leptospira
8	36	90.0	210	11 Q9EPG8	Q9EPG8 rattus norv
9	36	90.0	254	2 Q9LBY3	Q9LBY3 shewanella
10	36	90.0	330	16 Q8XYA4	Q8XYA4 ralsstonia s
11	36	90.0	380	8 Q47545	Q47545 chlamydomon
12	36	90.0	442	10 Q9PED7	Q9PED7 oryza sativ
13	36	90.0	460	8 Q8HIG1	Q8HIG1 parazen pac
14	36	90.0	460	8 Q8HL32	Q8HL32 apocycclus
15	36	90.0	460	16 Q8RL24	Q8RL24 salinonella
16	36	90.0	460	16 Q8ZJ28	Q8ZJ28 salinonella

17	36	90.0	464	16 Q8RC54	Q8RC54 thermocaneer
18	36	90.0	490	16 Q8FPI8	Q8FPI8 corynebacte
19	36	90.0	493	2 Q8GPG7	Q8GPG7 pantoea agg
20	36	90.0	520	11 Q9JH11	Q9JH11 mus musculu
21	36	90.0	520	11 Q99K28	Q99K28 mus musculu
22	36	90.0	534	11 Q9D758	Q9D758 mus musculu
23	36	90.0	590	16 Q91496	Q91496 pseudomonas
24	36	90.0	744	16 Q31087	Q31087 mycobacteri
25	36	90.0	767	16 Q8G651	Q8G651 bifidobacte
26	36	90.0	864	13 Q73637	Q73637 fugu rubrip
27	35	87.5	116	2 Q68039	Q68039 rhodobacter
28	35	87.5	135	2 Q05744	Q05744 mycobacteri
29	35	87.5	145	5 Q810L0	Q810L0 mycobacteri
30	35	87.5	194	16 Q8D964	Q8D964 vibrio vuln
31	35	87.5	280	5 Q22375	Q22375 caenorhabd
32	35	87.5	321	5 Q94515	Q94515 drosophila
33	35	87.5	518	16 Q98134	Q98134 rhizobium 1
34	35	87.5	599	8 Q47815	Q47815 geomya paze
35	35	87.5	740	6 Q95KV1	Q95KV1 bos taurus
36	35	87.5	741	12 Q8BC12	Q8BC12 gremmentell
37	35	87.5	745	11 Q8CBT3	Q8CBT3 mus musculu
38	35	87.5	756	6 Q95KV0	Q95KV0 bos taurus
39	35	87.5	770	3 Q9P491	Q9P491 trichoderma
40	35	87.5	777	3 Q59898	Q59898 ampelomyces
41	35	87.5	792	3 Q9P8J3	Q9P8J3 coniothyrix
42	34	85.0	69	2 Q87032	Q87032 vibrio chol
43	34	85.0	106	11 Q8CLU5	Q8CLU5 mus musculu
44	34	85.0	151	16 Q94K44	Q94K44 streptomyce
45	34	85.0	168	4 Q96E06	Q96E06 homo sapien

## ALIGNMENTS

RESULT 1  
Q9B964 ID Q9B964 PRELIMINARY: PRT: 526 AA.  
AC Q9B964; 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DR 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE Cytochrome oxidase subunit I (EC 1.9.3.1) (COI) (Cytochrome c oxidase polypeptide I) (Fragment).  
DS Polypeptide I (Fragment).  
OS Ceratopsolen nanus.  
OG Ceratopsolen nanus.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Psycota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;  
OC Agaonidae; Agaoninae; Ceratopsolen.  
OK NCBI\_TaxId=130016;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=G077;  
RA Weiblen G.D.;  
RT "Phylogenetic analyses of dioecious fig pollinators based on mitochondrial DNA sequences and morphology."  
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE CATALYTIC CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME C + 2 H(2)O.  
CC -1- PATHWAY: RESPIRATORY CHAIN, TERMINAL STEP.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL.  
CC -1- INNER MEMBRANE (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.  
DR EMBL; AF200382; AA00073.1; -.  
DR HSSP; P18401; 1PPT.  
DR InterPro; IPR00883; COX1.  
DR Pfam; PF00115; COX1; 1.



DR PRINTS; PRO1165; CYCOXIDASE1.  
 DR PROSITE; PS00077; COX1; 1.  
 KM Copper; Electron transport; Heme; Inner membrane; Membrane;  
 KM Oxidoreductase; Respiratory chain; Transmembrane; Transport;  
 KM Mitochondrion.  
 FT NON\_TER 1  
 SQ SEQUENCE 526 AA; 59586 MW; 587FE82D8C4F2B62 CRC64;

Query Match 95.0%; Score 38; DB 8; Length 526;  
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWSL 6  
 Db 10 LNMWSL 15

## RESULT 2

Q9GV77 PRELIMINARY; PRT; 3103 AA.

AC Q9GV77;  
 DT 01-MAR-2001 (TRENBLREL. 16, Created)  
 DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)  
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)  
 DE Embryonic blastocoelel extracellular matrix precursor.  
 GN ECM3.  
 OS Elychnus variegatus (Sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Echinacea; Temnopneuroidea; Toxopneustidae;  
 OC Elychnus.  
 OX NCBI\_TaxID=7654;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20340282; PubMed=10885756;  
 RA Hodor P.G., Illies M.R., Bradley S., Etensohn C.A.;  
 RT "Cell-substrate interactions during sea urchin gastrulation: migrating  
 primary mesenchyme cells interact with and align extracellular matrix  
 fibers that contain ECM3, a molecule with NG2-like and multiple  
 calcium-binding domains";  
 RT Dev. Biol. 222:181-194(2000).  
 RL EMBL; AF287478; AAC00570.1; -  
 DR InterPro; IPR002126; Cadherin.  
 DR InterPro; IPR003644; Calx\_beta.  
 DR Pfam; PF03160; Calx\_beta; 5.  
 DR SMART; SM00112; CA; 1.  
 DR SMART; SM00237; Calx\_beta; 5.  
 DR PROSITE; PS0268; CADHERIN\_2; 1.  
 KM Matrix protein; signal.  
 FT SIGNAL 1 19  
 SQ SEQUENCE 3103 AA; 343770 MW; 79D7EBDE1C54393 CRC64;

Query Match 95.0%; Score 38; DB 5; Length 3103;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWSL 6  
 Db 1724 LNMWSL 1729

## RESULT 3

Q9KER2 PRELIMINARY; PRT; 204 AA.

AC Q9KER2;  
 DT 01-OCT-2000 (TRENBLREL. 15, Created)  
 DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)  
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)  
 DE Hypothetical protein BH0787.  
 GN BH0787.  
 OS Bacillus halodurans.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 NCBI\_TaxID=86665;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=C-125 / JCM 9153;  
 RX MEDLINE=20512582; PubMed=11058132;  
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kihara S.,  
 RA Horikoshi K.;  
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
 RT halodurans and genomic sequence comparison with Bacillus subtilis";  
 RL Nucleic Acids Res. 28:4317-4331(2000).  
 DR EMBL; AP001509; BAB04506.1; -  
 DR InterPro; IPR006938; DUF624.  
 DR Pfam; PF04854; DUF624; 1.  
 KM Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 204 AA; 23786 MW; 7C476B67E71015B2 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 204;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWSL 6  
 Db 22 LNMWSL 27

## RESULT 4

Q92MU7 PRELIMINARY; PRT; 311 AA.

AC Q92MU7;  
 DT 01-DEC-2001 (TRENBLREL. 19, Created)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)  
 DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)  
 DE Putative sugar transport system permease ABC transporter protein.  
 GN R02512 OR SMC01978.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1021;  
 RX MEDLINE=21396507; PubMed=11481430;  
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Anpe F., Batut J.,  
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
 RA Godrie T., Goffeau A., Kahn D., Kise B., Lelaure V., Masny D.,  
 RA Pohl T., Portetelle D., Puchler A., Purnelle B., Rampeyger U.,  
 RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;  
 RT "Analysis of the chromosome sequence of the legume symbiont  
 RT Sinorhizobium meliloti strain 1021";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
 DR EMBL; AL591790; CAC47091.1; -  
 DR InterPro; IPR000515; BPD\_transp.  
 DR Pfam; PF00528; BPD\_transp; 1.  
 DR PROSITE; PS00402; BPD\_TRANS\_P\_NN\_MEMBER; 1.  
 KM Complete proteome.  
 SQ SEQUENCE 311 AA; 34300 MW; 4BF3497341A2C198 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 311;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWSL 6  
 Db 138 LNMWSL 143

## RESULT 5

Q8UB44 PRELIMINARY; PRT; 337 AA.

AC Q8UB44;  
 DT 01-JUN-2002 (TRENBLREL. 21, Created)  
 DT 01-JUN-2002 (TRENBLREL. 21, Last sequence update)  
 DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)  
 DE ABC transporter, membrane spanning protein.

GN ATU3173 OR AGR L 3372.  
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Rhizobium.  
 NCBI\_TaxID=176299;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21608550; PubMed=11743193;  
 RA Wood D.W., Seetahal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,  
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boye D. Sr.,  
 RA Chapman P., Clendenning J., Deatherage G., Gillet M., Grant C.,  
 RA Kueyavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,  
 RA Raymond C., Rouse G., Saenphimachak C., Xu Z., Romero P., Gordon D.,  
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
 RA Neeter E.W.;  
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
 RT C58.";  
 RL Science 294:2317-2323 (2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21608551; PubMed=11743194;  
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
 RA Qureshi B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,  
 RA Houmel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu P.,  
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,  
 RA Planagan C., Crowell C., Gursun J., Lomo C., Sear C., Strub G.,  
 RA Cielo C., Slater S.;  
 RT "Genome sequence of the plant pathogen and biotechnology agent  
 RT Agrobacterium tumefaciens C58.";  
 RL Science 294:2323-2328 (2001).  
 DR EMBL; AE009247; AAL43989.1; -  
 DR EMBL; AE008366; AAK90213.1; -  
 DR InterPro; IPR000515; BPD transp.  
 DR Pfam; PF00528; BPD transp. 1.  
 DR PROSITE; PS00402; BPD\_TRANSF\_INN\_MEMBER; 1.  
 DR Complete proteome.  
 KW SEQUENCE 337 AA; 37313 MW; 0F35B9A6E0D34813 CRC64;  
 SQ  
 Query Match 92.5%; Score 37; DB 16; Length 337;  
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6  
 Db 164 LNMAWL 169

RESULT 6  
 QWR80 PRELIMINARY; PRT; 464 AA.  
 ID QWR80  
 AC QWR80;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Hypothetical 52.0 kDa protein (ORF32).  
 OS Macaca mulatta rhadinovirus 17577, and  
 OS Macaca mulatta rhadinovirus 26-95.  
 OC Vitruvise; dsDNA vitruvise, no RNA stage; Herpesviridae;  
 OC Gammaherpesvirinae; Rhadinovirus.  
 NCBI\_TaxID=83534; 119193;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Macaca mulatta rhadinovirus 17577;  
 RX MEDLINE=99174001; PubMed=10074154;  
 RA Searles R.P., Bergsman E.P., Arthel M.K., Wong S.W.;  
 RT "Sequence and genomic analysis of a rhesus macaque rhadinovirus with  
 RT similarity to Kaposi's sarcoma-associated herpesvirus/human  
 RT herpesvirus 8.";  
 RL J. Virol. 73:3040-3053 (1999).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC SPECIES=Macaca mulatta rhadinovirus 26-95;  
 RC STRAIN=MACACA MULATTA RHADINOVIRUS ISOLATE 26-95;  
 RX MEDLINE=20173730; PubMed=10708456;  
 RA Alexander L., Denekamp L., Knapp A., Auerbach M.R., Damania B.,  
 RA DeRoosiers R.C.;  
 RT "The primary sequence of rhesus monkey rhadinovirus isolate 26-95:  
 RT sequence similarities to Kaposi's sarcoma-associated herpesvirus and  
 RT rhesus monkey rhadinovirus isolate 17577.";  
 RL J. Virol. 74:3388-3398 (2000).  
 DR EMBL; AF083501; AAD21358.1; -  
 DR EMBL; AF210726; AAP60010.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 464 AA; 51993 MW; ADB519AB96F511E5 CRC64;  
 Query Match 92.5%; Score 37; DB 12; Length 464;  
 Best Local Similarity 83.3%; Pred. No. 3.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6  
 Db 397 VNMSWL 402

RESULT 7  
 Q8P1E3 PRELIMINARY; PRT; 207 AA.  
 ID Q8P1E3  
 AC Q8P1E3;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Fritling body developmental protein S-like protein.  
 OS DEVS OR LA3193.  
 OS Leptospira interrogans.  
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.  
 OC NCBI\_TaxID=173;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar 1a1;  
 RA Ren S.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB011481; AAN50391.1; -  
 KW Complete proteome.  
 SQ SEQUENCE 207 AA; 23460 MW; 14775910CB7BB68 CRC64;  
 Query Match 90.0%; Score 36; DB 16; Length 207;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NMSWL 6  
 Db 157 NMSWL 161

RESULT 8  
 Q9EPG8 PRELIMINARY; PRT; 210 AA.  
 ID Q9EPG8  
 AC Q9EPG8;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Brain Na+/Ca++ exchanger-associated protein.  
 OS Rattus norvegicus (Rat).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RA Michaelis M.L., Hadwiger G.H., Islam S.I., Kumar K.N.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U53512; AAG38872.1; -  
 DR InterPro; IPR000456; Ribosomal\_L17.  
 DR Pfam; PF01196; Ribosomal\_L17; 1.

SQ SEQUENCE 210 AA; 24405 MW; 3C9170304235B02D CRC64;

Query Match 90.0%; Score 36; DB 11; Length 210;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMW 5

DB 126 LNMW 130

RESULT 9

Q9LBY3 PRELIMINARY; PRT; 254 AA.

AC Q9LBY3; 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

GN Quinol oxidase subunit III.

OS Shewanella violacea.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;

OC Alteromonadaceae; Shewanella.

OX NCBI\_TaxID=60217;

RN [1]

RP SEQUENCE FROM N.A.

RA Qureshi M.H., Kato C., Nakasone K., Yamada M., Horikoshi K.;

RT "Pressure-regulation of a membrane-bound quinol oxidase in a deep-sea

RT piezophilic bacterium, Shewanella violacea."

RL Submitted (JCT-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB033827; BAA94864.1; -.

DR HSSP; P18400; ICYW.

DR Interpro; IPR001505; Copper CuA.

DR Interpro; IPR006333; CyOA II.

DR Prodom; PD000131; Copper CuA; 1.

DR TIGRfam; TIGR01433; CyOA; 1.

DR SEQUENCE 254 AA; 28657 MW; F1870460580ACED CRC64;

Query Match 90.0%; Score 36; DB 2; Length 254;

Best Local Similarity 83.3%; Pred. No. 2.6e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNMW 6

DB 84 LNMW 89

RESULT 10

Q8XYA4 PRELIMINARY; PRT; 330 AA.

AC Q8XYA4; 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Probable transmembrane cytochrome O ubiquinol oxidase (Subunit II)

DE oxidoreductase protein (EC 1.10.3.-).

GN CyOA2 OR RSC1858 OR R803418.

OS Ralstonia solanacearum (Pseudomonas solanacearum).

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Ralstoniaceae; Ralstonia.

OX NCBI\_TaxID=305;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GM11000;

RA Salenoubat M., Genin S., Artiguenave F., Gouzy J., Mangeron S.,

RA Arlet M., Billault A., Brotier P., Camus J.C., Catolico L.,

RA Chander M., Chole N., Claudel-Renard C., Cunnac S., Demange N.,

RA Gaspin C., Lavie W., Moisan A., Robert C., Saurin W., Schlex T.,

RA Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,

RA Weisenbach J., Boucher C.A.;

RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";

RL Mature 415:497-502(2002).

DR EMBL; AL646067; CAD15560.1; -.

DR Interpro; IPR001505; Copper CuA.

DR Interpro; IPR006333; CyOA II.

DR Prodom; PD000131; Copper CuA; 1.

DR TIGRfam; TIGR01433; CyOA; 1.

KW Oxidoreductase; Complete proteome.

SQ SEQUENCE 330 AA; 36117 MW; B82DF114452359B8 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 330;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNMW 6

DB 153 LNMW 158

RESULT 11

Q47545 PRELIMINARY; PRT; 380 AA.

AC Q47545; 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

GN Apocytochrome b.

OS Chlamydomonas eugametos.

OG Mitochondrion.

OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

OC Chlamydomonadaceae; Chlamydomonas.

OX NCBI\_TaxID=3053;

RN [1]

RP SEQUENCE FROM N.A.

RA Denovan-Wright E.M., Nedelcu A.M., Lee R.W.;

RT "Complete sequence of the mitochondrial DNA of Chlamydomonas

RT eugametos."

RL Plant Mol. Biol. 36:285-295(1998).

Query Match 90.0%; Score 36; DB 8; Length 380;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMW 5

DB 26 LNMW 30

RESULT 12

Q9FED7 PRELIMINARY; PRT; 442 AA.

```

AC O9FED7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P0001B06.11 protein (P0671B11.33 protein).
GN P0001B06.11 OR P0671B11.33.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriactoidae; Oryzaceae; Oryza.
OX NCB1_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GAS) genomic DNA, chromosome 1, PAC
RT clone:P0001B06."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GAS) genomic DNA, chromosome 1, PAC
RT clone:P0671B11."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002537; BAB1658.1; -.
DR EMBL; AP002746; BAB1217.1; -.
DR Gramene; O9FED7; -.
DR InterPro; IPR000048; IQ_region.
DR Pfam; PF00612; IQ_3.
DR SMART; SM00015; IQ_1.
SQ SEQUENCE 442 AA; 48947 MW; 2F783FEBE3740632 CRC64;

Query Match
Best Local Similarity 90.0%; Score 36; DB 10; Length 442;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NMSWL 6
DB 274 NMSWL 278

RESULT 13
O8HLG1 PRELIMINARY; PRT; 460 AA.
AC O8HLG1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE NADH dehydrogenase subunit 4.
GN ND4.
OS Parazen pacificus (parazen).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Zelformes; Parazeniidae; Parazen.
OX NCB1_TaxID=181440;
RN [1]
RP SEQUENCE FROM N.A.
RA Miya M.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Miya M., Takehima H., Endo H., Ishiguro N.B., Inoue J.G., Mukai T.,
RA Satoh T.P., Yamaguchi M., Kawaguchi A., Mabuchi K., Shirai S.M.,
RA Nishida M.;
RT "Major Patterns of higher teleostean phylogenies: A new perspective
RT based on 100 complete mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 26:121-138(2002).
DR EMBL; AF004433; BAC23537.1; -.
RA Mitochondrion.
SQ SEQUENCE 460 AA; 51399 MW; 2CF21B48B7B6CD7A CRC64;

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Query Match
Best Local Similarity 90.0%; Score 36; DB 8; Length 460;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NMSWL 6
DB 388 NMSWL 392

RESULT 14
O8HL32 PRELIMINARY; PRT; 460 AA.
AC O8HL32;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE NADH dehydrogenase subunit 4.
GN ND4.
OS Apocycylus ventricosus (smooth lumpucker).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Scorpaeniformes;
OC Corioidae; Cyclopteridae; Apocycylus.
OX NCB1_TaxID=181459;
RN [1]
RP SEQUENCE FROM N.A.
RA Miya M.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Miya M., Takehima H., Endo H., Ishiguro N.B., Inoue J.G., Mukai T.,
RA Satoh T.P., Yamaguchi M., Kawaguchi A., Mabuchi K., Shirai S.M.,
RA Nishida M.;
RT "Major Patterns of higher teleostean phylogenies: A new perspective
RT based on 100 complete mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 26:121-138(2002).
DR EMBL; AF004443; BAC23666.1; -.
RA Mitochondrion.
SQ SEQUENCE 460 AA; 51277 MW; 335D673853B97A26 CRC64;

Query Match
Best Local Similarity 90.0%; Score 36; DB 8; Length 460;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSWL 5
DB 387 LMSWL 391

RESULT 15
O8ZL24 PRELIMINARY; PRT; 460 AA.
AC O8ZL24;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative glycosyl hydrolase family.
GN STM3775.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCB1_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L72 / SCS1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Portolillo S., All J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvany E.,
RA Ryan B., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium

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RT LT2."  
RL Nature 413:852-856(2001).  
DR EMBL; AE008876; AAL2633.1; -.  
DR InterPro; IPR001360; Glyco\_hydro\_1.  
DR Pfam; PF00232; Glyco\_hydro\_1; 1.  
DR PRINTS; PR00131; GLHYDRIASE1.  
DR ProDom; PD000650; Glyco\_hydro\_1; 1.  
DR PROSITE; PS00572; GLYCOSYL\_HYDROL\_F1\_1; 1.  
KW Hydrolase; Hypothetical protein; Complete proteome.  
SQ SEQUENCE 460 AA; 53173 MW; 1FC5P45D6E96709 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 460;  
Best Local Similarity 100.0%; Pred.No. 4.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWSWL 6  
|||||

DB 418 NWSWL 422

Search completed: February 18, 2004, 14:35:46  
Job time : 19.3684 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds  
(without alignments)  
79.423 Million cell updates/sec

Title: US-09-643-260-9  
Perfect score: 40  
Sequence: 1 LNM5WL 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	90.0	204	1 YTI6_CAEEL	Q10919 caenorhabdi
2	36	90.0	767	1 MERE_BIFLO	Q8651 bifidobacte
3	35	87.5	325	1 RIR2_MYCLE	Q9cbq2 mycobacteri
4	35	87.5	745	1 IKKA_HUMAN	Q15111 h inhibitor
5	35	87.5	745	1 IKKA_MOUSE	Q60680 m inhibitor
6	35	87.5	756	1 IKKG_HUMAN	Q14920 homo sapien
7	35	87.5	757	1 IKKG_MOUSE	Q88351 mus musculu
8	35	87.5	757	1 IKKG_RAT	Q9qy78 rattus norv
9	34	85.0	154	1 Y451_SYNY3	P29920 paracoccu
10	34	85.0	345	1 NUO8_PAPDS	P42032 rhododact
11	34	85.0	345	1 NUO8_RHOCA	P06591 escherichia
12	34	85.0	444	1 T1SD_ECOLI	Q10187 schizosacch
13	34	85.0	612	1 YAMD_SCHPO	Q24488 drosophila
14	34	85.0	685	1 ROR1_DROME	Q33822 aserina pe
15	33	82.5	54	1 ATP8_ASTPE	Q883d3 wiggleswort
16	33	82.5	157	1 RHM_WIGBR	P30535 bos tauris
17	33	82.5	169	1 PKB3_BOVIN	P30536 homo sapien
18	33	82.5	169	1 PKB3_HUMAN	P50637 mus musculu
19	33	82.5	169	1 PKB3_MOUSE	P16257 rattus norv
20	33	82.5	169	1 PKB3_MOUSE	P21995 mus musculu
21	33	82.5	330	1 EMB_MOUSE	Q02768 rhododact
22	33	82.5	444	1 CYB_RHOSH	P12768 streptomyce
23	33	82.5	455	1 PIR_STRGR	P31348 influenza a
24	33	82.5	470	1 NRAM_IKLE	P31349 influenza a
25	33	82.5	470	1 NRAM_IKLE	P03469 influenza a
26	33	82.5	470	1 NRAM_IKLE	P03469 influenza a
27	33	82.5	479	1 LMB_BACSU	P44105 haemophilus
28	33	82.5	514	1 YOP4_HAKIN	Q06531 caenorhabdi
29	33	82.5	529	1 YOP4_CAEEL	P36731 saccharomyc
30	33	82.5	627	1 YHE0_YEAST	P36731 saccharomyc
31	33	82.5	735	1 DHR2_YEAST	P13269 trypanosoma
32	33	82.5	752	1 8511_TRYCR	Q74377 schizosacch
33	33	82.5	877	1 SUIH_SCHPO	

34	33	82.5	1053	1 HMDH_SCHPO	Q10283 schizosacch
35	33	82.5	1564	1 N184_SCHPO	Q9p7m8 schizosacch
36	33	82.5	3951	1 VGF1_IBVD	P27920 avian infec
37	32	80.0	53	1 ATP8_ANOGA	P34836 anophelis g
38	32	80.0	53	1 ATP8_ANOOU	P33506 anophelis g
39	32	80.0	53	1 ATP8_ARTSF	Q37707 atemia san
40	32	80.0	54	1 ATP8_COHLO	Q9afp7 cochlomyia
41	32	80.0	54	1 ATP8_PANLI	P12697 paracentrot
42	32	80.0	55	1 ATP8_STRPU	P15997 strongyloce
43	32	80.0	151	1 CT78_HUMAN	Q9br46 homo sapien
44	32	80.0	154	1 Y86A_METUA	P81329 methanococc
45	32	80.0	181	1 ISP2_VIRCH	Q9krre2 vibrio chol

## ALIGNMENTS

## RESULT 1

ID	YTI6_CAEEL	STANDARD	PRT	204 AA.
AC	Q10919;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	Hypothetical 23.6 kDa protein B0252.6 in chromosome II.			
GN	B0252.6.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;			
OC	Rhabditidae; Pelodierinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RA	Du Z., Waterston R.;			
RL	Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.			
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CC	or send an email to <a href="mailto:license@jdb-ebi.ch">license@jdb-ebi.ch</a> ).			
CC	-----			
DR	EMBL; U23453; AAC46760.1; -			
DR	PIR; T15295; T15295.			
DR	WormPep; B0252.6; CB02422.			
KW	Hypothetical protein.			
SC	SEQUENCE 204 AA; 23610 MW; 59FBI5536CD22F43 CRC64;			

Query Match 90.0%; Score 36; DB 1; Length 204;  
Best local similarity 100.0%; Pred. No. 32;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NMSWL 6  
DB 96 NMSWL 100

## RESULT 2

ID	MERE_BIFLO	STANDARD	PRT	767 AA.
AC	Q8651;			
DT	15-SEP-2003 (Rel. 42, Created)			
DT	15-SEP-2003 (Rel. 42, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	5-methyltetrahydropteroylglutamate--homocysteine methyltransferase			
DE	(EC 2.1.1.14) (methionine synthase, vitamin-B12 independent isozyme)			
DE	(Cobalamin-independent methionine synthase).			
GN	MERE OR B10798.			
OS	Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;			
OC	Bifidobacterium longum.			
OC	Bifidobacteriaceae; Bifidobacterium.			

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OX NCB1_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787;
RA Schell M.A., Karmirantzou M., Snel B., Vlijanova D., Berger B.,
RA Peesl G., Zwaan M.-C., Desiere F., Bork P., Delley M.,
RA Fridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
CC -1- FUNCTION: Catalyzes the transfer of a methyl group from 5-
CC methyltetrahydrofolate to homocysteine resulting in methionine
CC formation (by similarity).
CC -1- CATALYTIC ACTIVITY: 5-methyltetrahydropteroyltri-L-glutamate + L-
CC homocysteine = tetrahydropteroyltri-L-glutamate + L-methionine.
CC -1- COFACTOR: zinc; binds one ion per subunit (by similarity).
CC -1- PATHWAY: Terminal step in the de novo biosynthesis of methionine.
CC -1- SIMILARITY: Belongs to the vitamin-B12 independent methionine
CC synthase family.
-----
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DR HAMAB; AE014702; AAN24613.1; -
DR InterPro: IPR002629; Methionine_synth.
DR InterPro: IPR006276; Met_synth_B12ind.
DR Pfam: PF01717; Methionine_synth; 1.
DR ProDom: PD004692; Methionine_synth; 2.
DR TIGRfam: TIGR01371; met_synth_B12ind; 1.
KW Transferase; Methyltransferase; Methionine biosynthesis; zinc; Repeat;
KW Complete proteome.
FT METAL 652 ZINC (BY SIMILARITY).
FT METAL 654 ZINC (BY SIMILARITY).
FT METAL 737 ZINC (BY SIMILARITY).
SQ SEQUENCE 767 AA; 85358 MW; 839AC62929F9D26 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 767;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMSW 5
DB 569 LNMSW 573

RESULT 3
RIR2_MYCLE STANDARD; PRT; 325 AA.
AC 09C8Q2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonucleoside-diphosphate reductase beta chain (EC 1.1.7.4.1)
DE (Ribonucleoside reductase small subunit).
GN NRDP OR ML1731.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteriia; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCB1_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11334002;
RA Cole S.T., Sigmeier K., Parikh J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore K., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,

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RA Davies R.M., Devlin K., Duthey S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornaby T., Jagels K., Lacroix C., Maclean J., Moulé S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus."
RL Nature 409:1007-1011(2001).
CC -1- FUNCTION: CATALYZES THE BIOSYNTHESIS OF DEOXYRIBONUCLEOTIDES FROM
CC THE CORRESPONDING RIBONUCLEOTIDES, PRECURSORS THAT ARE NECESSARY
CC FOR DNA SYNTHESIS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 2'-deoxyribonucleoside diphosphate + oxidized
CC thiorodoxin + (H2O) = ribonucleoside diphosphate + reduced
CC thiorodoxin.
CC -1- COFACTOR: BINDS 2 IRON IONS (BY SIMILARITY).
CC -1- PATHWAY: DNA replication pathway; first step.
CC -1- SUBUNIT: Tetramer of two alpha and two beta chains
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RIBONUCLEOSIDE DIPHOSPHATE REDUCTASE
CC SMALL CHAIN FAMILY. MORE SIMILAR TO ENTEROBACTERIAL NRDP THAN TO
CC NRDP.
-----
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DR EMBL; AL583923; CAC30684.1; -
DR PIR; B87125; B87125.
DR HSSP; P17424; 2R2F.
DR Leproma; ML1731; -
DR InterPro: IPR000358; Ribonucleotide.
DR Pfam: PF00268; ribonuc red sm; 1.
DR PROSITE: PS00369; RIBORED_SMALL; 1.
KW Oxidoreductase; DNA replication; iron; Complete proteome.
FT METAL 73 IRON 1 (BY SIMILARITY).
FT METAL 104 IRON 1 AND 2 (BY SIMILARITY).
FT METAL 107 IRON 1 (BY SIMILARITY).
FT METAL 164 IRON 2 (BY SIMILARITY).
FT METAL 198 IRON 2 (BY SIMILARITY).
FT METAL 201 IRON 2 (BY SIMILARITY).
FT ACT_SITE 111 BY SIMILARITY.
SQ SEQUENCE 325 AA; 37316 MW; A80D29751183358B CRC64;

Query Match 87.5%; Score 35; DB 1; Length 325;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMSWL 6
DB 15 INMNWL 20

RESULT 4
IKKA_HUMAN STANDARD; PRT; 745 AA.
ID IKKA_HUMAN
AC 01511; 014666; 013132; 092467;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
DE (I kappa-B kinase alpha) (IKK- $\alpha$ ) (IKK-A) (Ikkapab kinase)
DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).
GN CHUK OR IKKA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]

```

RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.  
RC TISSUE-T-cell;  
RX MEDLINE=9738646; PubMed=9244310;  
RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;  
RT "Identification and characterization of an IkappaB kinase."; *Cell* 90:373-383(1997).  
RN [2]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=97394468; PubMed=9252186;  
RA Didonato J.A., Hayekawa M., Rothwarf D.M., Zandi E., Karin M.;  
RT "A cytokine-responsive IkappaB kinase that activates the transcription factor NF-kappaB."; *Nature* 388:548-554(1997).  
RN [3]  
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND SER-176.  
RC TISSUE=Cervical carcinoma;  
RX MEDLINE=98008813; PubMed=9346484;  
RA Mercutio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L., Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;  
RT "IKK-1 and IKK-2: cytosolic-activated IkappaB kinases essential for NF-kappaB activation."; *Science* 278:860-866(1997).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RX MEDLINE=99032998; PubMed=9813230;  
RA Hu M.C.-T., Wang Y.-P.;  
RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and embryonic tissues but localized to different human chromosomes."; *Gene* 222:331-40(1998).  
RN [5]  
RP SEQUENCE OF 32-745 FROM N.A.  
RC TISSUE=Cervical carcinoma;  
RX MEDLINE=96258427; PubMed=8777433;  
RA Connolly M.A., Marcu K.B.;  
RT "CHUK, a new member of the helix-loop-helix and leucine zipper families of interacting proteins, contains a serine-threonine kinase catalytic domain."; *Cell* Mol. Biol. Res. 41:537-549(1995).  
RN [6]  
RP PHOSPHORYLATION BY MAP3K4/IKK, AND MUTAGENESIS OF SER-176, THR-179 AND SER-180.  
RX MEDLINE=98188283; PubMed=9550446;  
RA Ling L., Cao Z., Goeddel D.V.;  
RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of Ser-176."; *Proc. Natl. Acad. Sci. U.S.A.* 95:3792-3797(1998).  
RN [7]  
RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.  
RX MEDLINE=99413720; PubMed=10485710;  
RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M., Donner D.B.;  
RT "NF-kappaB activation by tumour necrosis factor requires the Akt serine-threonine kinase."; *Nature* 401:82-85(1999).  
RN [8]  
RP IKKA-IKKB BINDING.  
RX MEDLINE=99212141; PubMed=10195894;  
RA Delhase M., Hayakawa M., Chen Y., Karin M.;  
RT "Positive and negative regulation of IkappaB kinase activity through IKKbeta subunit phosphorylation."; *Science* 284:309-313(1999).  
RN [9]  
RP IKK PHOSPHORYLATION.  
RX MEDLINE=99038238; PubMed=9819420;  
RA Nemoto S., Didonato J.A., Lin A.;  
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappaB-inducing kinase."; *Mol. Cell. Biol.* 18:7336-7343(1998).  
RN [10]  
RP REVIEW.  
RX MEDLINE=20178139; PubMed=10712223;

RA	Jobin C. Sartor R.B.;	
RT	"the I kappa B/NF-kappa B system: a key determinant of mucosal	
RL	inflammation and protection.";	
RU	Ann. J. Physiol. 278:C451-C462(2000).	
RN	[11]	
RP	SUBUNIT OF A COMPLEX CONTAINING CREBBP; NCOA2; IKKB AND IKBK.	
RX	MEDLINE=21968797; PubMed=11971985;	
RA	Mu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,	
RT	O'Malley B.W.;	
RU	"regulation of SRC-3 (p61p/ACTR/AIB-1/RAC-3/TRAM-1) coactivator	
RL	activity by I kappa B Kinase.";	
RU	Mol. Cell. Biol. 22:3549-3561(2002).	
CC	-1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to	
CC	the dissociation of the inhibitor/NF-kappa-B complex and	
CC	ultimately the degradation of the inhibitor. Also phosphorylates	
CC	NCOA3.	
CC	-1- ENZYME REGULATION: Activated when phosphorylated and inactivated	
CC	when dephosphorylated.	
CC	-1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but	
CC	also as an homodimer. Directly interacts with IKK-GAMMA/NEMO.	
CC	Heterodimers form the active complex. The tripartite complex can	
CC	also bind to MAPK14/NIK, MEK1, IKKp and IKB-alpha-p65-p50	
CC	complex. A weak interaction with TRAF2 cannot be excluded. Part of	
CC	a complex composed of NCOA2, NCOA3, IKKB, IKBK and CREBBP.	
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.	
CC	-1- TISSUE SPECIFICITY: Widely expressed.	
CC	-1- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by	
CC	MEK1, and dephosphorylated by PP2A, Autophosphorylated.	
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.	
CC	IKAPAB KINASE SUBFAMILY.	
CC	-----	
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaborate	
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CC	the European Bioinformatics Institute. There are no restrictions on	
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CC	modified and this statement is not removed. Usage by and for commerc	
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/annou">http://www.isb-sib.ch/annou</a>	
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).	
CC	-----	
DR	EMBL; AF012890; AAC51662.1; -	
DR	EMBL; AF009225; AAC51671.1; -	
DR	EMBL; AF080157; AAD08996.1; -	
DR	EMBL; U25512; AAC50713.1; -	
DR	HSSP; Q63450; 1A06.	
DR	Genew; HGNC:1974; CHUK.	
DR	MIM; 600664; -	
DR	GO; GO:0005737; C:cytoplasm; TMS.	
DR	GO; GO:0008384; P:ikappab kinase activity; TMS.	
DR	GO; GO:0007345; P:embryogenesis and morphogenesis; TMS.	
DR	GO; GO:0007252; P:I-kappab phosphorylation; TMS.	
DR	GO; GO:0006955; P:immune response; TMS.	
DR	InterPro; IPR000719; Prot kinase.	
DR	InterPro; IPR002290; Ser thr kinase.	
DR	InterPro; IPR001245; Tyr kinase.	
DR	Pfam; PF00069; pkinase; 1	
DR	PRINTS; PR00109; TYRKINASE.	
DR	Prodom; PD000001; Prot kinase.	
DR	SMART; SM00220; S_TKC; 1.	
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.	
DR	PROSITE; PS00108; PROTEIN KINASE ST; 1.	
DR	PROSITE; PS50011; PROTEIN KINASE DOM; 1.	
KW	Transferase; Serine/chreonine-protein kinase; ATP-binding;	
KW	Phosphorylation.	
FT	DOMAIN 15 302	PROTEIN KINASE.
FT	DOMAIN 455 476	LEUCINE-ZIPPER (POTENTIAL).
FT	DOMAIN 738 743	NEMO-BINDING.
FT	NP BIND 21 29	ATP (BY SIMILARITY).
FT	BINDING 44 44	ATP (BY SIMILARITY).
FT	ACT SITE 144 144	BY SIMILARITY.
FT	MOD_RES 23 23	PHOSPHORYLATION (BY PKB/AKT1).
FT	MOD_RES 176 176	PHOSPHORYLATION (BY MAP3K14).
FT	MOTAGN 23 23	T->A. LOSS OF PHOSPHORYLATION AND DECREASE OF KINASE ACTIVITY.



FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.  
 FT MUTAGEN 44 44 K->M: LOSS OF AUTOPHOSPHORYLATION.  
 FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF ACTIVITY.  
 FT MUTAGEN 176 176 S->B: FULL ACTIVATION.  
 FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.  
 FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.  
 FT CONFLICT 543 543 E->G (IN REF. 2).  
 FT CONFLICT 604 604 L->R (IN REF. 5).  
 FT CONFLICT 679 680 TS->AY (IN REF. 5).  
 FT CONFLICT 684 684 P->A (IN REF. 3 AND 5).  
 FT CONFLICT 687 687 TS->DL (IN REF. 5).  
 SQ SEQUENCE 745 AA; 84653 MW; 7A90B598C98A56C2 CRC64;  
 Query Match 87.5%; Score 35; DB 1; Length 745;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6  
 Db 738 LDMSWL 743

RESULT 5  
 ID IKKA\_MOUSE STANDARD; PRT; 745 AA.  
 AC 060680; Q9D2X3;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Inhibitor of nuclear factor kappa-B kinase subunit (I $\kappa$ B 2.7.1.1.-)  
 DE (1-kappa-B kinase alpha) (IKK $\alpha$ ) (IKK-A) (I $\kappa$ B kinase)  
 DE (1-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous  
 kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKB1KX).  
 GN CHUK OR IKKA. (Mouse).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=BALB/c;  
 RX MEDLINE=9604444; PubMed=7558004;  
 RA Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.;  
 RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human  
 chromosome 10 and mouse chromosome 19.";  
 RL Genomics 27:348-351(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=BALB/c;  
 RX MEDLINE=96258427; PubMed=8777433;  
 RA Connolly M.A., Marcu K.B.;  
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper  
 families of interacting proteins, contains a serine-threonine kinase  
 catalytic domain.";  
 RL Cell. Mol. Biol. Res. 41:537-549(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RC STRAIN=C57BL/6J; TISSUE=Colon;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,  
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,  
 RA Kodora K., Matsuda H.A., Ashburner M., Batelov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kienl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Bocelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita K., Gariboldi M.,  
 RA Gietzenich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schenbach C., Seta T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wymshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Konteak S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [4]  
 RP ALTERNATIVE SPLICING;  
 RX MEDLINE=20198447; PubMed=10733566;  
 RA McKenzie F.R., Connolly M.A., Balzarano D., Mueller J.R.,  
 RA Gelezianus R., Marcu K.B.;  
 RT "Functional isoforms of I $\kappa$ B kinase alpha (IKK $\alpha$ ) lacking  
 RT leucine zipper and helix-loop-helix domains reveal that IKK $\alpha$  and  
 RT IKK $\beta$  have different activation requirements.";  
 RL Mol. Cell. Biol. 20:2635-2649(2000).  
 RN [5]  
 RP PHOSPHORYLATION BY MAP3K14/NIK.  
 RX MEDLINE=98188238; PubMed=9520401;  
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,  
 RA Okumura K.;  
 RT "Differential regulation of I $\kappa$ B kinase alpha and beta by two  
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated  
 RT protein kinase/ERK kinase kinase-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).  
 RN [6]  
 RP IKKA-IKKB BINDING.  
 RX MEDLINE=99212141; PubMed=10195894;  
 RA Delnase M., Hayakawa M., Chen Y., Karin M.;  
 RT "Positive and negative regulation of I $\kappa$ B kinase activity through  
 RT IKK $\beta$  subunit phosphorylation.";  
 RL Science 284:309-313(1999).  
 RN [7]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., DiDonato J.A., Lin A.;  
 RT "Coordinate regulation of I $\kappa$ B kinase by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [8]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Uebachs C., Sartor R.B.;  
 RT "The I $\kappa$ B kinase B system: a key determinant of mucosal  
 RT inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 CC the dissociation of the inhibitor/NF-kappa-B complex and  
 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3.  
 CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated  
 CC when dephosphorylated.  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but  
 CC also as an homodimer. Directly interacts with IKK-gamma/MEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MAP3K14/NIK, MEK1, IKAP and IKK-alpha-P65-P50  
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of  
 CC a complex composed of NCOA2, NCOA3, IKKB, IKKG and CREBBP (by  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1;  
 CC IsoId=Q60680-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Delta LH;  
 CC IsoId=Q60680-2; Sequence=VSP\_004866; VSP\_004867;  
 CC Name=3; Synonyms=Delta H;  
 CC IsoId=Q60680-3; Sequence=VSP\_004866, VSP\_004869;  
 CC TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and  
 CC 3 are expressed predominantly in brain and T-lymphocytes.  
 CC -1- DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by  
 CC E11, E15 and E17 days. In the limb development, its expression  
 CC predominates in the limb buds at E12.5 day.



RP IDENTIFICATION IN A COMPLEX WITH CREBBP, NCOA2, NCOA3, IKKA AND IKKB.  
 RX MEDLINE=21968797; PubMed=11971985;  
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,  
 O'Malley B.W.;  
 RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator  
 activity by I kappa B kinase";  
 RL Mol. Cell. Biol. 22:3549-3561(2002).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 the dissociation of the inhibitor/NF-kappa-B complex and  
 ultimately the degradation of the inhibitor. Also phosphorylates  
 NCOA3 (by similarity).  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-alpha-P65-P50  
 complex. Phosphorylated IKK-alpha is further released from the  
 complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB  
 and CREBBP.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal  
 muscle, kidney, pancreas, spleen, thymus, prostate, testis and  
 peripheral blood.  
 CC -1- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.  
 CC Weakly autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPAB KINASE SUBFAMILY.  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF029684; AAC51860.1; -;  
 DR EMBL; AF080158; AAD08997.1; -;  
 DR EMBL; AF031416; AAC64675.1; -;  
 DR EMBL; BC006231; AAH06231.1; -;  
 DR HSSP; Q63450; 1A06.  
 DR Genew; HGNC:5960; IKKB.  
 DR MIM; 603258; -;  
 DR GO; GO:0005737; C:cytoplasm; NAS.  
 DR GO; GO:0005524; P:ATP binding activity; NAS.  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; NAS.  
 DR GO; GO:0016563; P:transcriptional activator activity; NAS.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.  
 DR InterPro: IPR002290; Ser\_Thr\_kinase.  
 DR Pfam; PF00069; Kinase; 1.  
 DR Pfam; PF00240; Ubiquitin; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE\_NEG.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.  
 KM Transferrase; Serine/threonine-protein kinase; ATP-binding;  
 KM Phosphorylation.  
 FT DOMAIN 15 300 PROTEIN KINASE.  
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 FT NP BIND 737 742 NEMO-BINDING.  
 FT ACT\_SITE 21 29 ATP (BY SIMILARITY).  
 FT BINDING 44 44 ATP (BY SIMILARITY).  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 181 181 PHOSPHORYLATION.  
 FT MTAGN 44 44 K-2A: LOSS OF KINASE ACTIVITY AND NO  
 EFFECT ON BINDING TO NIK.  
 FT MTAGN 177 177 S-2A: DECREASE OF ACTIVITY.  
 FT MTAGN 177 177 S-2B: FULL ACTIVATION.  
 FT MTAGN 181 181 S-2A: DECREASE OF ACTIVITY.  
 FT MTAGN 181 181 S-2B: FULL ACTIVATION.  
 FT CONFLICT 231 255 WSKVRKSEVDIVSBDLNGTYVF -> CYRMPGTVAHS

FT FT CONFLICT 425 425 CNPSTLGGGRMI (IN REF. 5).  
 FT FT SEQUENCE 756 AA; 86563 MW; F9C4DF671AE9E14E CRC64;  
 SQ SQ  
 Query Match 87.5%; Score 35; DB 1; Length 756;  
 Best Local Similarity 83.3%;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNMSTL 6  
 Db 737 LDMSTL 742  
 RESULT 7  
 ID IKKB MOUSE STANDARD; PRT; 757 AA.  
 AC 088351; Q9RLJ6;  
 DT 16-OCT-2001 (Rel. 40. Created)  
 DT 28-FEB-2003 (Rel. 41. Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (IC 2.7.1.-)  
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase  
 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIB).  
 GN IKKB OR IKKB  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SOURCE: FROM N.A. AND PHOSPHORYLATION BY MEKK1.  
 RC STRAIN=C57BL/6; TISSUE=spleen;  
 RX MEDLINE=98188238; PubMed=9520401;  
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,  
 Okumura K.;  
 RT "Differential regulation of IkappaB kinase alpha and beta by two  
 upstream kinases, NF-kappaB-inducing kinase and mitogen-activated  
 protein kinase/ERK kinase-1";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;  
 RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that  
 constitutively phosphorylates serine residues of Ikb";  
 RL Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP DEVELOPMENTAL STAGE.  
 RX MEDLINE=99455228; PubMed=10523828;  
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;  
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling  
 pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a  
 developmentally regulated protein kinase";  
 RL Oncogene 18:5514-5524(1999).  
 RN [4]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., Diconato J.A., Lin A.;  
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein  
 kinase kinase kinase 1 and NF-kappaB-inducing kinase";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [5]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 inflammation and protection";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 the dissociation of the inhibitor/NF-kappa-B complex and  
 ultimately the degradation of the inhibitor. Also phosphorylates  
 NCOA3.  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can

CC also bind to MEK1, MAP3K14/NIK, IKAP and IKK-ALPHA-P55-P50  
 CC complex. Phosphorylated IKK-alpha is further released from the  
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKGA, IKKGB  
 CC and CREBBP (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.  
 CC -1- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout  
 CC the mouse embryo, at E9.5 day its expression begins to be  
 CC localized to the brain, neural ganglia, neural tube, and in liver  
 CC at E12.5 day. At E15.5 day, the expression is further restricted  
 CC to specific tissues of the embryo.  
 CC -1- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.  
 CC Weakly autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPB KINASE SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; AF026524; AAC23557.1; -  
 CC EMBL; AF088910; AAD52095.1; -  
 CC HSSP; Q63450; 1A06.  
 CC MGD; MGI:1338071; Ikbkb.  
 CC InterPro; IPR000719; Prot Kinase.  
 CC InterPro; IPR002290; Ser Thr kinase.  
 CC InterPro; IPR001245; Tyr kinase.  
 CC Pfam; PF00069; kinase; 1.  
 CC PRINTS; PR00109; TYRKINASE.  
 CC PRODOM; PD000001; Prot Kinase; 1.  
 CC PROSITE; PS00107; PROTEIN KINASE ATP; FALSE\_NEG.  
 CC PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 CC PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC Transferrase; Serine/threonine-protein kinase; ATP-binding;  
 CC phosphorylation.  
 CC KW  
 CC DOMAIN 15 300 PROTEIN KINASE.  
 CC FT 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 CC FT DOMAIN 737 742 NEMO-BINDING.  
 CC FT NP\_BIND 21 29 ATP (BY SIMILARITY).  
 CC FT BINDING 44 44 ATP (BY SIMILARITY).  
 CC FT ACT\_SITE 145 145 BY SIMILARITY.  
 CC FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 CC FT MOD\_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).  
 CC FT MOD\_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).  
 CC FT CONFLICT 56 56 N -> D (IN REF. 2).  
 CC FT CONFLICT 343 343 N -> D (IN REF. 2).  
 CC FT CONFLICT 356 356 K -> E (IN REF. 2).  
 CC FT CONFLICT 390 390 L -> F (IN REF. 2).  
 CC FT CONFLICT 406 406 P -> Q (IN REF. 2).  
 CC FT FT 573 K -> R (IN REF. 2).  
 CC FT CONFLICT 736 757 TIDMSWLMQWEDERCSLEQACD -> VTA (IN REF.  
 CC FT SEQUENCE 757 AA; 86690 MW; FED962095449C5E CRC64;  
 CC  
 CC Query Match 87.5%; Score 35; DB 1; Length 757;  
 CC Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 LMSWTL 6  
 CC DB 737 LMSWTL 742  
 CC  
 CC RESULT 8  
 CC ID IKKB\_RAT STANDARD; PRT; 757 AA.  
 CC AC Q9QY78;  
 CC DT 16-OCT-2001 (Rel. 40, Created)  
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (BC 2.7.1.-)  
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (I-kappa-B kinase  
 DE 2) (IKK) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).  
 GN IKKB OR IKK.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxId=10116;  
 OX (1)  
 RP SEQUENCE FROM N.A.  
 RA Zhang Y., Sun S., Ravid K.;  
 RT "IKK beta in megakaryocyte differentiation.";  
 RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN (2)  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., Didonato J.A., Lin A.;  
 RT "Coordinate regulation of Ikkappa kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN (3)  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 RT inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 CC the dissociation of the inhibitor/NF-kappa-B complex and  
 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3.  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MEK1, MAP3K14/NIK, IKAP and IKK-alpha-P55-P50  
 CC complex. Phosphorylated IKK-alpha is further released from the  
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKGA, IKKGB  
 CC and CREBBP (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.  
 CC Weakly autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPB KINASE SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; AF15282; AAF21978.1; -  
 CC HSSP; Q63450; 1A06.  
 CC InterPro; IPR000719; Prot Kinase.  
 CC InterPro; IPR002290; Ser Thr kinase.  
 CC InterPro; IPR001245; Tyr kinase.  
 CC Pfam; PF00069; kinase; 1.  
 CC PRINTS; PR00109; TYRKINASE.  
 CC PRODOM; PD000001; Prot Kinase; 1.  
 CC PROSITE; PS00107; PROTEIN KINASE ATP; FALSE\_NEG.  
 CC PROSITE; PS00108; PROTEIN KINASE DOM; 1.  
 CC PROSITE; PS50011; PROTEIN\_KINASE\_ST; 1.  
 CC Transferrase; Serine/threonine-protein kinase; ATP-binding;  
 CC phosphorylation.  
 CC KW  
 CC DOMAIN 15 300 PROTEIN KINASE.  
 CC FT 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 CC FT DOMAIN 737 742 NEMO-BINDING.  
 CC FT NP\_BIND 21 29 ATP (BY SIMILARITY).  
 CC FT BINDING 44 44 ATP (BY SIMILARITY).  
 CC FT ACT\_SITE 145 145 BY SIMILARITY.  
 CC FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).

FT MOD RES 177 177 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD RES 181 181 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 757 AA; 86866 MW; 3AF6A6A7DF91F9C CRC64;

Query Match 87.5%; Score 35; DB 1; Length 757;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWSL 6  
 DB 737 LNMWSL 742

RESULT 9  
 ID Y451\_S1YNY3 STANDARD; PRT; 154 AA.  
 AC P74576;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical protein s110451.  
 GN S110451.  
 OS Synechocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 OX NCBI\_TaxID=1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; PubMed=8905231;  
 RA Kaneke T., Sato S., Kotani H., Tanaka A., Asagiri E., Nakamura Y.,  
 RA Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,  
 RA Hosokuchi T., Matsuno A., Muraki A., Nakazaki N., Natsu K.,  
 RA Okumura S., Shimo S., Takeuchi C., Wada T., Watanabe A.,  
 RA Yamada M., Yasuda M., Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 RT entire genome and assignment of potential protein-coding regions.";  
 RL DNA Res. 3:109-136(1996).  
 CC -1- SIMILARITY: BELONGS TO THE UPF0039 (ELAA) FAMILY.

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CC EMBL; D90917; BAA18794.1; -;  
 DR PIR; S76882; S76882;  
 DR InterPro; IPR00182; GCS5acetyltransf.  
 DR Pfam; PF00583; Acetyltransf. 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 154 AA; 17612 MW; C84777660627F9C2 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 154;  
 Best Local Similarity 80.0%; Pred. No. 49;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWSL 5  
 DB 3 LNMWSL 7

RESULT 10  
 ID N008\_PARDE STANDARD; PRT; 345 AA.  
 AC P29920;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE NADH-quinone oxidoreductase chain 8 (EC 1.6.99.5) (NADH dehydrogenase  
 DE I, chain 8) (NDH-1, chain 8).  
 GN N008.

OS Paracoccus denitrificans.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;  
 OC Rhodobacteraceae; Paracoccus.  
 OX NCBI\_TaxID=266;

RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 13543; PubMed=8422400;  
 RX MEDLINE=93136200; PubMed=8422400;  
 RA Xu X., Matsumo-Yagi A., Yagi T.;  
 RT "DNA sequencing of the seven remaining structural genes of the gene  
 RT cluster encoding the energy-transducing NADH-quinone oxidoreductase  
 RT of Paracoccus denitrificans.";  
 RL Biochemistry 32:968-981(1993).  
 CC -1- FUNCTION: NDH-1 shuttles electrons from NADH, via FMN and iron-  
 CC sulfur (Fe-S) centers, to quinones in the respiratory chain. The  
 CC immediate electron acceptor for the enzyme in this species is  
 CC believed to be ubiquinone. Couples the redox reaction to proton  
 CC translocation (for every two electrons transferred, four hydrogen  
 CC ions are translocated across the cytoplasmic membrane), and thus  
 CC conserves the redox energy in a proton gradient.

CC -1- CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.  
 CC -1- SUBUNIT: COMPOSED OF 14 DIFFERENT SUBUNITS. SUBUNITS N007-14  
 CC CONSTITUTE THE MEMBRANE SECTOR OF THE COMPLEX.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.

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CC EMBL; L02354; AAA25592.1; -;  
 DR PIR; C45456; C45456;  
 DR InterPro; IPR001694; Resp\_NADH\_dh1.  
 DR Pfam; PF00146; NADHdh. 1.  
 DR PROSITE; PS00667; COMPLEX1\_ND1\_1; 1.  
 DR PROSITE; PS00668; COMPLEX1\_ND1\_2; 1.  
 KW Oxidoreductase; NAD; Quinone; Ubiquinone; Transmembrane.  
 FT TRANSMEM 15 35 POTENTIAL.  
 FT TRANSMEM 82 102 POTENTIAL.  
 FT TRANSMEM 115 135 POTENTIAL.  
 FT TRANSMEM 161 181 POTENTIAL.  
 FT TRANSMEM 190 210 POTENTIAL.  
 FT TRANSMEM 253 273 POTENTIAL.  
 FT TRANSMEM 278 298 POTENTIAL.  
 FT TRANSMEM 309 329 POTENTIAL.  
 SQ SEQUENCE 345 AA; 38751 MW; E33B667B5E9506B4 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 345;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNMWSL 6  
 DB 191 LNMWSL 196

RESULT 11  
 ID N00H\_RHOCA STANDARD; PRT; 345 AA.  
 AC P42032;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE NADH-quinone oxidoreductase chain H (EC 1.6.99.5) (NADH dehydrogenase  
 DE I, chain H) (NDH-1, chain H).  
 GN N00H OR NDHA.  
 OS Rhodobacter capsulatus (Rhodospirillum rubrum capsulata).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;  
 OC Rhodobacteraceae; Rhodobacter.

```

OX  NCBI_TaxID=1061;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=ATCC 33303 / B10;
RA  MEDLINE=92233948; PubMed=1568483;
RX  Dupuis A.;
RT  "Identification of two genes of Rhodobacter capsulatus coding for
RT  proteins homologous to the ND1 and 23 kDa subunits of the
RT  mitochondrial complex I."
RL  FEBS Lett. 301:215-218(1992).
CC  -1- FUNCTION: NDH-1 shuttles electrons from NADH, via FMN and iron-
CC  sulfur (Fe-S) centers, to quinones in the respiratory chain. The
CC  immediate electron acceptor for the enzyme in this species is
CC  believed to be ubiquinone. Couples the redox reaction to proton
CC  translocation (for every two electrons transferred, four hydrogen
CC  ions are translocated across the cytoplasmic membrane), and thus
CC  conserves the redox energy in a proton gradient.
CC  -1- CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
CC  -----
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CC  or send an email to license@1sb-sib.ch).
CC  -----
DR  EMBL; AF029365; AAC24997.1; -
DR  EMBL; Z11611; CAA77684.1; -
DR  PIR; S22368; S22368.
DR  InterPro; IPR001694; Resp_NADH_dh1.
DR  Pfam; PF00146; NADdh1.1.
DR  PROSITE; PS00667; COMPLEX1_ND1_1; 1.
DR  PROSITE; PS00668; COMPLEX1_ND1_2; 1.
KW  Oxidoreductase; NAD; Quinone; Ubiquinone; Transmembrane.
FT  TRANSMEM 14
FT  TRANSMEM 84 104
FT  TRANSMEM 115 135
FT  TRANSMEM 161 181
FT  TRANSMEM 190 210
FT  TRANSMEM 248 268
FT  TRANSMEM 277 297
FT  TRANSMEM 309 329
FT  TRANSMEM 345 AA; 37852 MW; 5f959d640d911854 CRC64;
SQ  SEQUENCE

Query Match      85.0%; Score 34; DB 1; Length 345;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RX  MEDLINE=83216118; PubMed=6304321;
RA  Gough J.A., Murray N.E.;
RT  "Sequence diversity among related genes for recognition of specific
RT  targets in DNA molecules."
RL  J. Mol. Biol. 166:1-19(1983).
CC  -1- FUNCTION: THE M AND S SUBUNITS TOGETHER FORM A METHYLTRANSFERASE
CC  (MTASE) THAT METHYLATES TWO ADENINE RESIDUES IN COMPLEMENTARY
CC  STRANDS OF BIPARTITE DNA RECOGNITION SEQUENCE. IN THE PRESENCE OF
CC  THE R SUBUNIT THE COMPLEX CAN ALSO ACT AS AN ENDONUCLEASE, BINDING
CC  TO THE SAME TARGET SEQUENCE BUT CUTTING THE DNA SOME DISTANCE FROM
CC  THIS SITE. WHETHER THE DNA IS CUT OR MODIFIED DEPENDS ON THE
CC  METHYLATION STATE OF THE TARGET SEQUENCE. WHEN THE TARGET SITE IS
CC  UNMODIFIED, THE DNA IS CUT. WHEN THE TARGET SITE IS
CC  METHYLATED, THE COMPLEX ACTS AS A MAINTENANCE MTASE MODIFYING
CC  THE DNA SO THAT BOTH STRANDS BECOME METHYLATED. SUBUNIT S DICTATES
CC  DNA SEQUENCES SPECIFICITY. THE ECODI ENZYME RECOGNIZES 5'-
CC  TTA(N7)GTCT-3'.
CC  -1- SUBUNIT: THE TYPE I RESTRICTION/MODIFICATION SYSTEM IS COMPOSED
CC  OF THREE POLYPEPTIDES R,M AND S.
CC  -1- DOMAIN: CONTAINS TWO DNA RECOGNITION DOMAINS, EACH SPECIFYING
CC  RECOGNITION OF ONE OF THE TWO DEFINED COMPONENTS OF THE TARGET
CC  SEQUENCE.
CC  -1- SIMILARITY: BELONGS TO THE TYPE-I RESTRICTION SYSTEM S METHYLASE
CC  FAMILY.
CC  -----
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CC  -----
DR  EMBL; V00287; CAA23553.1; -
DR  REBASE; 3640; S.ECODI.
DR  InterPro; IPR000055; Rest mod DNA.
DR  Pfam; PF01420; Methylase S; 2_
KW  Restriction system; DNA-Binding.
SQ  SEQUENCE 444 AA; 49893 MW; 14BE17B5325294F0 CRC64;

Query Match      85.0%; Score 34; DB 1; Length 444;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY  1 LNMWMTL 6
DB  191 LNMWMTL 196

RESULT 12
T1SD_ECOLI STANDARD; PRT; 444 AA.
AC  P06991;
DT  01-APR-1988 (Rel. 07, Created)
DT  01-APR-1988 (Rel. 07, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Type I restriction enzyme EcodI specificity protein (S protein)
DE  (S.EcodI).
GN  HSDS OR HSS.
OS  Escherichia coli.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC  Enterobacteriaceae; Escherichia.
OX  NCBI_TaxID=562;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=D / E166;

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QY  2 NMSWMTL 6
DB  215 NMSWMTL 219

RESULT 13
YAWD_SCHPO STANDARD; PRT; 612 AA.
AC  Q10187;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Hypothetical protein C3F10.13 in chromosome I.
GN  SPAC3F10.13.
OS  Schizosaccharomyces pombe (fission yeast).
OC  Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC  Schizosaccharomycetales; Schizosaccharomycetaceae;
OC  Schizosaccharomycetes.
OX  NCBI_TaxID=4896;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=972;
RX  MEDLINE=21848401; PubMed=11859360;
RA  Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA  Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA  Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA  Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA  Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA  Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,

```

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson S., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Voiclaert G., Aert R., Robben J., Gromprez B.,  
 RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs C., Holzer C., Holzer E., Moesli D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Medler H., Mambut R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mortier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurt S.M.,  
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Uesery D., Barrett B.G., Nurse P.,  
 RT "the genome sequence of Schizosaccharomyces pombe.",  
 RL Nature 415:871-880(2002).  
 CC -1- SIMILARITY: Contains 1 UBA domain.  
 CC -----  
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DR EMBL; 269369; CAA9311.1; -.  
 DR PIR; T38714; T38714.  
 DR GeneDB SPombe; SPAC3F10.13; -.  
 DR InterPro; IPR000449; UBA\_domain.  
 DR Pfam; PF00627; UBA\_1.  
 DR SMART; SMO0165; UBA\_1.  
 DR PROSITE; PS50030; UBA\_1.  
 KW Hydrophobic protein; Glycoprotein; Transmembrane.  
 FT TRANSMEM 91 111 POTENTIAL.  
 FT TRANSMEM 437 457 POTENTIAL.  
 FT DOMAIN 3 42 UBA.  
 FT CARBOHYD 128 128 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 220 220 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 296 296 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 315 315 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 416 416 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 612 AA; 68720 MW; 38BFD93808F554CD CRC64;

Query Match 85.0%; Score 34; DB 1; Length 612;  
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NMSWL 6  
 Db 296 NMSWI 300

RESULT 14  
 ROR1\_DROME STANDARD; PRT; 685 AA.  
 AC Q24488;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase transmembrane receptor Ror precursor  
 DE (EC 2.7.1.112) (drom).  
 GN ROR OR CG4926.  
 OS Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephyridiidae; Drosophilidae; Drosophila.  
 CC NCBI\_TaxID=7227;  
 RN [1]

RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
 RC STRAIN=Cancon-S; TISSUE=Larval brain;  
 RX MEDLINE=93344822; PubMed=8394009;  
 RT "Dros. a potential neurotrophic receptor gene, encodes a Drosophila  
 RT homolog of the vertebrate Ror family of Trk-related receptor tyrosine  
 RT kinases."  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7109-7113(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams W.D., Cenniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wen K.H., Doyle C., Baxter E.G., Holt G., Nelson C.R., Milos G.L.G.,  
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokerstein P., Brothier P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Folsch C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasner K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,  
 RA Jalali M., Kalish F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Murthy D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paclet J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Syrakas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 RN [3]  
 RP SEQUENCE OF 545-597 FROM N.A.  
 RX MEDLINE=98401146; PubMed=9731193;  
 RA Oates A.C., Wollberg P., Achen M.G., Milke A.F.;  
 RT "Sampling the genomic pool of protein tyrosine kinase genes using the  
 RT polymerase chain reaction with genomic DNA."  
 RT Biochem. Biophys. Res. Commun. 249:660-667(1998).  
 CC -1- FUNCTION: Tyrosine-protein kinase receptor that functions during  
 CC early stages of neuronal development.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: Expressed in neurons of the developing nervous  
 CC system.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. ROR  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: Contains 1 frizzled (FZ) domain.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way

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CC -----

DR EMBL; L20297; AAA28660.1; -

DR EMBL; AEO03628; AAF52885.1; -

DR EMBL; AJ002908; CAA05743.1; -

DR PIR; A48289; A48289.

DR HSP; P13362; 1RGK.

DR PLYBase; FBgn0010407; Ror.

DR GO; GO:0016021; C:integral to membrane; NMS.

DR GO; GO:0004713; P:protein tyrosine kinase activity; NMS.

DR GO; GO:0007417; P:central nervous system development; IEP.

DR GO; GO:0006468; P:protein amino acid phosphorylation; NMS.

DR InterPro; IPR0000024; Fz domain.

DR InterPro; IPR000001; Kringle.

DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR002011; RTKinaseII.

DR InterPro; IPR001245; Tyr\_kinase.

DR Pfam; PF00051; kringle; 1.

DR Pfam; PF00069; kinase; 1.

DR PRINTS; PRO0018; KRINGLE.

DR PRINTS; PRO0109; TYRKINASE.

DR ProDom; PD000395; Kringle; 1.

DR ProDom; PD000001; Prot\_kinase; 1.

DR SMART; SM00130; KR; 1.

DR SMART; SM00219; Tyrc; 1.

DR PROSITE; PSS0038; Fz; 1.

DR PROSITE; PSS0021; KRINGLE; 1; 1.

DR PROSITE; PSS0070; KRINGLE; 2; 1.

DR PROSITE; PSS0107; PROTEIN KINASE ATP; 1.

DR PROSITE; PSS0011; PROTEIN KINASE DOM; 1.

DR PROSITE; PSS0109; PROTEIN KINASE TYR; 1.

DR PROSITE; PSS0239; RECEPTOR\_TYR\_KIN\_II; 1.

DR Transferrase; Kinase; Tyrosine-protein kinase; ATP-binding; Receptor;

DR Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation;

KW Developmental protein.

KM

FT CHAIN 1 24

FT SIGNAL 25 685

FT DOMAIN 25 317

FT TRANSMEM 318 338

FT DOMAIN 339 685

FT DOMAIN 36 225

FT DOMAIN 236 310

FT DOMAIN 410 677

FT NP BIND 416 424

FT BINDING 442 442

FT ACT\_SITE 539 539

FT MOD\_RES 565 565

FT MOD\_RES 569 569

FT MOD\_RES 570 570

FT CARBOHYD 45 45

FT CARBOHYD 63 63

FT CARBOHYD 129 129

FT CARBOHYD 144 144

FT CARBOHYD 250 250

SQ SEQUENCE 685 AA; 78142 MW; 526162D27D5DF7C7 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 685;

Best Local Similarity 83.3%; Pred. No. 2.1e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LNMW 6

DB 259 LRWSWL 264

RESULT 15

ATP8\_ASTPE

ID ATP8\_ASTPE STANDARD; PRT; 54 AA.

AC Q33822;

DT 15-JUL-1998 (rel. 36, Created)

DT 15-JUL-1998 (rel. 36, Last sequence update)

DT 28-FEB-2003 (rel. 41, Last annotation update)

DE ATP synthase protein 8 (BC 3.6.3.14) (ATPase subunit 8) (A6L).

GN MTP8 OR ATP8

OS Asterina pectinifera (Starfish).

OC Mitochondrion.

OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;

OC Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.

OX NCBI\_TaxID=7594;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RX MEDLINE=93402698; PubMed=7672576;

RA Asakawa S., Himeho H., Miura K.-I., Watanabe K.;

RT "Nucleotide sequence and gene organization of the starfish Asterina pectinifera mitochondrial genome."

RL Genetics 140:1047-1060(1995).

CC -1- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.

CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate + H(+) (out).

CC -1- SUBCELLULAR LOCATION: Membrane-bound.

CC -1- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.

CC -----

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CC -----

DR EMBL; D16387; BAA03883.1; -

DR PIR; S70600; S70600.

DR InterPro; IPR001421; ATPase8\_mit.

DR Pfam; PF00895; ATP-synt\_8; 1.

KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.

FT TRANSMEM 8 28

FT SIGNAL 54 AA; 6241 MW; 9EABDACB93CDF5F1 CRC64;

SQ SEQUENCE

Query Match 82.5%; Score 33; DB 1; Length 54;

Best Local Similarity 80.0%; Pred. No. 25;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMW 5

DB 49 LNMW 53

Search completed: February 18, 2004, 14:28:07

Job time : 4.55263 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds

(Without alignments)  
87.531 Million cell updates/sec

Title: US-09-643-260-9

Perfect score: 40

Sequence: 1 LNMWML 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR 76:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	204	2 C83748	hypothetical prote
2	37	92.5	337	2 AG2946	hypothetical prote
3	37	92.5	337	2 C98336	probable integral
4	36	90.0	204	2 T15295	hypothetical prote
5	36	90.0	380	2 T11041	ubiquinol-cytochro
6	36	90.0	460	2 AG0965	probable glycosyl
7	36	90.0	590	2 C83491	hypothetical prote
8	36	90.0	744	2 T10035	hypothetical prote
9	35	87.5	116	2 T03472	conserved hypotet
10	35	87.5	321	2 T24773	hypothetical prote
11	35	87.5	325	2 B87125	ribonucleotide red
12	35	87.5	745	1 T49101	conserved helix-10
13	35	87.5	777	2 T09056	glucan 1,3-beta-gl
14	34	85.0	154	2 S76882	hypothetical prote
15	34	85.0	345	2 C45456	NADH2 dehydrogenas
16	34	85.0	345	2 S22368	NADH2 dehydrogenas
17	34	85.0	355	2 F70983	probable serine pr
18	34	85.0	632	2 T38714	hypothetical prote
19	34	85.0	685	1 A48289	neurotrophic recep
20	34	85.0	903	2 E88221	protein T01H3.2 [1
21	34	85.0	919	2 T37062	probable transcrip
22	34	85.0	980	2 T24336	hypothetical prote
23	34	85.0	1147	2 T35781	hypothetical prote
24	33	82.5	52	2 D90532	hypothetical prote
25	33	82.5	54	2 S70600	H+-transporting tw
26	33	82.5	72	2 AD2464	hypothetical prote
27	33	82.5	169	2 T38724	mitochondrial benz
28	33	82.5	169	2 JCI393	benzodiazepine rec
29	33	82.5	169	2 I57953	peripheral-type be

30	33	82.5	169	2 A53405	peripheral-type be
31	33	82.5	169	2 S14257	benzodiazepine rec
32	33	82.5	169	2 A39473	peripheral-type be
33	33	82.5	169	2 JB0149	peripheral benzod
34	33	82.5	275	2 AB2466	ABC transporter su
35	33	82.5	281	2 AF2161	cation-efflux syst
36	33	82.5	289	2 AB2953	ATP synthase A cha
37	33	82.5	310	2 C84701	hypothetical prote
38	33	82.5	315	2 A86710	transposase of 159
39	33	82.5	315	2 G86712	transposase of 159
40	33	82.5	315	2 D86741	transposase of 159
41	33	82.5	315	2 G86787	transposase of 159
42	33	82.5	315	2 G86794	transposase of 159
43	33	82.5	315	2 C86814	transposase of 159
44	33	82.5	315	2 B86837	transposase of 159
45	33	82.5	315	2 B86860	transposase of 159

#### ALIGNMENTS

RESULT 1  
C83748 hypothetical protein BH0787 [imported] - Bacillus halodurans (strain C-125)  
C/Species: Bacillus halodurans  
C/Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #ext\_change 15-Jun-2001  
C/Accession: C83748  
R/Takami, H., Nakasone, K., Takaki, Y., Maeno, G., Sasaki, R., Maeda, N., Fujii, F., Hi  
Nucleic Acids Res. 28, 4317-4331, 2000  
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans an  
A/Reference number: AB3650, NCBI:20512582, PMID:11058132  
A/Accession: C83748  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-204 <STO>  
A/Cross-references: GB:AP001509; GB:BA000004; NID:gl0173176; PIDN:BA804506.1; GSPDB:GN  
A/Experimental source: strain C-125  
C/Genetics:  
A/Gene: BH0787  
C/Superfamily: Bacillus subtilis conserved hypothetical protein ysel

Query Match  
Best Local Similarity 92.5% Score 37; DB 2; Length 204;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWML 6  
|||  
Db 22 LNMWML 27

RESULT 2  
AG2946 hypothetical protein Atcu3173 [imported] - Agrobacterium tumefaciens (strain C58, Dupont  
C/Species: Agrobacterium tumefaciens  
C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #ext\_change 16-Nov-2002  
C/Accession: AG2946  
R/Wood, D.W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E., Chen, Y., Woo,  
erige, G., Gilliet, W., Grant, C., Guenther, D., Kutyavin, T., Levy, R., Li, M., McClell  
; Karp, P., Romero, P., Zhang, S.  
Science 294, 2317-2323, 2001  
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A/Reference number: AB2577, NCBI:21608550; PMID:11743193  
A/Accession: AG2946  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-337 <KUR>  
A/Cross-references: GB:AB008689; PIDN:AAL43989.1; PID:gl7741546; GSPDB:GN00187  
A/Experimental source: strain C58 (Dupont)  
C/Genetics:  
A/Gene: Atcu3173  
A/Map position: linear chromosome



adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Larbig, K.; Lim,  
 .; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho  
 A/Reference number: A82950; MUID:20437337; PMID:10984043  
 A/Accession: C83491  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-590 <STO>  
 A/Cross-references: GB:AE004553; GB:AE004091; NID:G9947164; PIDN:AG04631.1; GSPDB:GN001  
 A/Experimental source: strain PA01  
 C/Genetics:  
 A/Gene: PA1242

Query Match 90.0%; Score 36; DB 2; Length 590;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNM5W 5  
 Db 360 LNM5W 364

RESULT 8  
 T10035  
 Hypothetical protein MLCB628.16c - *Mycobacterium leprae*  
 C/Species: *Mycobacterium leprae*  
 C/Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 21-Jul-2000  
 C/Accession: T10035  
 R/Bigmeter, K.; Honore, N.; Woods, S.A.; Caudron, B.; Cole, S.T.  
 Mol. Microbiol. 7, 197-206, 1993  
 A/Title: Use of an ordered cosmid library to deduce the genomic organization of *Mycobact*  
 A/Reference number: Z16917; MUID:93188700; PMID:8446027  
 A/Accession: T10035  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-744 <BIG>  
 A/Cross-references: EMBL:Y14967; NID:G2370268; PIDN:CA45203.1; PID:G2370283  
 C/Genetics:  
 A/Note: MLCB628.16c

Query Match 90.0%; Score 36; DB 2; Length 744;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NMSWL 6  
 Db 265 NMSWL 269

RESULT 9  
 T03472  
 conserved hypothetical protein - *Rhodobacter capsulatus*  
 C/Species: *Rhodobacter capsulatus*  
 C/Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 08-Oct-1999  
 C/Accession: T03472  
 R/Vlcek, C.; Paces, V.; Matisev, N.; Paces, J.; Haselkorn, R.; Fomstein, M.  
 Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997  
 A/Title: Sequence of a 189-kb segment of the chromosome of *Rhodobacter capsulatus* SB1003  
 A/Reference number: Z14955; MUID:97404404; PMID:9256421  
 A/Accession: T03472  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-116 <VLC>  
 A/Cross-references: EMBL:AF010496; NID:G3128256; PIDN:AC16125.1; PID:G3128273  
 C/Genetics:  
 A/Map position: 1

Query Match 87.5%; Score 35; DB 2; Length 116;  
 Best Local Similarity 83.3%; Pred. No. 56;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNM5W 6

Db 63 LNM5W 68

RESULT 10  
 T24773  
 Hypothetical protein T10B10.8 - *Caenorhabditis elegans*  
 C/Species: *Caenorhabditis elegans*  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
 C/Accession: T24773  
 R/Sims, M.  
 submitted to the EMBL Data Library, May 1996  
 A/Reference number: Z19934  
 A/Accession: T24773  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-321 <ML>  
 A/Cross-references: EMBL:Z72514; PIDN:CA96680.1; GSPDB:GN00028; CESP:T10B10.8  
 A/Experimental source: clone T10B10  
 C/Genetics:  
 A/Gene: CESP:T10B10.8  
 A/Map position: X  
 A/Introns: 40/3; 54/2; 64/3; 123/3; 229/2; 262/3

Query Match 87.5%; Score 35; DB 2; Length 321;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNM5W 6  
 Db 221 LNM5W 226

RESULT 11  
 B87125  
 ribonucleotide reductase small subunit (imported) - *Mycobacterium leprae*  
 C/Species: *Mycobacterium leprae*  
 C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
 C/Accession: B87125  
 R/Cole, S.T.; Bigmeyer, K.; Parthill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; I  
 R.; Davies, R.M.; Devlin, K.; Duthey, S.; Felwell, T.; Fraser, A.; Hamlin, N.; Holroy  
 eam, M.A.; Rutherford, K.M.  
 Nature 409, 1007-1011, 2001  
 A/Title: Massive gene decay in the leprosy bacillus.  
 A/Reference number: A86909; MUID:21128732; PMID:11234002  
 A/Accession: B87125  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-325 <STO>  
 A/Cross-references: GB:AL450380; NID:G13093483; PIDN:CAC30684.1; GSPDB:GN00147  
 C/Genetics:  
 A/Gene: nrdf  
 C/Superfamily: ribonucleotide-diphosphate reductase beta

Query Match 87.5%; Score 35; DB 2; Length 325;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNM5W 6  
 Db 15 LNM5W 20

RESULT 12  
 I49101  
 conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.-) CHUK - mouse  
 C/Species: *Mus musculus* (house mouse)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C/Accession: I49101  
 R/Mock, B.A.; Connolly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.  
 Genomics 27, 348-351, 1995  
 A/Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome

A:Reference number: 149101; MUID:96044444; PMID:7558004  
 A:Accession: 149101  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-745 <PSS>  
 A:Cross-references: EMBL:U12473; NID:g1079492; PIDN:AAC52589.1; PID:g1079493  
 C:Gene: CHUK  
 C:Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homolo  
 C:Keywords: ATP; phosphotransferase  
 F:13-283/Domain: protein kinase homology <KIN>

Query Match 87.5%; Score 35; DB 1; Length 745;  
 Best Local Similarity 83.3%; Pred. No. 3.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6  
 DB 738 LDMSWL 743

RESULT 13  
 T09056  
 glucan 1,3-beta-glucosidase (EC 3.2.1.58) - *Ampelomyces quisqualis*  
 N:Alternate names: exo-beta-1,3-glucanase  
 C:Species: *Ampelomyces quisqualis*  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: T09056  
 R:Rotem, Y.; Yarden, O.; Stetzberg, A.  
 submitted to the EMBL Data Library, October 1997  
 A:Reference number: Z16541  
 A:Accession: T09056  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-777 <ROT>  
 A:Cross-references: EMBL:AF029354; NID:g3004862; PID:g3004863  
 A:Experimental source: strain AQ10  
 C:Gene: exga  
 C:Genetics:  
 A:Function:  
 A:Description: catalyzes the hydrolysis of beta-D-glucose units from the non-reducing en  
 C:Keywords: glycosidase; hydrolase

Query Match 87.5%; Score 35; DB 2; Length 777;  
 Best Local Similarity 66.7%; Pred. No. 3.8e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6  
 DB 266 MNMNL 271

RESULT 14  
 S76882  
 hypothetical protein - *Synechocystis* sp. (strain PCC 6803)  
 C:Species: *Synechocystis* sp.  
 A:Variety: PCC 6803  
 C>Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
 C:Accession: S76882  
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
 O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
 DNA Res. 3, 109-116, 1996  
 A>Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*  
 B.  
 A:Reference number: S74322; MUID:97061201; PMID:8905231  
 A:Accession: S76882  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-154 <KAN>  
 A:Cross-references: EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BAAL8794.1; PID:g165388  
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
 C:Genetics:  
 A:Start codon: GTG

C:Superfamily: hypothetical protein b2267

Query Match 85.0%; Score 34; DB 2; Length 154;  
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSW 5  
 DB 3 INMSW 7

RESULT 15  
 C45456  
 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - *Paracoccus denitrificans*  
 N:Alternate names: NADH-quinone oxidoreductase chain I  
 C:Species: *Paracoccus denitrificans*  
 C>Date: 24-Feb-1994 #sequence\_revision 15-Oct-1994 #text\_change 03-Jun-2002  
 C:Accession: C45456  
 R:Xu, X.; Matsuno-Fagi, A.; Yagi, T.  
 Biochemistry 32, 968-981, 1993  
 A>Title: DNA sequencing of the seven remaining structural genes of the gene cluster en  
 A:Reference number: A45456; MUID:93136200; PMID:8422400  
 A:Accession: C45456  
 A:Molecule type: DNA  
 A:Residues: 1-345 <XU>  
 A:Cross-references: GB:L02354; NID:g150606; PIDN:AA25592.1; PID:g150608  
 A:Note: sequence extracted from NCBI backbone (NCBIN:123409, NCBI:123413)  
 C:Genetics:  
 A:Gene: NQ08  
 C:Superfamily: NADH dehydrogenase (ubiquinone) chain 1  
 C:Keywords: membrane-associated complex; NAD; oxidative phosphorylation; oxidoreductase

Query Match 85.0%; Score 34; DB 2; Length 345;  
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNMSWL 6  
 DB 191 LNMYWL 196

Search completed: February 18, 2004, 14:38:43  
 Job time : 7.5921 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds

(without alignments)  
35.929 Million cell updates/sec

Title: US-09-643-260-9

Perfect score: 40

Sequence: 1 LNWMTL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	90.0	117	4	US-09-149-476-360
2	36	90.0	609	2	US-09-252-991A-20134
3	35	87.5	745	2	US-08-887-518-3
4	35	87.5	745	2	US-09-023-321-3
5	35	87.5	745	2	US-08-890-853-4
6	35	87.5	745	2	US-09-032-475-3
7	35	87.5	745	2	US-09-099-125A-4
8	35	87.5	745	2	US-09-099-125A-4
9	35	87.5	745	2	US-09-032-475-4
10	35	87.5	745	3	US-08-890-854-4
11	35	87.5	745	3	US-09-023-324-4
12	35	87.5	745	3	US-09-168-629-2
13	35	87.5	745	3	US-08-910-820-10
14	35	87.5	745	3	US-08-810-131A-2
15	35	87.5	745	4	US-09-109-986-4
16	35	87.5	745	4	US-09-844-908-10
17	35	87.5	745	4	US-09-868-758-3
18	35	87.5	756	2	US-08-887-518-4
19	35	87.5	756	2	US-09-023-321-4
20	35	87.5	756	2	US-08-890-853-2
21	35	87.5	756	2	US-09-032-475-4
22	35	87.5	756	2	US-09-099-125A-2
23	35	87.5	756	2	US-09-099-125A-2
24	35	87.5	756	3	US-09-032-476-2
25	35	87.5	756	3	US-08-890-854-2
26	35	87.5	756	3	US-09-023-324-2
27	35	87.5	756	3	US-09-168-629-15

28	35	87.5	756	3	US-08-910-820-9	Sequence 9, Appl1
29	35	87.5	756	4	US-09-109-986-2	Sequence 2, Appl1
30	35	87.5	756	4	US-09-844-908-9	Sequence 9, Appl1
31	35	87.5	756	4	US-09-868-758-4	Sequence 4, Appl1
32	35	87.5	956	4	US-09-417-197-123	Sequence 123, App
33	35	87.5	997	4	US-09-417-197-121	Sequence 121, App
34	34	85.0	144	4	US-09-252-991A-21138	Sequence 21138, A
35	34	85.0	355	3	US-08-818-112-79	Sequence 79, Appl
36	34	85.0	355	4	US-08-818-111-80	Sequence 80, Appl
37	34	85.0	355	4	US-09-056-556-79	Sequence 79, Appl
38	34	85.0	355	4	US-09-072-596-80	Sequence 80, Appl
39	34	85.0	454	4	US-09-252-991A-28780	Sequence 28780, A
40	33	82.5	151	4	US-09-252-991A-23526	Sequence 23526, A
41	33	82.5	303	4	US-09-252-991A-19160	Sequence 19160, A
42	33	82.5	396	4	US-09-134-001C-4443	Sequence 4443, Ap
43	33	82.5	455	2	US-08-272-255-14	Sequence 14, Appl
44	33	82.5	455	5	PCT-US95-08565-14	Sequence 14, Appl
45	33	82.5	471	4	US-08-311-731A-168	Sequence 168, App

## ALIGNMENTS

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RESULT 1
US-09-149-476-360
; Sequence 360, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149, 476
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
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; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
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EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/04/7,587
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/04/7,492
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/04/7,598
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/04/7,613
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/04/7,582
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/04/7,596
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/04/7,612
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/04/7,632
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/04/7,601
EARLIER	FILING DATE: 1997-05-23
EARLIER	APPLICATION NUMBER: 60/04/3,580
EARLIER	FILING DATE: 1997-04-11
EARLIER	APPLICATION NUMBER: 60/04/3,568
EARLIER	FILING DATE: 1997-04-11
EARLIER	APPLICATION NUMBER: 60/04/3,614
EARLIER	FILING DATE: 1997-04-11
EARLIER	APPLICATION NUMBER: 60/04/3,569
EARLIER	FILING DATE: 1997-04-11
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EARLIER	FILING DATE: 1997-04-11
EARLIER	APPLICATION NUMBER: 60/04/3,613
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EARLIER	FILING DATE: 1997-04-11
EARLIER	APPLICATION NUMBER: 60/04/3,612
EARLIER	FILING DATE: 1997-04-11
EARLIER	APPLICATION NUMBER: 60/04/8,974
EARLIER	FILING DATE: 1997-06-06
EARLIER	APPLICATION NUMBER: 60/05/6,886
EARLIER	FILING DATE: 1997-08-22
EARLIER	APPLICATION NUMBER: 60/05/6,877
EARLIER	FILING DATE: 1997-08-22
EARLIER	APPLICATION NUMBER: 60/05/6,889
EARLIER	FILING DATE: 1997-08-22
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EARLIER	FILING DATE: 1997-08-22
EARLIER	APPLICATION NUMBER: 60/05/6,630
EARLIER	FILING DATE: 1997-08-22
EARLIER	APPLICATION NUMBER: 60/05/6,878
EARLIER	FILING DATE: 1997-08-22
EARLIER	APPLICATION NUMBER: 60/05/6,662
EARLIER	FILING DATE: 1997-08-22
EARLIER	APPLICATION NUMBER: 60/05/6,872
EARLIER	FILING DATE: 1997-08-22
EARLIER	APPLICATION NUMBER: 60/05/6,882
EARLIER	FILING DATE: 1997-08-22
EARLIER	APPLICATION NUMBER: 60/05/6,637
EARLIER	FILING DATE: 1997-08-22
EARLIER	APPLICATION NUMBER: 60/05/6,903
EARLIER	FILING DATE: 1997-08-22
EARLIER	APPLICATION NUMBER: 60/05/6,888
EARLIER	FILING DATE: 1997-08-22
EARLIER	APPLICATION NUMBER: 60/05/6,879
EARLIER	FILING DATE: 1997-08-22
EARLIER	APPLICATION NUMBER: 60/05/6,880

[illegible]

EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 90.0%; Score 36; DB 4; Length 117;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSW 5  
| | | | |  
DB 30 LNMSW 34

RESULT 2  
US-09-252-991A-20134  
Sequence 20134, Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 20134

LENGTH: 609

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-20134

Query Match 90.0%; Score 36; DB 4; Length 609;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSW 5  
| | | | |  
DB 379 LNMSW 383

RESULT 3  
US-08-887-518-3  
Sequence 3, Application US/0887518  
Patent No. 5843721

GENERAL INFORMATION:

APPLICANT: Roche, Mike

APPLICANT: Wu, Lin

TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-887-518-3

Query Match 87.5%; Score 35; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6  
| | | | |  
DB 738 LNMSWL 743

RESULT 4  
US-09-023-321-3  
Sequence 3, Application US/09023321  
Patent No. 5844073

GENERAL INFORMATION:

APPLICANT: Roche, Mike

APPLICANT: Wu, Lin

TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,321  
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/887,518

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-008

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

Query Match 87.5%; Score 35; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6

Db 738 LDMSWL 743

## RESULT 5

US-08-890-853-4  
Sequence 4, Application US/08890853  
Patent No. 5851812  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
ATTORNEY/AGENT INFORMATION:  
MORONICZ, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-853-4

Query Match 87.5%; Score 35; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6

Db 738 LDMSWL 743

## RESULT 6

US-09-032-475-3  
Sequence 3, Application US/09032475  
Patent No. 5854003  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
ATTORNEY/AGENT INFORMATION:  
MORONICZ, John  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,475  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/887,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-032-475-3

Query Match 87.5%; Score 35; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6

Db 738 LDMSWL 743

## RESULT 7

US-09-099-125A-4  
Sequence 4, Application US/09099125A  
Patent No. 5916760  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
ATTORNEY/AGENT INFORMATION:  
MORONICZ, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,125A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid



STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-099-125A-4

Query Match  
Best Local Similarity 87.5%; Score 35; DB 2; Length 745;  
Pred. No. 7.3e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWTL 6  
DB 738 LDMWTL 743

RESULT 8  
US-09-099-124A-4  
Sequence 4, Application US/09099124A  
Patent No. 5939302  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Moronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,124A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-099-124A-4

Query Match  
Best Local Similarity 87.5%; Score 35; DB 2; Length 745;  
Pred. No. 7.3e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWTL 6  
DB 738 LDMWTL 743

RESULT 9  
US-09-032-476-4  
Sequence 4, Application US/09032476  
Patent No. 6235492  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike

APPLICANT: Cao, Zhaoan  
APPLICANT: R gnter, Catherine  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,476  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/890,854  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-032-476-4

Query Match  
Best Local Similarity 87.5%; Score 35; DB 3; Length 745;  
Pred. No. 7.3e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWTL 6  
DB 738 LDMWTL 743

RESULT 10  
US-08-890-854-4  
Sequence 4, Application US/08890854  
Patent No. 6235512  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
APPLICANT: Cao, Zhaoan  
APPLICANT: R gnter, Catherine  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,854  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-854-4

Query Match 87.5%; Score 35; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6  
|:||||  
Db 738 LDMSWL 743

RESULT 11  
US-09-023-324-4  
Sequence 4, Application US/09023324  
Patent No. 6235513  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
APPLICANT: Cao, Zhaodan  
APPLICANT: R. gnier, Catherine  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,324  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/890,854  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-324-4

Query Match 87.5%; Score 35; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6  
|:||||  
Db 738 LDMSWL 743

RESULT 12  
US-09-168-629-2  
Sequence 2, Application US/09168629  
Patent No. 6242253  
GENERAL INFORMATION:  
APPLICANT: Karin, Michael  
APPLICANT: Didonato, Joseph A.  
APPLICANT: Rothwarf, David M.  
APPLICANT: Hayakawa, Makio  
APPLICANT: Zandi, Ebrahim  
TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same  
FILE REFERENCE: P-UD 3295  
CURRENT APPLICATION NUMBER: US/09/168,629  
CURRENT FILING DATE: 1998-10-08  
EARLIER APPLICATION NUMBER: 60/061,470  
EARLIER FILING DATE: 1997-10-09  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO: 2  
LENGTH: 745  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-168-629-2

Query Match 87.5%; Score 35; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6  
|:||||  
Db 738 LDMSWL 743

RESULT 13  
US-08-910-820-10  
Sequence 10, Application US/08910820  
Patent No. 6258579  
GENERAL INFORMATION:  
APPLICANT: Mercurio, Frank  
APPLICANT: Zhu, Hengyi  
APPLICANT: Barbosa, Miguel  
APPLICANT: Li, Gian  
APPLICANT: Murray, Brian W.  
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE  
TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,820  
FILING DATE: 12-AUG-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 860098.413C1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-910-820-10

Query Match 87.5%; Score 35; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6  
|:||||  
DB 738 LDWSSL 743

RESULT 14  
US-08-810-131A-2  
Sequence 2, Application US/08810131A  
Patent No. 6268194  
GENERAL INFORMATION:  
APPLICANT: Karin, Michael  
APPLICANT: Didonato, Joseph A.  
APPLICANT: Rochwart, David M.  
APPLICANT: Hayakawa, Makio  
APPLICANT: Zandi, Ebrahim  
TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using  
TITLE OF INVENTION: Same  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/810,131A  
FILING DATE: 25-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 2408  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULAR TYPE: protein  
US-08-810-131A-2

Query Match 87.5%; Score 35; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6  
|:||||  
DB 738 LDWSSL 743

RESULT 15  
US-09-109-986-4  
Sequence 4, Application US/09109986  
Patent No. 6479266  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
APPLICANT: Cao, Zhadan  
APPLICANT: R guler, Catherine  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/109,986  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/890,854  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
US-09-109-986-4

Query Match 87.5%; Score 35; DB 4; Length 745;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6  
|:||||  
DB 738 LDWSSL 743

Search completed: February 18, 2004, 14:41:48  
Job time : 8.06579 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds  
(without alignments)  
89.145 Million cell updates/sec

Title: US-09-643-260-8  
Perfect score: 39  
Sequence: 1 LEWSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP\_Archea:\*  
2: SP\_Bacteria:\*  
3: SP\_Fungi:\*  
4: SP\_Human:\*  
5: SP\_Invertebrate:\*  
6: SP\_Mammal:\*  
7: SP\_Mhc:\*  
8: SP\_Organelle:\*  
9: SP\_Phage:\*  
10: SP\_Plant:\*  
11: SP\_Rodent:\*  
12: SP\_Virus:\*  
13: SP\_Vertebrate:\*  
14: SP\_Unclassified:\*  
15: SP\_Virus:\*  
16: SP\_Bacteriophage:\*  
17: SP\_Archea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	92.3	387	10	Q8LJE0
2	36	92.3	482	5	Q9VQ45
3	36	92.3	544	10	Q9FEB1
4	36	92.3	645	8	Q63620
5	36	92.3	740	6	Q95KVL
6	36	92.3	745	11	Q8CMT3
7	36	92.3	756	6	Q95KVO
8	35	89.7	48	16	Q8VK32
9	35	89.7	110	16	Q8DY14
10	35	89.7	173	17	Q9HH7
11	35	89.7	196	13	Q9YH31
12	35	89.7	276	2	Q47020
13	35	89.7	311	5	Q94380
14	35	89.7	371	5	Q25333
15	35	89.7	387	16	Q8YFW8
16	35	89.7	390	16	Q8G212

Result No.	Score	Query Match	Length	ID	Description
17	35	89.7	391	2	Q8KPQ4
18	35	89.7	391	16	Q8YPT8
19	35	89.7	469	10	Q8RXB1
20	35	89.7	481	11	Q8VCV5
21	35	89.7	522	10	Q9SJ13
22	35	89.7	522	10	Q8LH9
23	35	89.7	522	10	Q8LH75
24	35	89.7	604	4	Q9Y475
25	35	89.7	645	2	Q69315
26	35	89.7	645	2	Q8GEA9
27	35	89.7	683	4	Q96DU7
28	35	89.7	823	5	Q8SC00
29	35	89.7	1173	16	Q8ERJ0
30	35	89.7	1345	16	Q9L060
31	35	89.7	1367	16	Q9PPR8
32	35	89.7	1379	13	P79701
33	35	89.7	1591	3	Q9HFW1
34	35	89.7	2054	5	Q9GZ13
35	34	87.2	116	2	Q68039
36	34	87.2	135	2	Q05744
37	34	87.2	145	5	Q810L0
38	34	87.2	248	4	Q8W205
39	34	87.2	321	5	Q94515
40	34	87.2	355	16	Q07175
41	34	87.2	395	17	Q97V10
42	34	87.2	398	16	P74568
43	34	87.2	465	16	Q8P701
44	34	87.2	469	16	Q8PG82
45	34	87.2	471	16	Q8P416

## ALIGNMENTS

## RESULT 1

ID	Q8LJE0	PRELIMINARY;	PRT;	387 AA.
AC	Q8LJE0			
DT	01-OCT-2002 (TEMBLrel. 22, Created)			
DT	01-OCT-2002 (TEMBLrel. 22, Last sequence update)			
DT	01-MAR-2003 (TEMBLrel. 23, Last annotation update)			
DE	P0496H05.7 protein.			
GN	P0496H05.7.			
OS	Oryza sativa (japonica cultivar-group).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Ehharctoideae; Oryzae; Oryza.			
OX	NCBI_TaxID:3947;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Nipponbare;			
RA	Sasaki T., Matsumoto T., Yamamoto K.;			
RT	"Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC			
RT	clone:P0496H05."			
RL	Submitted (PEB-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AP003267; BAC03279.1; -			
DR	Genbank; Q8LJE0; -			
SQ	SEQUENCE 387 AA; 41273 MW; C3D070B59608ACB CRC64;			

Query Match 92.3%; Score 36; DB 10; Length 387;  
Best Local Similarity 83.3%; Pred. No. 4.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6

DB 242 VEWMSWL 247

## RESULT 2

ID	Q9VQ45	PRELIMINARY;	PRT;	482 AA.
AC	Q9VQ45			
DT	01-MAY-2000 (TEMBLrel. 13, Created)			

DT 01-OCT-2002 (Tremblrel. 22, last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, last annotation update)  
 DE CG31664 protein.  
 GN CG31933 OR CG15622.  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NC NCB1\_Taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=1073112;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolahav S.,  
 RA Borkov D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Deacon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kienison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshirei A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacble J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupel M.P., Smith T.,  
 RA Slier E., Spradling A.C., Stepieton M., Strong R., Sun B.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
 RA Fortiera S., Frise E., Galle R.F., Garg N.S., George R.A.,  
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
 RA Idegam C., Jalali M., Kruse D., Li P., Mattei B., Moshirei A.,  
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
 RA Pacble J., Pargass V., Park S., Patel S., Pfeiffer B.,  
 RA Phouenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 RA Strapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RT "Sequencing of Drosophila melanogaster genome";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Miera S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kankner J.S., Prochuk S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,

RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Searle S.M.J., Smith B., Shu S., Smutnick F., Whitefield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,  
 RT "Annotation of Drosophila melanogaster genome";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Flybase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB003585; AAF5136.2; -;  
 DR Flybase; PBgn0051664; CG31664.  
 DR Flybase; PBgn0051933; CG31933.  
 DR InterPro; IPR004245; DUF229.  
 DR Pfam; PF02995; DUF229; 1.  
 SQ SEQUENCE 482 AA; 55495 MW; A91F2D2DFDPC5D CRC64;

Query Match 92.3%; Score 36; DB 5; Length 482;  
 Best Local Similarity 83.3%; Pred. No. 5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEWSWL 6  
 Db 57 VEWMSWL 62

RESULT 3  
 ID Q9FEE1 PRELIMINARY; PRT; 544 AA.  
 AC Q9FEE1  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, last sequence update)  
 DE Putative cytochrome P450.  
 GN P0688A04.9 OR P0006C01.24.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Eriactroideae; Oryzeae; Oryza.  
 NC NCB1\_Taxid=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Nipponbare;  
 RA Saeki T., Matsunoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC  
 clone: P0688A04.";  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Nipponbare;  
 RA Saeki T., Matsunoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC  
 clone: P0688A04.";  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Nipponbare;  
 RA Saeki T., Matsunoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC  
 clone: P0006C01.";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1-SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 DR EMBL; AP002839; BAB19103.1; -;  
 DR EMBL; AP002744; BAB19082.1; -;  
 DR Gramene; Q9FEE1; -;  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR Pfam; PF00067; P450; 1.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
 KW Heme; Monooxygenase; Oxidoreductase.  
 SQ SEQUENCE 544 AA; 60867 MW; 273BAR596DD1A024 CRC64;

Query Match 92.3%; Score 36; DB 10; Length 544;  
 Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
 Db 48 LEWAML 53

## RESULT 4

063620 PRELIMINARY; PRT; 645 AA.  
 AC 063620;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE NADH dehydrogenase subunit 5.  
 OS Balanoglossus carnosus.  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Hemichordata; Enteropneusta; Ptychodermidae;  
 OC Balanoglossus.  
 OC NCBI\_TaxID=35080;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99016090; PubMed=9799263;  
 RT Caestreana J., Feldmaier-Fuchs G., Yokobori S., Satoh N., Paabo S.;  
 RT "The mitochondrial genome of the hemichordate Balanoglossus carnosus  
 and the evolution of deuterostome mitochondria."  
 RL Genetics 150:1115-1123(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98188267; PubMed=9520430;  
 RT Caestreana J., Feldmaier-Fuchs G., Paabo S.;  
 RT "Codon reassignment and amino acid composition in hemichordate  
 mitochondria."  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3703-3707(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RT Caestreana J., Feldmaier-Fuchs G., Paabo S.;  
 RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AF051097; AAD11945.1; -  
 DR InterPro; IPR003916; NADH dehydrog.  
 DR InterPro; IPR001750; Oxidored\_q1.  
 DR InterPro; IPR001516; Oxidored\_q1\_N.  
 DR Pfam; PF00662; oxidored\_q1; 1.  
 DR Pfam; PF00662; oxidored\_q1\_N; 1.  
 DR PRINTS; PR01434; NADHGNAS5.  
 KM NAD; Oxidoreductase; Ubiquinone; Mitochondrion.  
 SQ SEQUENCE 645 AA; 69455 MW; C8A98941B61F92 CRC64;

Query Match 92.3%; Score 36; DB 8; Length 645;  
 Best Local Similarity 83.3%; Pred. No. 6.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
 Db 96 LEWAML 101

## RESULT 5

095KV1 PRELIMINARY; PRT; 740 AA.  
 AC 095KV1;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE 1kb kinase-alpha.  
 GN BIKKALPHA.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RT Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;  
 RA "Identification and characterization of the bovine 1kb kinases (IKTs)

RT alpha, beta and gamma".  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1-SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; AJ414555; CAC93686.1; -  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser Thr\_kinase.  
 DR Pfam; PF00069; kinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 740 AA; 84343 MW; 01903BE1F4D176 CRC64;

Query Match 92.3%; Score 36; DB 6; Length 740;  
 Best Local Similarity 83.3%; Pred. No. 7.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
 Db 738 LDMSWL 738

## RESULT 6

08CBT3 PRELIMINARY; PRT; 745 AA.  
 AC 08CBT3;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Conserved helix-loop-helix ubiquitous kinase.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=urinary bladder;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA "The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RL 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK035326; BAC29034.1; -  
 SQ SEQUENCE 745 AA; 84770 MW; 48C9B01C17A61184 CRC64;

Query Match 92.3%; Score 36; DB 11; Length 745;  
 Best Local Similarity 83.3%; Pred. No. 7.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
 Db 738 LDMSWL 743

## RESULT 7

095KV0 PRELIMINARY; PRT; 756 AA.  
 AC 095KV0;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE 1kb kinase-beta.  
 GN BIKKBETA.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Rotenberg S., Dobbelaere D.A.E., Heusler V.T.  
 RT "Identification and characterization of the bovine Ikb kinases (IKKs)  
 RT alpha, beta and gamma."  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL: AJ144556; CAC3687.1; -  
 DR InterPro: IPR00719; Prot\_Kinase.  
 DR InterPro: IPR02290; Ser\_thr\_kinase.  
 DR InterPro: IPR01245; Tyr\_kinase.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR PRODOM: PD000001; Prot\_kinase; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SO SEQUENCE 756 AA; 86647 MW; A072D15614A176B5 CRC64;

Query Match 92.3%; Score 36; DB 6; Length 756;  
 Best Local Similarity 83.3%; Pred. No. 7.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSML 6  
 |||||  
 Db 737 LEWSML 742

RESULT 8  
 ID Q8VKB2 PRELIMINARY; PRT; 48 AA.  
 AC Q8VKB2.  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Hypothetical protein MT0946.  
 GN MT0946  
 OS Mycobacterium tuberculosis  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 OX 11  
 RN RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., Deboy R., Dodson R., Gwin M.L., Haft D., Hickey B.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bhat W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains."  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AE006980; AAK45193.1; -  
 DR TIGR: MT0946; -  
 KW Hypothetical protein.  
 SO SEQUENCE 48 AA; 5265 MW; COBRA9D6A2EFBD6 CRC64;

Query Match 89.7%; Score 35; DB 16; Length 48;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EWSML 6  
 |||||  
 Db 14 EWSML 18

RESULT 9  
 ID Q8DY14 PRELIMINARY; PRT; 110 AA.  
 AC Q8DY14.  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 GN SAG1496.

OS Streptococcus agalactiae (serotype V).  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=216466;  
 OX 11  
 RN RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=2603 V/R / Serotype V;  
 RX MEDLINE=22222988; PubMed=12200547;  
 RA Tetteilin H., Maignan V., Cieleszyc M.J., Eisen J.A., Peterson S.,  
 RA Wessels M.R., Paulsen I.T., Nelson K.E., Margalit I., Read T.D.,  
 RA Messels L.C., Wolf A.M., Beman M.J., Brinkac L.M., Daugherty S.C.,  
 RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,  
 RA Radu D., Fedorova N.B., Scanlan D., Khouri H., Scallan S.,  
 RA Cary H.A., Cline R.T., Van Aken S.E., Gill J., Scallan S.,  
 RA Jacobson E.T., Breton C., Gall G., Martini L., Vengli F., Malone D.,  
 RA Rinaldo D., Rappaport R., Telford J.L., Kasper D.L., Grandi G.,  
 RA Fraser C.M.;  
 RT "Complete genome sequence and comparative genomic analysis of an  
 RT emerging human pathogen, serotype V Streptococcus agalactiae."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).  
 DR EMBL: AE014260; AAN00363.1; -  
 DR TIGR: SAG1496; -  
 KW Hypothetical protein; Complete proteome.  
 SO SEQUENCE 110 AA; 12689 MW; 243D6B93029709A4 CRC64;

Query Match 89.7%; Score 35; DB 16; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSM 5  
 |||||  
 Db 14 LEWSM 18

RESULT 10  
 ID Q9HHP7 PRELIMINARY; PRT; 173 AA.  
 AC Q9HHP7.  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE Vng6292C.  
 GN Vng6292C.  
 OS Halobacterium sp. (strain NRC-1).  
 OC Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;  
 OC Halobacteriaceae; Halobacterium.  
 OX NCBI\_TaxID=64091;  
 OX 11  
 RN RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20504483; PubMed=11016950;  
 RA Ng W.V., Kennedy S.P., Mahatras G.G., Bergulat B., Pan M.,  
 RA Shukla H.D., Laaky S.R., Baliga N.S., Thorsen V., Shroona J.,  
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Meli R., Go Y.A.,  
 RA Leitauer B., Keller K., Cruz R., Daneon M.J., Hough D.W.,  
 RA Maddocks D.G., Jablonaki P.E., Krebs M.P., Angevine C.W., Dale H.,  
 RA Ienparger T.A., Beck R.F., Pohlischer M., Spudich J.L., Jung K.-H.,  
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,  
 RA Hardard H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;  
 RT "Genome sequence of Halobacterium species NRC-1."  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).  
 DR EMBL: AE005159; AAG20929.1; -  
 DR InterPro: IPR001584; Rve.  
 DR Pfam: PF00665; rve; 1.  
 KW Plasmid; Complete proteome.  
 SO SEQUENCE 173 AA; 20267 MW; E8B02BDC76ED4371 CRC64;

Query Match 89.7%; Score 35; DB 17; Length 173;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EWSML 6  
 |||||





RN [12]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K-12;  
 RX MEDLINE=87279948; PubMed=3301821;  
 RA Coulton J.W., Mason P., Allatt D.D.;  
 RT "fhuc and fhd genes for iron (III)-ferrichrome transport into  
 RT Escherichia coli K-12.";  
 RL J. Bacteriol. 169:3844-3849(1987).  
 RN [13]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K-12;  
 RX MEDLINE=88058963; PubMed=3316212;  
 RA Taber C.W., Taber H.;  
 RT "The speeoped operon of Escherichia coli: Formation and processing of  
 RT a proenzyme form of S-adenosylmethionine decarboxylase.";  
 RL J. Biol. Chem. 262:16037-16040(1987).  
 RN [14]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K-12;  
 RX MEDLINE=88152237; PubMed=2450046;  
 RA Gebhard W., Schreilmueller T., Hochstrasser K.;  
 RT "Complementary DNA and derived amino acid sequence of the precursor of  
 RT one of the three protein components of the inter-alpha-trypsin  
 RT inhibitor complex.";  
 RL FEBS Lett. 229:63-67(1988).  
 RN [15]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K-12;  
 RX MEDLINE=89061679; PubMed=2904262;  
 RA Andrews S.C., Guest J.R.;  
 RT "Nucleotide sequence of the gene encoding the GMP reductase of  
 RT Escherichia coli K12.";  
 RL Biochem. J. 255:35-43(1988).  
 RN [16]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K-12;  
 RX MEDLINE=88227880; PubMed=3372485;  
 RA Mellano M.A., Cooksey D.A.;  
 RT "Nucleotide sequence and organization of copper resistance genes from  
 RT Pseudomonas syringae pv. tomato.";  
 RL J. Bacteriol. 170:2879-2883(1988).  
 RN [17]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K-12;  
 RX MEDLINE=89155419; PubMed=2537812;  
 RA Liu J., Parkinson J.S.;  
 RT "Genetic and sequence analysis of the pcnB locus, an Escherichia coli  
 RT gene involved in plasmid copy number control.";  
 RL J. Bacteriol. 171:1254-1261(1988).  
 RN [18]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K-12;  
 RX MEDLINE=89008347; PubMed=3049588;  
 RA Sung Y., Fuchs J.A.;  
 RT "Characterization of the cym operon in Escherichia coli K12.";  
 RL J. Biol. Chem. 263:14769-14775(1988).  
 RN [19]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K-12;  
 RX MEDLINE=89057448; PubMed=3057437;  
 RA Lipinska B., Sharma S., Georgopoulos C.;  
 RT "Sequence analysis and regulation of the htrA gene of Escherichia  
 RT coli: A sigma-32-independent mechanism of heat-inducible  
 RT transcription.";  
 RL Nucleic Acids Res. 16:10053-10067(1988).  
 RN [20]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K-12;  
 RX MEDLINE=90126278; PubMed=2693214;  
 RA Romero M.I., Jepsen L.P., Stroman P., van Heeswijk R.;  
 RT "Characterization of a leuA gene and an Ars element from Nucor  
 RT Circinellolides.";  
 RL Gene 84:335-343(1989).

RN [21]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K-12;  
 RX MEDLINE=89327165; PubMed=2666401;  
 RA Xie Q.W., Taber C.W., Taber H.;  
 RT "Spermidine biosynthesis in Escherichia coli: the promoter and the  
 RT termination regions of the speD operon.";  
 RL J. Bacteriol. 171:4457-4465(1989).  
 RN [22]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K-12;  
 RX MEDLINE=90113890; PubMed=2691840;  
 RA Lindquist S., Gallant M., Lindberg F., Normark S.;  
 RT "Regulating proteins in enterobacterial ampC beta-lactamase  
 RT regulation.";  
 RL Mol. Microbiol. 3:1091-1102(1989).  
 RN [23]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K-12;  
 RX MEDLINE=90202727; PubMed=2180916;  
 RA Kang P.J., Craig E.A.;  
 RT "Identification and characterization of a new Escherichia coli gene  
 RT that is a dosage-dependent suppressor of a dnaK deletion mutation.";  
 RL J. Bacteriol. 172:2055-2064(1990).  
 RN [24]

Query Match 89.7%; Score 35; DB 2; Length 276;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EMSWL 6  
 Db 9 EMSWL 13

RESULT 13  
 ID 094380 PRELIMINARY; PRT; 311 AA.  
 AC 094380;  
 DT 01-FEB-1997 (TRMBLrel. 02, Created)  
 DT 01-MAY-2000 (TRMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)  
 DE ZC47.13 protein.  
 GN ZC47.13.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBT\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA McMurray A.A.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode C.elegans: A platform for  
 RT investigating biology.";  
 RT Science 282:2012-2018(1998).  
 DR EMBL; Z81141; CAB03488.2; -  
 DR WormDep; ZC47.13; CE25668.  
 DR InterPro; IPR002900; DUF38.  
 DR InterPro; IPR001810; F-box.  
 DR Pfam; PF00646; F-box; 1.  
 DR Pfam; PF01827; FTH; 1.  
 SQ SEQUENCE 311 AA; 36603 MW; 928464208868C48B CRC64;

Query Match 89.7%; Score 35; DB 5; Length 311;  
 Best Local Similarity 83.3%; Pred. No. 4.7e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 EMSWL 6

Db 295 LEWEMWL 300

## RESULT 14

Q25333 PRELIMINARY; PRT; 371 AA.  
 AC Q25333;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE Surface antigen P2 (Fragment).  
 OS Leishmania major.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 OX NCBI\_TaxID=5664;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=V121;  
 RX MEDLINE=92105105; PubMed=1761547;  
 RA Murray P.J., Spithill T.W.;  
 RT "Variants of a Leishmania Surface Antigen Derived from a Multigenic Family."  
 RL J. Biol. Chem. 266:24477-24484 (1991).  
 DR EMBL; X57134; CAA40413.1; -.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR007090; LRR\_plant.  
 DR InterPro; IPR02965; P-rich\_extensn.  
 DR Pfam; PF00560; LRR; 2.  
 DR PRINTS; PR01217; PRICHEXTENS.  
 DR PROSITE; PSS0502; LRR\_PS; 1.  
 FT NON\_TER  
 SQ SEQUENCE 371 AA; 39765 MW; 820A0BE163E247D CRC64;

Query Match 89.7%; Score 35; DB 5; Length 371;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EMSWL 6  
 |||||  
 Db 1 EMSWL 5

## RESULT 15

Q8YFW8 PRELIMINARY; PRT; 387 AA.  
 AC Q8YFW8;  
 DT 01-MAR-2002 (TReMBLrel. 20, Created)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
 DE Mannose-6-phosphate isomerase (EC 5.3.1.8).  
 GN BMEI1394.  
 OS Brucella melitensis.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Brucellaceae; Brucella.  
 OX NCBI\_TaxID=29459;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=16M / ATCC 23456 / Biotype 1;  
 RX MEDLINE=20020109; PubMed=11756688;  
 RA DelVecchio V.G., Kapratel V., Redkar R.J., Patra G., Mujer C., Los T.,  
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,  
 RA Jabloncki L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,  
 RA Selkov E., Elzer P.H., Haglid S., O'Callaghan D., Teleson J.-J.,  
 RA Haseikorn R., Kyriades N., Overbeek R.;  
 RT "The genome sequence of the facultative intracellular pathogen  
 Brucella melitensis."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).  
 DR EMBL; AB009577; AAU52575.1; -.  
 KW isomerase; Complete proteome.  
 SQ SEQUENCE 387 AA; 44267 MW; 4E1F33C6446163F CRC64;

Query Match 89.7%; Score 35; DB 16; Length 387;  
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EMSWL 6

Db 245 EMSWL 249

Search completed: February 18, 2004, 14:35:44  
 Job time : 18.3684 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 / Search time 3.55263 Seconds  
(without alignments)  
79,423 Million cell updates/sec

Title: US-09-643-260-8

Perfect score: 39  
Sequence: 1 LEWSWL 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt 41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	92.3	745	1 IKXA_HUMAN	O15111 h inhibitor
2	36	92.3	745	1 IKXA_MOUSE	O60680 m inhibitor
3	36	92.3	756	1 IKXB_HUMAN	O14620 homo sapien
4	36	92.3	757	1 IKXB_MOUSE	O88351 mus musculu
5	36	92.3	757	1 IKXB_RAT	O90778 rattus norv
6	35	89.7	400	1 HOPC_ECOLI	P36646 escherichia
7	34	87.2	334	1 GTRB_BOVIN	P58354 bos taurus
8	34	87.2	477	1 GTRB_HUMAN	O90764 homo sapien
9	34	87.2	477	1 GTRB_MOUSE	O91121 rattus norv
10	34	87.2	478	1 GTRB_RAT	O91121 rattus norv
11	34	87.2	685	1 RORI_DROME	O24488 drosophila
12	33	84.6	512	1 VG29_BPMU	O91121 rattus norv
13	33	84.6	777	1 TDRI_HUMAN	O91121 rattus norv
14	33	84.6	928	1 TDRI_MOUSE	O91121 rattus norv
15	33	84.6	1698	1 Y076_HUMAN	O91121 rattus norv
16	33	82.1	83	1 VG41_BPMU	O91121 rattus norv
17	32	82.1	94	1 VG41_MOUSE	O91121 rattus norv
18	32	82.1	296	1 CYOA_BUCAL	P57544 buchnera ap
19	32	82.1	307	1 OOK2_ACEAC	P50653 acetobacter
20	32	82.1	314	1 CYOA_PSEPU	O90771 pseudomonas
21	32	82.1	362	1 DCUP_YEAST	P32347 baccharomyc
22	32	82.1	375	1 D12_CREAL	O81931 crepis alpi
23	32	82.1	387	1 MANA_RHIME	P29954 rhizobium m
24	32	82.1	561	1 RK_BOVIN	P28327 bos taurus
25	32	82.1	563	1 RK_HUMAN	O15835 homo sapien
26	32	82.1	564	1 RK_MOUSE	O90714 mus musculu
27	32	82.1	564	1 RK_RAT	O63651 rattus norv
28	32	82.1	576	1 GRKE_HUMAN	P43350 homo sapien
29	32	82.1	576	1 GRKE_MOUSE	O70293 mus musculu
30	32	82.1	576	1 GRKE_RAT	P97711 rattus norv
31	32	82.1	578	1 GRK4_HUMAN	P33298 homo sapien
32	32	82.1	590	1 GRKS_BOVIN	P43249 bos taurus
33	32	82.1	590	1 GRKS_HUMAN	P34947 homo sapien

34	32	82.1	590	1 GRKS_RAT	O62833 rattus norv
35	32	82.1	642	1 YORI_CABEL	O09537 caenorhabdit
36	32	82.1	714	1 GRK2_DROME	P32866 drosophila
37	32	82.1	775	1 ECEL_MOUSE	O91010 mus musculu
38	32	82.1	775	1 ECEL_RAT	O91013 rattus norv
39	32	82.1	826	1 CRVA_BACCH	O98597 bacillus th
40	32	82.1	842	1 AMPN_LACDL	P37896 lactobacilli
41	32	82.1	983	1 BEPA3_CHICK	P29318 gallus galli
42	32	82.1	983	1 BEPA3_HUMAN	P29320 homo sapien
43	32	82.1	983	1 BEPA3_MOUSE	P29319 mus musculu
44	32	82.1	984	1 BEPA3_RAT	O08680 rattus norv
45	32	82.1	1039	1 GUNB_CAUSA	P10474 c endoglucan

## ALIGNMENTS

RESULT 1  
ID IKXA\_HUMAN STANDARD, PRT, 745 AA.  
AC O15111; 014666; 013132; 092467;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)  
DE (I kappa-B kinase alpha) (IKBA) (IKK-alpha) (IKK-A) (Ikkappa kinase)  
DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).  
GN CHUK OR IKKA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.  
RC TISSUE=T-cell;  
RX MEDLINE=97386461; PubMed=9244310;  
RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;  
RT "Identification and characterization of an Ikkappa kinase";  
RL Cell 90:373-383(1997).  
RN [2]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC MEDLINE=97394468; PubMed=9252186;  
RX DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi B., Karin M.;  
RA "A cytokine-responsive Ikkappa kinase that activates the transcription factor NF-kappaB";  
RT Nature 388:548-554(1997).  
RN [3]  
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND SER-176.  
RC TISSUE=Cervical carcinoma;  
RX MEDLINE=96008013; PubMed=9346484;  
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,  
RT Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;  
RT "IKK-1 and IKK-2: cytokine-activated Ikkappa kinases essential for NF-kappaB activation";  
RL Science 278:860-866(1997).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RX MEDLINE=99032998; PubMed=9813330;  
RA Hu M.C.-T., Wang Y.-P.;  
RT "Ikkappa kinase-alpha and -beta genes are coexpressed in adult and embryonic tissues but localized to different human chromosomes";  
RL Gene 222:31-40(1998).  
RN [5]  
RP SEQUENCE OF 32-745 FROM N.A.  
RC TISSUE=Cervical carcinoma;  
RX MEDLINE=96258427; PubMed=8777433;  
RA Connolly M.A., Marcu K.B.;  
RT "CHUK, a new member of the helix-loop-helix and leucine zipper families of interacting proteins, contains a serine-threonine kinase catalytic domain";

RL Cell. Mol. Biol. Res. 41:537-549(1995).

RP [6] PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179 AND SER-180.

RX MEDLINE=98188283; PubMed=9520446;

RA Ling L., Cao Z., Goeddel D.V.;

RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of Ser-176.";

RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).

RN [7]

RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.

RX MEDLINE=99413720; PubMed=10485710;

RA Ozes O.N., Mayo L.D., Guebin J.A., Pfeiffer S.R., Pfeiffer L.M., Donner D.B.;

RT "NF-kappaB activation by tumor necrosis factor requires the Akt serine-threonine kinase.";

RL Nature 401:82-85(1999).

RN [8]

RP IKK-ALPHA BINDING.

RX MEDLINE=99212141; PubMed=10195894;

RA Delhaese M., Hayakawa M., Chen Y., Karin M.;

RT "Positive and negative regulation of IkappaB kinase activity through IkappaB subunit phosphorylation.";

RL Science 284:309-313(1999).

RN [9]

RP IKK PHOSPHORYLATION.

RX MEDLINE=99038238; PubMed=9819420;

RA Nemoto S., Didonato J.A., Lin A.;

RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappaB-inducing kinase.";

RL Mol. Cell. Biol. 18:7336-7343(1998).

RN [10]

RP REVIEW.

RX MEDLINE=20178139; PubMed=10712233;

RA Jobin C., Sartor R.B.;

RT "The I-kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";

RL Am. J. Physiol. 278:C451-C462(2000).

RN [11]

RP SUBUNIT OF A COMPLEX CONTAINING CREBBP, NCOA2, NCOA3, IKKB AND IKKG.

RX MEDLINE=21968797; PubMed=11971985;

RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J., O'Malley B.W.;

RT "Regulation of SRC-3 (PCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator activity by I kappa B kinase.";

RL Mol. Cell. Biol. 22:3549-3561(2002).

CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates NCOA3.

CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated when dephosphorylated.

CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but also as an homodimer. Directly interacts with IKK-GAMMA/NEMO. Heterodimers form the active complex. The tripartite complex can also bind to MAP3K14/NIK, MEKK1, IKAP and IKK-alpha-P65-P50 complex. A weak interaction with TRAF2 cannot be excluded. Part of a complex composed of NCOA2, NCOA3, IKKB, IKKG and CREBBP.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- TISSUE SPECIFICITY: Widely expressed.

CC -1- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by MEKK1, and dephosphorylated by PP2A. Autophosphorylated.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. IKAPAB KINASE SUBFAMILY.

CC -----

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CC -----

DR EMBL; AF012890; AAC51662.1; -

DR EMBL; AF009225; AAC51671.1; -

DR EMBL; AF080157; AAD08996.1; -

DR EMBL; U22512; AAC50713.1; -

DR HSSP; 063450; 1A06.

DR Genew; HGNC:1974; CHUK.

DR MIM; 600664; -

DR GO; GO:0005737; Cytoplasm; TAS.

DR GO; GO:0008384; F-ikappaB kinase activity; TAS.

DR GO; GO:0007345; P-embryogenesis and morphogenesis; TAS.

DR GO; GO:0007252; P-I-kappaB phosphorylation; TAS.

DR GO; GO:0006955; P-immune response; TAS.

DR InterPro; IPR000719; Prot. kinase.

DR InterPro; IPR002290; Ser. thr. kinase.

DR InterPro; IPR001245; Tyr. kinase.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PD00109; TYRKINASE.

DR ProDom; PD000001; Prot. kinase; 1.

DR SMART; SM00220; S\_TKc; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.

DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.

DR KX Transferrase; Serine/threonine-protein kinase; ATP-binding; phosphorylation.

KW Phosphorylation.

KW DOMAIN 15 302

FT DOMAIN 15 302

FT DOMAIN 455 476

FT DOMAIN 738 743

FT NP BIND 21 29

FT BINDING 44 44

FT ACT SITE 144 144

FT MOD RES 23 23

FT MOD RES 176 176

FT MUTAGEN 23 23

FT MUTAGEN 44 44

FT MUTAGEN 44 44

FT MUTAGEN 176 176

FT MUTAGEN 176 176

FT MUTAGEN 176 176

FT MUTAGEN 179 179

FT MUTAGEN 180 180

FT CONFLICT 543 543

FT CONFLICT 604 604

FT CONFLICT 679 680

FT CONFLICT 684 684

FT CONFLICT 686 687

SO SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;

Query Match 92.3%; Score 36; DB 1; Length 745;

Best Local Similarity 83.3%; Pred. No. 1.2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEMSWL 6

DB 738 LMSWL 743

RESULT 2

IKKA MOUSE

ID IKKA MOUSE STANDARD; PRT; 745 AA.

AC 060650; Q9D2X3; -

DT 16-OCT-2001 (Rel. 40; Created)

DT 16-OCT-2001 (Rel. 40; Last sequence update)

DT 15-SEP-2003 (Rel. 42; Last annotation update)

DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)

DE (I-kappa-B kinase alpha) (IKK-alpha) (IKK-A) (IkappaB kinase)

DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKB1KX).

GN CHUK OR IKKA.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxId=10090;

RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN-BALB/c;  
 RX MEDLINE=3604444; PubMed=755804;  
 RA Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.;  
 RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human  
 chromosome 10 and mouse chromosome 19.";  
 RL Genomics 27:348-351(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN-BALB/c;  
 RX MEDLINE=96258427; PubMed=8777433;  
 RA Connolly M.A., Marcu K.B.;  
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper  
 families of interacting proteins, contains a serine-threonine kinase  
 catalytic domain.";  
 RL Cell. Mol. Biol. Res. 41:537-549(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RC STRAIN-C57BL/6J; TISSUE=Colon;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai Y., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi Y., Fukuda S.,  
 RA Atawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,  
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kankawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batzlov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King M., Kochiwa H.,  
 RA Knehl P., Lewis S., Matsuo Y., Nishikido I., Pesole G., Quackenbush J.,  
 RA Schirral L.M., Scambly F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barth G.,  
 RA Blake J., Bonfelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Guelincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Maehima M., Mazzarelli J., Mombaerts P.,  
 RA Norodone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Saeki K., Sato K., Schonbach C., Seyer T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whiteaker C., Wilmink L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontuski S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [4]  
 RP ALTERNATIVE SPLICING.  
 RX MEDLINE=20198447; PubMed=10733566;  
 RA McKenzie F.R., Connolly M.A., Balzarano D., Mueller J.R.,  
 RA Gelezunas R., Marcu K.B.;  
 RT "Functional isoforms of Ikappab kinase alpha (IKKalpha) lacking  
 leucine zipper and helix-loop-helix domains reveal that IKKalpha and  
 IKKbeta have different activation requirements.";  
 RL Cell. Biol. 20:2635-2649(2000).  
 RN [5]  
 RP PHOSPHORYLATION BY MAP3K4/NIK.  
 RX MEDLINE=98188238; PubMed=9520401;  
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yasita H.,  
 RA Okumura K.;  
 RT "Differential regulation of Ikappab kinase alpha and beta by two  
 upstream kinases, NF-kappaB-inducing kinase and mitogen-activated  
 protein kinase/ERK kinase kinase-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).  
 RN [6]  
 RA IKK-1 BINDING.  
 RX MEDLINE=99212141; PubMed=10195894;  
 RA Delhaese M., Hayakawa M., Chen Y., Karin M.;  
 RT "Positive and negative regulation of Ikappab kinase activity through  
 IKKbeta subunit phosphorylation.";  
 RL Science 284:309-313(1999).  
 RN [7]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., Didonato J.A., Lin A.;  
 RT "Coordinate regulation of Ikappab kinases by mitogen-activated protein  
 kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).

[8]  
RN REVIEW  
RX MEDLINE=20176139; PubMed=10712233;  
RA Josin C., Sator R.B.  
RT "The I kappa B/NF-Kappa B system: a key determinant of mucosal inflammation and protection."  
RL Am. J. Physiol. 276:C451-C462(2000).  
CC -I- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates NCOA3.  
CC -I- ENZYME REGULATION: Activated when phosphorylated and inactivated when dephosphorylated.  
CC -I- SUBUNIT: Preferentially found as a heterodimer w/lt IKK-beta but also as an homodimer. Directly interacts with IKK-gamma/MEMO. Heterodimers form the active complex. The tripartite complex can also bind to MAP3K14/NIK, MEKK1, IKAP and IKB-alpha-P65-P50 complex. A weak interaction with TRAF2 cannot be excluded. Part of a complex composed of NCOA2, NCOA3, IKKB, IKBG and CREBBP (by similarity).  
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -I- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Name=1;  
CC IsoId=Q60680-1; Sequence=displayed;  
CC Name=2; Synonyms=Delta LH;  
CC IsoId=Q60680-2; Sequence=VSP\_004866, VSP\_004867;  
CC Name=3; Synonyms=Delta H;  
CC IsoId=Q60680-3; Sequence=VSP\_004868, VSP\_004869;  
CC -I- TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and 3 are expressed predominantly in brain and T-lymphocytes.  
CC -I- DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by E11, E15 and E17 days. In the limb development, its expression predominates in the limb buds at E12.5 day.  
CC -I- PPM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by MEKK1, and dephosphorylated by PP2A, Autophosphorylated.  
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. IKAPPAB KINASE SUBFAMILY.  
CC -----  
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CC -----  
DR EMBL, U13473; AAC52589.1; -.  
DR EMBL, AK018671; BAB31335.1; -.  
DR PIR, I49101; I49101.  
DR HSSP, Q63450; IA06.  
DR MGD, MGI:99484; Chuk.  
DR InterPro, IPRO00719; Prot\_kinase.  
DR InterPro, IPRO02290; Ser\_Thr\_kinase.  
DR InterPro, IPRO01245; Tyr\_kinase.  
DR InterPro, PF00069; pkinase; 1.  
DR PRINTS, PR00109; TYRKINASE.  
DR ProDom, PD000001; Prot\_kinase; 1.  
DR PROSITE, PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE, PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE, PSS0011; PROTEIN\_KINASE\_DOM; 1.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation; Alternative splicing.  
KV DOMAIN 15 300  
FT LEUCINE\_ZIPPER (POTENTIAL).  
FT DOMAIN 455 476  
FT NP\_BIND 738 743  
FT BINDING 21 29  
FT ACT\_SITE 144 144  
FT MOD\_RES 23 23  
FT MOD\_RES 176 176  
FT PHOSPHORYLATION (BY MAP3K14) (BY SIMILARITY).

FT	VARSPLIC	452	471
FT	MULTIPLYNUTRINKUTLIS -> IFRKQVKSMBRNGBRK		
FT	SUF (in isoform 2).		
FT	VARSPLIC	472	745
FT	/PrId=VSP_004866.		
FT	VARSPLIC	577	584
FT	Missing (in isoform 2).		
FT	VARSPLIC	585	745
FT	DHLYDST -> GKTLQ9CY (in isoform 3).		
FT	CONFLICT	236	236
FT	CONFLICT	400	400
FT	SEQUENCE	745 AA,	84728 MM,
FT	3FEF5582AF92233 CRC64;		
OY	1 LBWSWL	6	
Db	738 LDWSWL	743	
Query Match			
Best Local Similarity		83.3%	Score 36; DB 1; Length 745;
Matches		5; Conservative	1; Mismatches
		0; Indels	0; Gaps
<hr/>			
RESULT 3			
IKKB_HUMAN	STANDARD;	PRT;	756 AA.
ID	IKKB_HUMAN		OL14920; O75327;
AC	16-OCT-2001	(Rel. 40, Created)	
DT	16-OCT-2001	(Rel. 40, Last sequence update)	
DT	15-SEP-2003	(Rel. 42, Last annotation update)	
DE	Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)		
DE	(I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase 2) (IKK2) (NFkappaB factor NF-kappa-B inhibitor kinase beta) (NFKBIKB).		
GN	IKKB OR IKKB.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
CX	NCBI_TaxID=9606;		
RN	[1]		
RN	SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.		
RC	TISSUE=Cervical carcinoma;		
RP	MEDLINE=98008813; PubMed=9346484;		
RX	Mercutio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,		
RA	Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;		
RT	"IKK-1 and IKK-2: cytokine-activated Ikappab kinases essential for		
RL	NF-kappab activation."		
RL	Science 278:860-866(1997).		
RN	[2]		
RN	SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.		
RC	MEDLINE=98008814; PubMed=9346485;		
RP	Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;		
RA	"Ikappab kinase-beta: NF-kappaB activation and complex formation with		
RT	Ikapab kinase-alpha and NIK."		
RL	Science 278:866-869(1997).		
RN	[3]		
RN	SEQUENCE FROM N.A.		
RC	TISSUE=Heart;		
RP	MEDLINE=98032998; PubMed=9813230;		
RX	Hu W.C.-T., Wang Y.-P.;		
RA	"Ikappab kinase-alpha and -beta genes are coexpressed in adult and		
RT	embryonic tissues but localized to different human chromosomes."		
RL	Genet. 222:31-40(1998).		
RN	[4]		
RN	SEQUENCE FROM N.A., AND GENE MAPPING.		
RC	MEDLINE=98438415; PubMed=9786565;		
RX	Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;		
RA	"Assignment of Ikappab kinase beta (IKKB) to human chromosome band		
RT	8p12--p11 by in situ hybridization."		
RL	Cytogenet. Cell Genet. 82:32-33(1998).		
RN	[5]		
RN	SEQUENCE OF 1-256 FROM N.A.		
RC	TISSUE=Lung;		
RX	Stralander R.L., Felngold E.A., Grouse L.H., Derge J.G.;		
RA	MEDLINE=22388257; PubMed=12477932;		

RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA DiGiuseppe L., Maruoka K., Farmer A.F., Rubin G.M., Hong L.,  
 RA Stepien M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedlin T.B., Toshitsuyuki S., Cavarni P., Prange C.,  
 RA Rata S.S., Luguelano N.A., Peters G.J., Abramson R.D., Mullish S.J.,  
 RA Roark S.A., McGwan P.J., McKernan K.J., Malek J.A., Gundrathe P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holys S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Farley J., Helton E., Kettelman W., Madan A.C., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko J., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield J.S.N., Krzywinski M.I., Skelton J., Smallus D.B.,  
 RA Scherch A., Schein J.R., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences."  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RT [6]  
 RP IKK PHOSPHORYLATION.  
 RP MEDLINE=99038238; PubMed=9819420;  
 RX Nemoto S., Didonato J.A., Lin A.;  
 RT "Coordinate regulation of Ikkappa kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappa-inducing kinase."  
 RT Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [7]  
 RN REVIEW.  
 RP MEDLINE=20178139; PubMed=10712233;  
 RX Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 RT inflammation and protection."  
 RT Am. J. Physiol. 278:C451-C462(2000).  
 RN [8]  
 RP IDENTIFICATION IN A COMPLEX WITH CREBBP, NCOA2, NCOA3, IKKA AND IKKB.  
 RX MEDLINE=21968797; PubMed=11971985;  
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,  
 RA O'Malley B.W.;  
 RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TEAM-1) coactivator  
 RT activity by I kappa B kinase."  
 RT Mol. Cell. Biol. 22:3549-3561(2002).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 CC the dissociation of the inhibitor/NF-kappa-B complex and  
 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3 (By similarity).  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MEKK1, MAP3K4/NIK. IKAP and IKB-alpha-955-P50  
 CC complex. Phosphorylated IKB-alpha is further released from the  
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG  
 CC and CREBBP.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal  
 CC muscle, kidney, pancreas, spleen, thymus, prostate, testis and  
 CC peripheral blood.  
 CC -1- PM: Phosphorylated by MEKK1 and probably also by MAP3K4/NIK.  
 CC weakly autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SSR/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPPA-B KINASE SUBFAMILY.  
 CC  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC  
 CC EMBL; AF029684; AAC51860.1; -  
 CC EMBL; AF080158; AAD08997.1; -  
 CC EMBL; AF031416; AAC64675.1; -  
 CC EMBL; BC006231; AAH06231.1; -

DR HSSP; 063450; 1A06.  
 DR Genew; HGNC:5960; IKKB.  
 DR MIM; 603258; -.  
 DR GO; GO:0005737; C:cytoplasm; NAS.  
 DR GO; GO:0005524; F:ATP binding activity; NAS.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.  
 DR GO; GO:0016563; F:transcriptional activator activity; NAS.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00240; ubiquitin; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Transferrase; Serine/threonine-protein kinase; ATP-binding;  
 KM Phosphorylation.  
 FT DOMAIN 15 300 PROTEIN KINASE.  
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 FT DOMAIN 737 742 NEMO-BINDING.  
 FT NP\_BIND 21 29 ATP (BY SIMILARITY).  
 FT BINDING 44 44 ATP (BY SIMILARITY).  
 FT ACT\_SITE 145 145 BY SIMILARITY.  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 177 177 PHOSPHORYLATION.  
 FT MOD\_RES 181 181 PHOSPHORYLATION.  
 FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO EFFECT ON BINDING TO NIK.  
 FT MUTAGEN 177 177 S->A: DECREASE OF ACTIVITY.  
 FT MUTAGEN 181 181 S->A: FULL ACTIVATION.  
 FT MUTAGEN 181 181 S->E: DECREASE OF ACTIVITY.  
 FT MUTAGEN 181 181 S->E: FULL ACTIVATION.  
 FT CONFLICT 231 255 WSKVRCKSEVDIVSDLDNGTYKF -> CRRMMPGVTHAS  
 FT CONFLICT 425 425 O -> H (IN REF. 1).  
 FT CONFLICT 425 425 O -> H (IN REF. 1).  
 SQ SEQUENCE 756 AA; 86563 MM; P9CADPF671ABE14E CRC64;

Query Match 92.3%; Score 36; DB 1; Length 756;  
 Best Local Similarity 83.3%; Pred. NO. 1.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LEWSWL 6  
 Db 737 LDWSWL 742

RESULT 4  
 IKKB\_MOUSE STANDARD; PRT; 757 AA.  
 ID ID\_MOUSE  
 AC 088351; Q9RIJ6; PRT; 757 AA.  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (BC 2.7.1.-)  
 DE (1-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase  
 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).  
 GN IKKB OR IKKB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NCBI\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A. AND PHOSPHORYLATION BY MEKK1.  
 RC STRAIN=C57BL/6; TISSUE=Spleen;  
 RX MEDLINE=98188238; PubMed=9520401;  
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,  
 "Differential regulation of I-kappa B kinase alpha and beta by two  
 RT upstream kinases, NF-kappa B-inducing kinase and mitogen-activated  
 RT protein kinase/SRK kinase kinase-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;  
 RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that  
 RT constitutively phosphorylates serine residues of IKB.";  
 RL Submitted (Aug-1998) to the EMBL/GenBank/DDA databases.  
 RN [3]  
 RP DEVELOPMENTAL STAGE.  
 RX MEDLINE=94455228; PubMed=10523828;  
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;  
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling  
 RT pathway activates I-kappa B kinases (IKK-alpha/beta) and IKK-beta is a  
 RT developmentally regulated protein kinase.";  
 RL Oncogene 18:5514-5524(1999).  
 RN [4]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., Didenko J.A., Iln A.;  
 RT "Coordinate regulation of I-kappa B kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappa B-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [5]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 RT inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 CC the dissociation of the inhibitor/NF-kappa-B complex and  
 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3.  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The trimeric complex can  
 CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-ALPHA-P65-P50  
 CC complex. Phosphorylated IKK-alpha is further released from the  
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBK  
 CC and CREBBP (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.  
 CC -1- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout  
 CC the mouse embryo, at E9.5 day its expression begins to be  
 CC localized to the brain, neural ganglia, neural tube, and in liver  
 CC at E12.5 day. At E15.5 day, the expression is further restricted  
 CC to specific tissues of the embryo.  
 CC -1- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.  
 CC Weakly autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPAB KINASE SUBFAMILY.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL; AF026524; AAC23557.1; -  
 CC EMBL; AF086910; AAD52095.1; -  
 DR HSSP; 063450; 1A06.  
 DR MGI; MGI:1338071; Ikbb.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KM Transferrase; Serine/threonine-protein kinase; ATP-binding;  
 KM Phosphorylation.

```

FT DOMAIN 15 300 PROTEIN KINASE.
FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 737 742 NEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 145 145 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 56 56 N -> D (IN REF. 2).
FT CONFLICT 343 343 N -> E (IN REF. 2).
FT CONFLICT 356 356 L -> F (IN REF. 2).
FT CONFLICT 390 390 P -> Q (IN REF. 2).
FT CONFLICT 406 406 K -> R (IN REF. 2).
FT CONFLICT 573 573 TLDMSWLQMEDEERCSLEQACD -> VTA (IN REF. 2).
FT CONFLICT 736 757

SQ SEQUENCE 757 AA; 86690 MW; PED962F095449C5E CRC64;

Query Match 92.3%; Score 36; DB 1; Length 757;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
DB 737 LDMSWL 742

RESULT 5
ID IKK_RAT STANDARD; PRT; 757 AA.
AC Q9QY78;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
DE (1-kappa-B-kinase beta) (IKKB) (IKK-beta) (1-kappa-B kinase
DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
GN IKKB OR IKK2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;

RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Sun S., David K.;
RT "IKK beta in megakaryocyte differentiation."
RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP IKK PHOSPHORYLATION.
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., Didonato J.A., Lin A.;
RT "Coordinate regulation of Ikkappa kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase."
RL Mol. Cell. Biol. 18:7336-7343(1998).
RN [3]
RP REVIEW.
RX MEDLINE=20178139; PubMed=10712233;
RA Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT inflammation and protection."
RL Am. J. Physiol. 278:C451-C462(2000).
CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC the dissociation of the inhibitor/NF-kappa-B complex and
CC ultimately the degradation of the inhibitor. Also phosphorylates
CC NCOA3.
CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.
CC Heterodimers form the active complex. The tripartite complex can
CC also bind to MEK1, MAP3K14/NIK, IKAP and IKK-alpha-P65-P50
CC complex. Phosphorylated IKK-alpha is further released from the
CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB
CC and CREBBP (by similarity).

```

```

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.
CC Weakly autophosphorylated.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPAB KINASE SUBFAMILY.
-----
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-----
CC EMBL; AF15282; AAF21978.1; -.
DR HSSP; 063450; 1A06.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 15 300 PROTEIN KINASE.
FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 737 742 NEMO-BINDING.
FT NP_BIND 21 29 ATP (BY SIMILARITY).
FT BINDING 44 44 ATP (BY SIMILARITY).
FT ACT_SITE 145 145 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 757 AA; 86866 MW; 3AFB46A7DF91F9C CRC64;

Query Match 92.3%; Score 36; DB 1; Length 757;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
DB 737 LDMSWL 742

RESULT 6
ID HOFC_ECOLI STANDARD; PRT; 400 AA.
AC P36346; P75648;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein transport protein hofc.
DE HOFC OR HOFC OR BO106.
GN HOFC OR HOFC OR BO106.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxId=562;

RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=K12;
RX MEDLINE=95047556; PubMed=7959070;
RA Whitchurch C.B., Mattick J.S.;
RT "Escherichia coli contains a set of genes homologous to those
RT involved in protein secretion, DNA uptake and the assembly of type-4
RT fimbriae in other bacteria."
RL Gene 150:9-15(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=K12 / WJ110;
RX MEDLINE=94261430; PubMed=8202364;

```



RA Fujita N., Mori H., Yura T., Ishihama A.;  
 "Systematic sequencing of the *Escherichia coli* genome: analysis of  
 the 2.4-4.1 min (110,917-193,643 bp) region.";  
 Nucleic Acids Res. 22:1637-1639(1994).  
 RL [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of *Escherichia coli* K-12.";  
 RL Science 277:123-124(1997).  
 RN [4]  
 RP SEQUENCE OF 165-400 FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=89061679; PubMed=2904262;  
 RA Andrews S.C., Guest J.R.;  
 RT "Nucleotide sequence of the gene encoding the GMP reductase of  
*Escherichia coli* K12.";  
 RL Biochem. J. 255:35-43(1988).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
 (Probable).  
 CC -1- SIMILARITY: BELONGS TO THE PUF/OUTP/EXEP/XSPS/XCBS FAMILY.  
 CC -1- CAUTION: REF.2 AND REF.4 SEQUENCES DIFFER IN THE N- AND C-TERMINAL  
 AS WELL AS IN THE CENTRAL PART DUE TO FRAMESHIFTS.  
 CC -----  
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 CC -----  
 DR EMBL; L28105; AAC36925.1; -  
 DR EMBL; D26562; -; NOT ANNOTATED\_CDS.  
 DR EMBL; AE000119; AAC73217.1; -  
 DR EMBL; X07917; -; NOT ANNOTATED\_CDS.  
 DR PIR; B64733; B64733.  
 DR EcGene; EG11798; hocC.  
 DR InterPro; IPR003004; Bac\_GSPF.  
 DR InterPro; IPR001992; Bac\_sec\_sylCII.  
 DR Pfam; PF00482; GSPF\_1.  
 DR PRINTS; PR00812; BCTERIALGSPF.  
 DR PROSITE; PS00874; T2SP\_F\_1.  
 KW Transport; Transmembrane; Inner membrane; Complete proteome.  
 FT TRANSMEM 165 185 POTENTIAL.  
 FT TRANSMEM 209 229 POTENTIAL.  
 FT TRANSMEM 370 390 POTENTIAL.  
 FT CONFLICT 1 39 -> MAVSNGAGAAVAVQVLT (IN REF. 1).  
 SQ SEQUENCE 400 AA; 44450 MW; 9D37333B87AE07D5 CRC64;  
 Query Match 89.7%; Score 35; DB 1; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 EWSWL 6  
 DB 215 EWSWL 219  
 RESULT 7  
 GTR8\_BOVIN STANDARD; PRT; 334 AA.  
 AC P58354;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Solute carrier family 2, facilitated glucose transporter, member 8  
 (Glucose transporter type 8) (Glucose transporter type XI) (Fragment).

GN SLC2A8 OR GLUT8 OR GLUTX1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_Taxid=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=2148267; PubMed=11599048;  
 RA Augustin R., Pocar P., Navarrete-Santos A., Wrenzycki C., Gandolfi F.,  
 RA Niemann H., Fischer B.;  
 RT "Glucose transporter expression is developmentally regulated in in  
 RT vitro derived bovine preimplantation embryos.";  
 RL Mol. Reprod. Dev. 60:370-376(2001).  
 CC -1- FUNCTION: Insulin-regulated facilitative glucose transporter.  
 CC Binds cytochalasin B in a glucose-inhibitable manner. Seems to be  
 CC a dual-specific sugar transporter as it is inhibitable by  
 CC fructose (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Principally  
 CC intracellular. May move between intracellular vesicles and the  
 CC plasma membrane. The dileucine internalization motif is critical  
 CC for intracellular sequestration (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE  
 CC TRANSPORTERS SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AF321324; AAK69606.1; -  
 DR InterPro; IPR007114; MFS.  
 DR InterPro; IPR005828; Sug\_transporter.  
 DR Pfam; PF00083; sugar\_tr\_1.  
 DR PROSITE; PS00216; SUGAR\_TRANSPORT\_1; 1.  
 DR PROSITE; PS00217; SUGAR\_TRANSPORT\_2; PARTIAL.  
 KW Transport; Sugar transporter; Transmembrane; Multigene family.  
 FT DOMAIN 1 14  
 FT TRANSMEM 15 14  
 FT DOMAIN 15 35  
 FT TRANSMEM 36 39  
 FT DOMAIN 39 58  
 FT TRANSMEM 60 113  
 FT DOMAIN 114 134  
 FT TRANSMEM 135 149  
 FT TRANSMEM 150 170  
 FT DOMAIN 171 176  
 FT TRANSMEM 177 197  
 FT DOMAIN 198 224  
 FT TRANSMEM 225 245  
 FT DOMAIN 246 261  
 FT TRANSMEM 262 282  
 FT DOMAIN 283 295  
 FT TRANSMEM 296 316  
 FT DOMAIN 317 334  
 SQ SEQUENCE 334 AA; 36699 MW; 0BE9B670DAB71DD CRC64;  
 Query Match 87.2%; Score 34; DB 1+02; Length 334;  
 Best Local Similarity 83.3%; Pred. No. 11e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LEWSWL 6  
 DB 35 LEWSWL 40  
 RESULT 8  
 GTR8\_HUMAN STANDARD; PRT; 477 AA.

AC Q9NT64; Q9NSC4;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Solute carrier family 2, facilitated glucose transporter, member 8  
 GN (Glucose transporter type 8) (Glucose transporter type XI).  
 GN SLC2A8 OR GLUT8 OR GLUTX1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RC MEDLINE=20283667; PubMed=10821868;  
 RA Doege H., Schuermann A., Bahrenberg G., Brauers A., Joest H.-G.;  
 RT "GLUT8, a novel member of the sugar transporter facilitator family with  
 RT glucose transport activity.";  
 RL J. Biol. Chem. 275:16275-16280(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20138191; PubMed=10671487;  
 RA Ibberson M.R., Uldry M.A., Thorens B.;  
 RT "GLUTX1, a novel mammalian glucose transporter expressed in the  
 RT central nervous system and insulin-sensitive tissues.";  
 RL J. Biol. Chem. 275:4607-4612(2000).  
 CC -1- FUNCTION: Insulin-regulated facilitative glucose transporter.  
 CC Binds cytochalasin B in a glucose-inhibitable manner. Seems to be  
 CC a dual-specific sugar transporter as it is inhibitable by  
 CC fructose (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Principally  
 CC intracellular. May move between intracellular vesicles and the  
 CC plasma membrane. The dileucine internalization motif is critical  
 CC for intracellular sequestration (By similarity).  
 CC -1- TISSUE SPECIFICITY: Highly expressed in testis, but not in  
 CC testicular carcinoma. Lower amounts present in most other tissues.  
 CC -1- INDUCTION: In testis, downregulated by estrogen.  
 CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE  
 CC TRANSPORTERS SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL, Y17801; CAB89809.1; -;  
 CC EMBL, AJ245937; CAB875702.1; -;  
 CC Genew; HGNC:13812; SLC2A8.  
 DR MIM; 605245; -;  
 DR GO; GO:0005887; C:Integral to plasma membrane; TAS.  
 DR GO; GO:0005355; P:glucose transporter activity; TAS.  
 DR GO; GO:0005975; P:carbohydrate metabolism; TAS.  
 DR GO; GO:0015758; P:glucose transport; TAS.  
 DR InterPro; IPR007114; MFS.  
 DR InterPro; IPR005828; Sub\_transporter.  
 DR InterPro; IPR005829; Sug\_transporter.  
 DR InterPro; IPR003663; Sug\_transp.  
 DR Pfam; PF00083; sugar tr; 1.  
 DR PRINTS; PR00171; SUGRTNSPORT.  
 DR TIGRPRAM; TIGR00879; SP; 1.  
 DR PROSITE; PS00216; SUGAR\_TRANSPORT\_1; 2.  
 DR PROSITE; PS00217; SUGAR\_TRANSPORT\_2; 1.  
 DR Transport; Sugar transport; Transmembrane; Glycoprotein;  
 KW Multigene family.  
 KM  
 FT DOMAIN 1 25 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 26 46 1 (POTENTIAL).  
 FT DOMAIN 47 70 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 71 91 2 (POTENTIAL).  
 FT DOMAIN 92 96 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 97 117 3 (POTENTIAL).

FT DOMAIN 118 127 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 128 148 4 (POTENTIAL).  
 FT DOMAIN 149 156 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 157 177 5 (POTENTIAL).  
 FT DOMAIN 178 182 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 183 202 6 (POTENTIAL).  
 FT DOMAIN 204 226 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 227 277 7 (POTENTIAL).  
 FT DOMAIN 278 292 8 (POTENTIAL).  
 FT TRANSMEM 293 313 9 (POTENTIAL).  
 FT DOMAIN 314 319 9 (POTENTIAL).  
 FT TRANSMEM 320 340 9 (POTENTIAL).  
 FT DOMAIN 341 367 10 (POTENTIAL).  
 FT TRANSMEM 368 388 10 (POTENTIAL).  
 FT DOMAIN 389 404 11 (POTENTIAL).  
 FT TRANSMEM 405 425 11 (POTENTIAL).  
 FT DOMAIN 426 438 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 439 459 12 (POTENTIAL).  
 FT DOMAIN 460 477 12 (POTENTIAL).  
 FT SITE 12 13 DILEUCINE INTERNALIZATION MOTIF (BY  
 FT SIMILARITY).  
 FT CARBOHYD 349 349 N-LINKED (GLCNAC. .) (By similarity).  
 FT CONFLICT 377 377 S -> N (IN REF. 2).  
 FT CONFLICT 456 457 FS -> LF (IN REF. 2).  
 FT CONFLICT 462 462 T -> I (IN REF. 2).  
 SQ SEQUENCE 477 AA; 50792 MW; 0848094B40A8E76 CRC64;  
 Query Match 87.2%; Score 34; DB 1; Length 477;  
 Best Local Similarity 83.3%; Pred. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LEWSL 6  
 DB 179 LEWRWL 184  
 RESULT 9  
 GTR8\_MOUSE STANDARD; PRT; 477 AA.  
 ID GTR8\_MOUSE  
 AC Q9UIF3; Q9UIP4; Q9UIZ0;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Solute carrier family 2, facilitated glucose transporter, member 8  
 GN SLC2A8 OR GLUT8 OR GLUTX1.  
 GN SLC2A8 OR GLUT8 OR GLUTX1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20138191; PubMed=10671487;  
 RA Ibberson M.R., Uldry M.A., Thorens B.;  
 RT "GLUTX1, a novel mammalian glucose transporter expressed in the  
 RT central nervous system and insulin-sensitive tissues.";  
 RL J. Biol. Chem. 275:4607-4612(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RC MEDLINE=20283667; PubMed=10821868;  
 RA Doege H., Schuermann A., Bahrenberg G., Brauers A., Joest H.-G.;  
 RT "GLUT8, a novel member of the sugar transporter facilitator family with  
 RT glucose transport activity.";  
 RL J. Biol. Chem. 275:16275-16280(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129; TISSUE=Embryonic carcinoma;  
 RC MEDLINE=20319023; PubMed=10860996;  
 RA Carayannopoulos M.O., Chi M.-Y., Cui Y., Pingsterhaue J.M.,  
 RA McKnight R.A., Mueckler S.U., Devaskar S.U., Moley K.H.;  
 RT "GLUT8 is a glucose transporter responsible for insulin-stimulated  
 RT glucose uptake in the blastocyst.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:7313-7318(2000).  
 RP [41]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=129/Ola; TISSUE=Spleen;  
 RX MEDLINE=21547794; PubMed=11689004;  
 RA Scheepers A., Doege H., Joost H.-G., Schnermann A.;  
 RT "Mouse GLUT8, genomic organization and regulation of expression in  
 RT 3T3-L1 adipocytes by glucose";  
 RL Biochem. Biophys. Res. Commun. 288:969-974(2001).  
 CC -1- FUNCTION: Insulin-regulated facilitative glucose transporter.  
 CC Binds cytochalasin B in a glucose-inhibitable manner. Seems to be  
 CC a dual-specific sugar transporter as it is inhibitable by  
 CC fructose.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Principally  
 CC intracellular. May move between intracellular vesicles and the  
 CC plasma membrane. The dileucine internalization motif is critical  
 CC for intracellular sequestration (by similarity). Insulin induces a  
 CC change in the intracellular localization and gives rise to  
 CC insertion in the plasma membrane.  
 CC -1- TISSUE SPECIFICITY: Highest level of expression in placenta and  
 CC testis. Highly expressed in adult and pubertal testis, but not  
 CC prepubertal testis. Lower levels of expression in brain, liver,  
 CC heart, kidney, fat and skeletal muscle.  
 CC -1- DEVELOPMENTAL STAGE: High expression in blastocysts.  
 CC -1- INDUCTION: Inhibited under glucose deprivation.  
 CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE  
 CC TRANSPORTERS SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AJ245936; CAB5719.1; -.  
 DR EMBL: Y17802; CAB89815.1; -.  
 DR EMBL: AF232061; AAF78366.1; -.  
 DR EMBL: AJ413951; CAC88690.1; -.  
 DR MGI: 1860103; SLC2A8.  
 DR GO: GO:0005887; C: integral to plasma membrane; IDA.  
 DR GO: GO:0005536; F: glucose binding activity; IDA.  
 DR GO: GO:0005355; F: glucose transporter activity; IDA.  
 DR GO: GO:0015758; F: glucose transporter; IDA.  
 DR GO: GO:0008286; P: insulin receptor signaling pathway; IDA.  
 DR GO: GO:0001666; P: response to hypoxia; IDA.  
 DR InterPro: IPR007114; MFS.  
 DR InterPro: IPR005828; Sub transporter.  
 DR InterPro: IPR005829; Sug transporter.  
 DR InterPro: IPR003663; Sugar\_transpt.  
 DR Pfam: PF00083; sugar\_tr; 1.  
 DR PRINTS: PRO0171; SUGRTNSPT.  
 DR TIGRFAMs: TIGR00879; SP; 1.  
 DR PROSITE: PS00216; SUGAR\_TRANSPORT\_1; 1.  
 DR PROSITE: PS00217; SUGAR\_TRANSPORT\_2; 1.  
 KW Transport; Sugar transport; Transmembrane; Glycoprotein;  
 KW Multigene family.  
 FT DOMAIN 1 25  
 FT TRANSMEM 26 46  
 FT DOMAIN 47 70  
 FT TRANSMEM 71 91  
 FT DOMAIN 92 96  
 FT TRANSMEM 97 117  
 FT DOMAIN 118 127  
 FT TRANSMEM 128 148  
 FT DOMAIN 149 156  
 FT TRANSMEM 157 177  
 FT DOMAIN 178 182  
 FT TRANSMEM 183 203  
 FT DOMAIN 204 257  
 FT TRANSMEM 258 278  
 FT DOMAIN 279 293  
 EXTRA-CELLULAR (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 1 (POTENTIAL).  
 EXTRA-CELLULAR (POTENTIAL).  
 2 (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 3 (POTENTIAL).  
 EXTRA-CELLULAR (POTENTIAL).  
 4 (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 5 (POTENTIAL).  
 EXTRA-CELLULAR (POTENTIAL).  
 6 (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 7 (POTENTIAL).  
 EXTRA-CELLULAR (POTENTIAL).

FT TRANSMEM 294 314 8 (POTENTIAL).  
 FT DOMAIN 315 320 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 321 341 9 (POTENTIAL).  
 FT DOMAIN 342 367 EXTRA-CELLULAR (POTENTIAL).  
 FT TRANSMEM 368 388 10 (POTENTIAL).  
 FT DOMAIN 389 404 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 405 425 11 (POTENTIAL).  
 FT DOMAIN 426 438 EXTRA-CELLULAR (POTENTIAL).  
 FT TRANSMEM 439 459 12 (POTENTIAL).  
 FT DOMAIN 460 477 CYTOPLASMIC (POTENTIAL).  
 FT SITE 12 13 DILEUCINE INTERNALIZATION MOTIF (BY  
 FT SITE 12 13 SIMILARITY).  
 FT CARBOHYD 350 350 N-LINKED (GLCNAC...) (By similarity).  
 FT CONFLICT 39 39 S -> N (IN REF. 1).  
 FT CONFLICT 94 94 S -> A (IN REF. 2 AND 4).  
 FT CONFLICT 429 429 S -> N (IN REF. 1).  
 SQ SEQUENCE 477 AA; 51523 MW; A3753FB34E452P9A CRC64;  
 Query Match 87.2%; Score 34; DB 1; Length 477;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LEWSMTL 6  
 DB 179 LEWSMTL 184  
 RESULT 10  
 GTR8\_RAT  
 ID GTR8\_RAT STANDARD; PRT; 478 AA.  
 AC Q9J721; Q9J7A6;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Solute carrier family 2, facilitated glucose transporter, member 8  
 DE (glucose transporter type 8) (Glucose transporter type X1).  
 GN SLC2A8 OR GLUT8 OR GLUTX1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 ON NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., CHARACTERIZATION, AND MUTAGENESIS OF LEU-12 AND  
 RP LEU-13.  
 RC TISSUE=Testis;  
 RX MEDLINE=20138191; PubMed=10671487;  
 RA Ibberson M.R., Uldry M.A., Thorens B.;  
 RT "GLUTX1, a novel mammalian glucose transporter expressed in the  
 RT central nervous system and insulin-sensitive tissues";  
 RL J. Biol. Chem. 275:4607-4612(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RA Ishihashi K.;  
 RT "Molecular cloning of a new putative glucose transporter";  
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=20283667; PubMed=10821868;  
 RA Doege H., Schnermann A., Bahrendberg C., Brauers A., Joost H.-G.;  
 RT "GLUT8, a novel member of the sugar transport facilitator family with  
 RT glucose transport activity";  
 RL J. Biol. Chem. 275:16275-16280(2000).  
 CC -1- FUNCTION: Insulin-regulated facilitative glucose transporter.  
 CC Binds cytochalasin B in a glucose-inhibitable manner. Seems to be  
 CC a dual-specific sugar transporter as it is inhibitable by  
 CC fructose.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Principally  
 CC intracellular. May move between intracellular vesicles and the  
 CC plasma membrane. The dileucine internalization motif is critical  
 CC for intracellular sequestration.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in adult and pubertal testis,  
 CC but not prepubertal testis. Moderate expression in hypothalamus,

CC cerebellum, brainstem, hippocampus, and adrenal gland. Lower  
 CC amounts present in most other tissues.  
 CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE  
 CC TRANSPORTERS SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: AJ245935; CAB75729.1; -  
 CC EMBL: AB034318; BAA94383.1; -  
 CC InterPro: IPR007114; MFS.  
 CC InterPro: IPR005828; Sub\_transporter.  
 CC InterPro: IPR005829; Sug\_transporter.  
 CC InterPro: IPR003663; Sugar\_transp.  
 CC Pfam: PF00083; sugar\_tr; 1.  
 CC PRINTS: PR00171; SUGTRANSPORT.  
 CC TIGRfam: TIGR00879; SP; 1.  
 CC PROSITE: PS00216; SUGAR\_TRANSPORT\_1; 2.  
 CC PROSITE: PS00217; SUGAR\_TRANSPORT\_2; 1.  
 CC Transprot; Sugar transport; Transmembrane; glycoprotein;  
 CC Multigene family.  
 CC FT DOMAIN 1 25 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 26 46 1 (POTENTIAL).  
 CC FT DOMAIN 47 70 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 71 91 2 (POTENTIAL).  
 CC FT DOMAIN 92 96 3 (POTENTIAL).  
 CC FT DOMAIN 97 117 4 (POTENTIAL).  
 CC FT DOMAIN 118 127 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 128 146 4 (POTENTIAL).  
 CC FT DOMAIN 149 156 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 157 177 5 (POTENTIAL).  
 CC FT DOMAIN 178 182 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 183 203 6 (POTENTIAL).  
 CC FT DOMAIN 204 257 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 258 278 7 (POTENTIAL).  
 CC FT DOMAIN 279 293 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 294 314 8 (POTENTIAL).  
 CC FT DOMAIN 315 320 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 321 341 9 (POTENTIAL).  
 CC FT DOMAIN 342 368 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 369 389 10 (POTENTIAL).  
 CC FT DOMAIN 390 405 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 406 426 11 (POTENTIAL).  
 CC FT DOMAIN 427 439 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 440 460 12 (POTENTIAL).  
 CC FT DOMAIN 461 478 CYTOPLASMIC (POTENTIAL).  
 CC FT SITE 12 13 DILEUCINE INTERNALIZATION MOTIF.  
 CC FT CARBOHYD 350 350 N-LINKED (GLCNAC...) (PROBABLE).  
 CC FT MOTAGEN 12 13 LT->AA: CHANGES SUBCELLULAR LOCATION.  
 CC FT MAINLY TO THE PLASMA MEMBRANE, THEREBY  
 CC INCREASING TRANSPORT ACTIVITY.  
 CC FT CONFLICT 83 84 GG -> GGA (IN REF. 2).  
 CC FT SEQUENCE 478 AA; 51458 MW; 95841PCLF18C9E9 CRC64;  
 CC Query Match 87.2%; Score 34; DB 1; Length 478;  
 CC Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 CC Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 CC Db 179 LEMSWL 184  
 CC 1 LEMSWL 6  
 CC RESULT 11  
 CC ROR1 DROME  
 CC ID ROR1 DROME STANDARD; PRT; 685 AA.  
 CC AC Q24468;  
 CC DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase transmembrane receptor Ror precursor  
 DE (EC 2.7.1.112) (drom).  
 DE ROR OR G64926.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OK NCBI\_TaxId=7227;  
 RN [1]  
 RN SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
 RP STRAIN=Canton-S; TISSUE=Larval brain;  
 RC MEDLINE=93348222; PubMed=8394009;  
 RX Wilson C., Guberhan D.C.I., Steller H.;  
 RT "Drosophila, a potential neurotrophic receptor gene, encodes a Drosophila  
 RT homolog of the vertebrate Ror family of Trk-related receptor tyrosine  
 RT kinases."  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7109-7113(1993).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=Berkley;  
 RC MEDLINE=20196006; PubMed=10731132;  
 RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers J.-H.C., Blazek R.G., Champagne M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter B.G., Holt G., Nelson C.R., Miklos G.L.G.,  
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Planck C., Baldwin D.,  
 RA Ballew R.M., Baer A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.V., Benos P.V., Bernan B.P., Brannan D., Bolshakov S.,  
 RA Borkova D., Botchan M.A., Bouck J., Brockstein P., Broclet P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos R., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Dong L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,  
 RA Foster C., Gabrielian A.B., Gary N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.V., Wei M.-H., Idagawa C.,  
 RA Jaitli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Paclet J.M.,  
 RA Palazolo M., Plittman G.S., Pan S., Pollard J., Part V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinerock K.G., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 RN [3]  
 RN SEQUENCE OF 545-597 FROM N.A.  
 RX MEDLINE=98401146; PubMed=9731193;  
 RA Oates A.C., Wolberg P., Achen M.G., Wilks A.F.;  
 RT "Sampling the genomic pool of protein tyrosine kinase genes using the  
 RT polymerase chain reaction with genomic DNA."  
 CC Biochem. Biophys. Res. Commun. 249:660-667(1998).  
 CC -1- FUNCTION: Tyrosine-protein kinase receptor that functions during  
 CC early stages of neuronal development.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).



RA Nakajima Y., Mituno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,  
RA Yamada K., Fujii Y., Oaki K., Hiraio M., Omori Y., Ota T., Suzuki Y.,  
RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,  
RA Isegaki T., Sugano S.,  
RT "NEBO human cDNA sequencing project";  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- TISSUE SPECIFICITY: Testis and ovary specific.  
CC -1- SIMILARITY: Contains 3 Tudor domains.  
CC -----  
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DR EMBL; AF285591; AK31970.1; -  
DR EMBL; AK024735; BAB14982.1; -  
DR GenBank; HGNC:11712; TDRD1.  
DR MIM; 605796; -  
DR InterPro; IPR001097; Maternal\_tudor.  
DR InterPro; IPR002999; Tudor.  
DR Pfam; PF00567; TUDOR; 3.  
DR SMART; SM00333; TUDOR; 3.  
DR PROSITE; PS50304; TUDOR; 3.  
KW Repeat.  
FT DOMAIN 138 197 TUDOR 1.  
FT DOMAIN 359 418 TUDOR 2.  
FT DOMAIN 587 645 TUDOR 3.  
FT CONFLICT 737 737 T -> M (IN REF. 2).  
FT CONFLICT 775 777 VKS -> KKKKK (IN REF. 2).  
SQ SEQUENCE 777 AA; 86762 MW; A733B80D3D76ABBC CRC64;

Query March 84.6%; Score 33; DB 1; Length 777;  
Best Local Similarity 66.7%; Pred. No. 3.5e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSM 6  
Db 300 LEWTV 305

RESULT 14  
TDR1\_MOUSE STANDARD; PRT; 928 AA.  
AC O99MT1;  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Tudor domain containing protein 1.  
DE TDRD1.  
GN Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary, and Testis;  
RX MEDLINE=21175148; PubMed=11279525;  
RA Wang P.J., McCarrey J.R., Yang F., Page D.C.,  
RT "An abundance of X-linked genes expressed in spermatogonia";  
RL Nat. Genet. 27:422-426(2001).  
CC -1- TISSUE SPECIFICITY: Testis and ovary specific.  
CC -1- SIMILARITY: Contains 4 Tudor domains.  
CC -----  
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CC -----  
CC EMBL; AF285591; AK31970.1; -  
DR MGD; MG1:1933218; Tdrcl.  
DR InterPro; IPR001097; Maternal\_tudor.  
DR InterPro; IPR002999; Tudor.  
DR Pfam; PF00567; TUDOR; 4.  
DR SMART; SM00333; TUDOR; 4.  
DR PROSITE; PS50304; TUDOR; 4.  
KW Repeat.  
FT DOMAIN 63 123 TUDOR 1.  
FT DOMAIN 292 351 TUDOR 2.  
FT DOMAIN 512 571 TUDOR 3.  
FT DOMAIN 738 796 TUDOR 4.  
SQ SEQUENCE 928 AA; 103050 MW; 9CCF0DBA3AF671AF CRC64;

Query March 84.6%; Score 33; DB 1; Length 928;  
Best Local Similarity 66.7%; Pred. No. 4.2e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSM 6  
Db 453 LEWTV 458

RESULT 15  
Y076\_HUMAN STANDARD; PRT; 1698 AA.  
AC Q14959;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Hypothetical protein KIAA0076.  
GN KIAA0076.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RX MEDLINE=96051398; PubMed=7584044;  
RA Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S.,  
RA Seki N., Kawarabayashi Y., Ishikawa K.-I., Tabata S.,  
RT "Prediction of the coding sequences of unidentified human genes. II.  
RT The coding sequences of 40 new genes (KIAA0041-KIAA0080) deduced by  
RT analysis of cDNA clones from human cell line KG-1.";  
RL DNA Res. 1:223-229(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bye;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Diatchenko L., Marisela K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raja S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullaney S.J.,  
RA Bosak S.A., McKernan K.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzyzanski M.I., Skalska U., Smallie D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Human and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: D38548; BAA07551.1; -.  
DR EMBL: BC033647; AAH33647.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 1698 AA; 19118 MW; 57B11CC478E3EEDA CRC64;

Query Match 84.6%; Score 33; DB 1; Length 1698;  
Best Local Similarity 66.7%; Pred. No. 7.5e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEWSWL 6  
|:|:|  
Db 1446 LOWTWL 1451

Search completed: February 18, 2004, 14:28:06  
Job time : 4.55263 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds  
(without alignments)  
87.531 Million cell updates/sec

Title: us-09-643-260-8

Perfect score: 39

Sequence: 1 LEWSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 761:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	92.3	645	2 T11137	NADH2 dehydrogenas
2	36	92.3	745	1 I49101	conserved helix-lo
3	35	89.7	150	2 PNO444	ig heavy chain V r
4	35	89.7	242	2 T27590	hypothetical prote
5	35	89.7	371	2 S20075	promastigote surfa
6	35	89.7	387	2 AD3426	mannose-6-phosphat
7	35	89.7	391	2 AG2318	hypothetical prote
8	35	89.7	400	2 B64733	protein transport
9	35	89.7	474	1 G2MS11	ig gamma-2b chain
10	35	89.7	522	2 A84606	hypothetical prote
11	35	89.7	1367	2 H82874	conserved hypotet
12	35	89.7	1379	2 UC4954	vascular endotheli
13	35	89.7	2054	2 T32413	probable acetyl-Co
14	34	87.2	116	2 T03472	conserved hypotet
15	34	87.2	117	2 S03289	ig heavy chain pre
16	34	87.2	133	2 PC1155	ig heavy chain pre
17	34	87.2	355	2 F70983	probable serine pr
18	34	87.2	395	2 E90438	hypothetical prote
19	34	87.2	398	2 S76763	neurotrophic recep
20	34	87.2	685	1 A48289	probable transcrip
21	34	87.2	919	2 T37062	probable potassium
22	34	87.2	1139	2 A10379	hypothetical prote
23	33	84.6	160	2 E71560	conserved hypotet
24	33	84.6	161	2 C81711	hypothetical prote
25	33	84.6	267	2 G90579	hypothetical prote
26	33	84.6	273	2 AB1696	PTS mannose-specif
27	33	84.6	272	2 AH1324	PTS mannose-specif
28	33	84.6	272	2 A13395	NADH2 dehydrogenas
29	33	84.6	358	2 AD2878	iron-chelator utli

30	33	84.6	358	2 P97654	mxCB protein (AF29
31	33	84.6	480	2 T24087	hypothetical prote
32	33	84.6	700	2 T24092	hypothetical prote
33	33	84.6	723	2 T32136	hypothetical prote
34	33	84.6	783	2 F88808	protein R09E10.3 (
35	33	84.6	903	2 T20804	hypothetical prote
36	33	84.6	1753	2 T00350	hypothetical prote
37	32	82.1	72	2 AD2464	hypothetical prote
38	32	82.1	83	2 S10986	gene 41 protein -
39	32	82.1	94	2 F72804	gp41 protein - Myc
40	32	82.1	100	2 AG0447	probable phage-rel
41	32	82.1	122	2 S63909	ig V-D-J region (M
42	32	82.1	132	2 S65785	mel-13a protein -
43	32	82.1	154	2 A72029	conserved hypotet
44	32	82.1	154	2 H86594	CT556 hypothetical
45	32	82.1	203	2 T50421	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

T11137

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - acorn worm mitochondrion

C/Species: mitochondrion Balanoglossus carnosus

C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #ext\_change 03-Jun-2002

C/Accession: T11137

R/Castresana, J.; Faldutier-Fuchs, G.; Yokobori, S.; Sach, N.; Paabo, S.

Genetics 150, 1115-1123, 1998

A/Title: The mitochondrial genome of the hemichordate Balanoglossus carnosus and the e

A/Reference number: Z17250; MIMD:99016080; PMID:9799263

A/Accession: T11137

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-645 <CAS>

A/Cross-references: EMBL:AF051097; NID:G3065680; PID:G3065682; PIDN:AAD11945.1

C/Genetics:

A/Genome: mitochondrion

C/Superfamily: NADH dehydrogenase (ubiquinone) chain 5

C/Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation

Query Match

Best Local Similarity 92.3%; Score 36; DB 2; Length 645;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6

DB 96 LEWSWL 101

##### RESULT 2

I49101

conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.1-) CHUK - mouse

C/Species: Mus musculus (house mouse)

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #ext\_change 10-Sep-1999

C/Accession: I49101

R/Mock, B.A.; Connolly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.

Genomics 27, 348-351, 1995

A/Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome

A/Reference number: I49101; MIMD:96044444; PMID:7558004

A/Accession: I49101

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-745 <RBS>

A/Cross-references: EMBL:U12473; NID:G1079492; PIDN:AAC52589.1; PID:G1079493

C/Genetics:

A/Gen: CHUK

C/Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homo-

C/Keywords: ATP; phosphotransferase

F/13-283/Domain: protein kinase homology <KIN>

Query Match

Best Local Similarity 92.3%; Score 36; DB 1; Length 745;



Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LEWSML 6  
 Db 738 LDMSWL 743

## RESULT 3

IG heavy chain V region precursor - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000

C/Accession: P00444

R/Kaluz, B.; Betzel, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.

Gene 122, 321-328, 1992

A/Title: A general method for chimerization of monoclonal antibodies by inverse polymerase

A/Reference number: P00444; MUID:93138402; PMID:1339379

A/Accession: P00444

A/Molecule type: mRNA

A/Residues: 1-150 <KAL>

A/Cross-references: GB:I02346

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-150/Product: Ig heavy chain V region #status predicted <MAT>

F:20-117/Domain: variable region <VRG>

F:34-117/Domain: immunoglobulin homology <IMM>

## Query Match

Best Local Similarity 89.7%; Score 35; DB 2; Length 150;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSML 6

Db 1 MEMSML 6

## RESULT 4

T27590

hypothetical protein ZC47.13 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000

C/Accession: T27590

R/McMurray, A.

submitted to the EMBL Data Library, October 1996

A/Reference number: Z20391

A/Accession: T27590

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-242 <WIL>

A/Cross-references: EMBL:281141; PIDN:CA803488.1; CESP:ZC47.13

A/Experimental source: clone ZC47

C/Genetics:

A/Introns: 172/3

C/Superfamily: Caenorhabditis elegans hypothetical protein ZC47.9

## Query Match

Best Local Similarity 89.7%; Score 35; DB 2; Length 242;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEWSML 6

Db 226 LEWML 231

## RESULT 5

S20075

promastigote surface antigen P2 (clone 2.5) precursor - Leishmania major (fragment)

C/Species: Leishmania major

C/Date: 13-Jan-1995 #sequence\_revision 06-Feb-1998 #text\_change 31-Jan-2000

C/Accession: S20075; C41710

R/Murray, P.J.; Spithill, T.W.

J. Biol. Chem. 266, 24477-24484, 1991

A/Title: Variants of a Leishmania surface antigen derived from a multigenic family.

A/Reference number: A41710; MUID:92105105; PMID:1761547

A/Accession: S20075

A/Molecule type: mRNA

A/Residues: 1-371 <MUR>

A/Cross-references: EMBL:X57134; NID:99580; PID:99581

C/Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol link;

F:1-343/Product: promastigote surface antigen P2 (fragment) #status predicted <PSA>

F:344-371/Domain: carboxyl-terminal propeptide #status predicted <CTP>

F:343/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Aap) (in mature fo:

## Query Match

Best Local Similarity 89.7%; Score 35; DB 2; Length 371;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EWSML 6

Db 1 EWSML 5

## RESULT 6

AD3426

mannose-6-phosphate isomerase (EC 5.3.1.8) [imported] - Brucella melitensis (strain 161

C/Species: Brucella melitensis

C/Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002

C/Accession: AD3426

R/DelVecchio, V.G.; Kapural, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A/Title: The genome sequence of the facultative intracellular pathogen Brucella melite:

A/Reference number: AD3426; PMID:11756688

A/Accession: AD3426

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1387 <KUR>

A/Cross-references: GB:AB008917; PIDN:AML52575.1; PID:gl7983392; GSPDB:GN00190

A/Experimental source: strain 16M

C/Genetics:

A/Map position: 1

C/Keywords: intramolecular oxidoreductase; isomerase

## Query Match

Best Local Similarity 89.7%; Score 35; DB 2; Length 387;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EWSML 6

Db 245 EWSML 249

## RESULT 7

AG2318

hypothetical protein all4102 [imported] - Nostoc sp. (strain PCC 7120)

C/Species: Nostoc sp. PCC 7120

A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002

C/Accession: AG2318

R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Itiguci

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,

DNA Res. 8, 205-213, 2001

A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A

A/Reference number: AB1807; MUID:21595285; PMID:11759840

A/Accession: AG2318

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1391 <KUR>

A/Cross-references: GB:BA000019; PIDN:BAB75801.1; PID:gl7133237; GSPDB:GN00179

A/Experimental source: strain PCC 7120

C/Genetics:

A/Gene: all4102

Query Match 89.7%; Score 35; DB 2; Length 391;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEWSML 6  
 |||||  
 DB 37 LEWMDL 42

## RESULT 8

protein transport protein hofc - Escherichia coli (strain K-12)  
 B64733  
 C/Species: Escherichia coli  
 C/Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #ext\_change 01-Mar-2002  
 C/Accession: B64733; S45184; S45183  
 R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
 A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A/Title: The complete genome sequence of Escherichia coli K-12.  
 A/Reference number: A64720; MUID:97426617; PMID:9278503  
 A/Accession: B64733  
 A/Status: nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-400 <BLAT>  
 A/Cross-references: GB:AE000119; GB:U00096; NID:91786283; PIDN:AACT3217.1; PID:91786295;  
 A/Experimental source: strain K-12, substrain MG1655  
 R/Fujita, N.  
 submitted to the EMBL Data Library, January 1994  
 A/Reference number: S45181  
 A/Accession: S45184  
 A/Molecule type: DNA  
 A/Residues: 'MGR', '8-147', 'PK', '150-173', 'NHGGCGNAFCVCRSLPSTREPTPHRH' <FUS>  
 A/Cross-references: EMBL:D26562; NID:9473770; PIDN:BA05563.1; PID:9473774  
 A/Experimental source: strain K-12  
 A/Accession: S45183  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 207-366, 'NRVADHNGNNTYAGCGNANPFRPCDEMGITACSTPALGDYRLKKRFGSCCTR', 'INVN  
 A/Cross-references: EMBL:D26562; NID:9473770; PIDN:BA05562.1; PID:9473773  
 A/Experimental source: strain K-12  
 C/Genetics:  
 A/Gene: hofc; hopc  
 C/Superfamily: secretion protein xcpS  
 C/Keywords: protein transport; transmembrane protein  
 F/167-183/Domain: transmembrane #status predicted <TM1>  
 F/719-735/Domain: transmembrane #status predicted <TM2>  
 F/369-385/Domain: transmembrane #status predicted <TM3>

Query Match 89.7%; Score 35; DB 2; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EMSML 6  
 |||||  
 DB 215 EMSML 219

## RESULT 9

G2MS11  
 IG gamma-2b chain - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 31-Mar-1980 #sequence\_revision 01-Dec-2000 #ext\_change 01-Dec-2000  
 C/Accession: S25057; A02157; A26232; A26233; A53598  
 R/Fischer, R.; Voss, A.; Nierbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
 submitted to the EMBL Data Library, July 1992  
 A/Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific R  
 A/Reference number: S25057  
 A/Accession: S25057  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-474 <FIS>  
 A/Cross-references: EMBL:X67210; NID:954826; PIDN:CAA7649.1; PID:954827  
 R/Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Odate, M.; Honjo, T.

Nature 283, 786-789, 1980  
 A/Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from  
 A/Reference number: A02157; MUID:80120716; PMID:6766534  
 A/Contents: a allele  
 A/Accession: A02157

A/Molecule type: DNA  
 A/Residues: 138-161, 'L', '163-189', 'FP', '193-474 <YAN>  
 A/Cross-references: GB:J00461  
 A/Note: the sequence was determined from the germline gene  
 R/Tucker, P.W.; Marcu, K.B.; Slichter, J.L.; Blattner, F.R.  
 Science 206, 1299-1303, 1979  
 A/Title: Structure of the constant and 3' untranslated regions of the murine gamma2b h

A/Reference number: A26233; MUID:80081501; PMID:117548

A/Contents: MPC 11

A/Accession: A26235

A/Molecule type: mRNA  
 A/Residues: 138-172, 'P', '174-189', 'FP', '193-376', 'T', '378-474 <TVU>  
 A/Note: Lys-474 is probably removed posttranslationally  
 R/Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
 Science 206, 1303-1306, 1979

A/Title: Sequence of the cloned gene for the constant region of murine gamma2b immunog

A/Reference number: A26232; MUID:80081502; PMID:117549

A/Accession: A26232

A/Molecule type: DNA

A/Residues: 138-172, 'P', '174-189', 'FP', '193-376', 'T', '378-474 <TVU>  
 R/Ollo, R.; Rougeon, F.  
 Nature 296, 761-763, 1982

A/Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gai

A/Reference number: A26233; MUID:82173203; PMID:6803173

A/Contents: b allele

A/Accession: A26233

A/Molecule type: DNA

A/Residues: 138-161, 'L', '163-189', 'FP', '193-300', 'R', '302-331', 'A', '333-437', 'DI', '440-474 <QLL  
 A/Cross-references: GB:J00461

R/Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takaha

J. Biol. Chem. 269, 12345-12350, 1994  
 A/Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.

A/Reference number: A53598; MUID:94216359; PMID:7512967

A/Accession: A53598

A/Status: preliminary

A/Molecule type: protein

A/Residues: 234-251 <KIM>  
 C/Comment: The a allele sequence is shown.

C/Genetics:

C/Intron: 138/1; 236/1; 258/1; 368/1

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k) hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob

F/157-222/Domain: immunoglobulin homology <IM1>

F/236-257/Region: hinge

F/281-350/Domain: immunoglobulin homology <IM2>

F/387-454/Domain: immunoglobulin homology <IM3>

F/152/Disulfide bonds: interchain (to light chain) #status predicted

F/164-220,288-348,394-452/Disulfide bonds: #status predicted

F/247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted

F/324/Binding site: carbohydrate (Aen) (covalent) #status predicted

QY 1 LEWSML 6  
 |||||  
 DB 1 MEMSWI 6

## RESULT 10

A84606  
 hypothetical protein At2g21860 [imported] - Arabidopsis thaliana  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #ext\_change 02-Feb-2001  
 C/Accession: A84606

R,lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Taiton, L.; Euse, D.; Nieman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A>Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: A84606  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-522 <STO>  
A:Cross-references: GB:AE002093; NID:g4417279; PIDN:AAD20404.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g21860  
A:Map position: 2

Query Match 89.7%; Score 35; DB 2; Length 522;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSW 5  
Db 341 LEWSW 345

RESULT 11  
H82874  
conserved hypothetical ATP/GTP-binding protein UUS71 [imported] - Ureaplasma urealyticum  
C:Species: Ureaplasma urealyticum  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: H82874  
R:Glass, J.I.; Letkowitz, E.J.; Glass, J.S.; Helner, C.R.; Chen, E.Y.; Cassell, G.H.  
submitted to GenBank, February 2000  
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min  
A:Reference number: A82870  
A:Accession: H82874  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1367 <GLA>  
A:Cross-references: GB:AE002155; GB:AF222894; NID:g6899572; PIDN:AAF30985.1; GSPDB:GN001  
A:Experimental source: serovar 3, biovar 1  
C:Genetics:  
A:Gene: UUS71  
A:Genetic code: SGC3

Query Match 89.7%; Score 35; DB 2; Length 1367;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EWSWL 6  
Db 786 EWSWL 790

RESULT 12  
JC4954  
vascular endothelial growth factor receptor 2 precursor - Japanese quail  
N:Alternate names: Quail endothelial kinase 2; Quak 2  
C:Species: Coturnix coturnix japonica (Japanese quail)  
C>Date: 31-Dec-1996 #sequence\_revision 31-Dec-1996 #text\_change 24-Sep-1999  
C:Accession: JC4954  
R:Elchmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.  
Gene 174, 3-8, 1996  
A>Title: Molecular cloning of Quak 1 and 2, two quail vascular endothelial growth factor  
A:Reference number: JC4953; MUID:97017121; PMID:8663722  
A:Accession: JC4954  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-1379 <ETC>  
A:Cross-references: EMBL:X83287; NID:g619865; PIDN:CAA58267.1; PID:e283815; PID:g1707416  
C:Comment: This protein is an endothelial-specific receptor and binds vascular endothelial  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homoid  
C:Keywords: ATP; embryo; factor receptor; transmembrane protein  
F,1-20/Domain: signal sequence #status predicted <SIG>

F,789-810/Domain: transmembrane #status predicted <TMM>  
F,856-1188/Domain: protein kinase homology <KIN>  
F,864-872/Region: protein kinase ATP-binding motif

Query Match 89.7%; Score 35; DB 2; Length 1379;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSW 5  
Db 57 LEWSW 61

RESULT 13  
T32413  
probable acetyl-CoA carboxylase (EC 6.4.1.2) W09B6.1 [similarity] - Caenorhabditis ele  
C:Species: Caenorhabditis elegans  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 18-Aug-2000  
C:Accession: T32413  
R:Goela, D.; Maggi, L.; Andrews, S.  
submitted to the EMBL Data Library, September 1997  
A:Description: The sequence of C. elegans cosmid W09B6.  
A:Reference number: Z21162  
A:Accession: T32413  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2054 <GOE>  
A:Cross-references: EMBL:AF025469; PIDN:AAJ71048.1; GSPDB:GN00020; CESP:W09B6.1  
A:Experimental source: strain Bristol N2; clone W09B6  
C:Genetics:  
A:Gene: CESP:W09B6.1  
A:Map position: 2  
A:Intons: 18/3; 50/3; 97/1; 734/2; 793/3; 1975/2; 2037/2  
C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/bioti  
C:Keywords: ligase

Query Match 89.7%; Score 35; DB 2; Length 2054;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSW 5  
Db 773 LEWSW 777

RESULT 14  
T03472  
conserved hypothetical protein - Rhodobacter capsulatus  
C:Species: Rhodobacter capsulatus  
C>Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 08-Oct-1999  
C:Accession: T03472  
R:VLcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fomstein, M.  
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997  
A>Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB10.  
A:Reference number: Z14955; MUID:97404404; PMID:9256491  
A:Accession: T03472  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-116 <VLC>  
A:Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AAC16125.1; PID:g3128273  
C:Genetics:  
A:Map position: 1

Query Match 87.2%; Score 34; DB 2; Length 116;  
Best Local Similarity 83.3%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LEWSWL 6  
Db 63 LEWSWL 68

RESULT 15

S03289  
Ig heavy chain precursor V region (VAR100) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 23-Jul-1999  
C/Accession: S03289  
R/Blankenstein, T.; Bonhomme, F.; Krawinkel, U.  
Immunogenetics 26, 237-248, 1987  
A/Title: Evolution of pseudogenes in the immunoglobulin V(H)-gene family of the mouse.  
A/Reference number: S03289; MUID:8806305; PMID:2820872  
A/Accession: S03289  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-117 <BLA>  
A/Cross-references: EMBL:X06866; NID:G52454; PIDN:CAA2991.1; PID:G758157  
C/Genetics:  
A/Introns: 16/1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 87.2%; Score 34; DB 2; Length 117;  
Best Local Similarity 66.7%; Pred. No. 74;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSVL 6  
:||||:  
Db 1 MEWSNV 6

Search completed: February 18, 2004, 14:38:42  
Job time : 8.5921 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds

(Without alignments)  
35.929 Million cell updates/sec

Title: US-09-643-260-8

Sequence: 39  
1 LEWSWL 6

Scoring table: BIOSUM62  
Gap 10.0, Gapext 0.5

Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A COMB pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B COMB pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A COMB pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B COMB pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS COMB pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1 pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	100.0	454	4 US-09-252-991A-28780	Sequence 28780, A
2	36	92.3	745	2 US-08-887-518-3	Sequence 3, App1
3	36	92.3	745	2 US-09-023-321-3	Sequence 3, App1
4	36	92.3	745	2 US-08-890-853-4	Sequence 4, App1
5	36	92.3	745	2 US-09-032-475-3	Sequence 3, App1
6	36	92.3	745	2 US-09-099-125A-4	Sequence 4, App1
7	36	92.3	745	2 US-09-099-125A-4	Sequence 4, App1
8	36	92.3	745	3 US-09-032-476-4	Sequence 4, App1
9	36	92.3	745	3 US-08-890-854-4	Sequence 4, App1
10	36	92.3	745	3 US-09-023-324-4	Sequence 2, App1
11	36	92.3	745	3 US-09-168-829-2	Sequence 10, App1
12	36	92.3	745	3 US-08-910-820-10	Sequence 4, App1
13	36	92.3	745	4 US-09-109-986-4	Sequence 2, App1
14	36	92.3	745	4 US-09-844-908-10	Sequence 10, App1
15	36	92.3	745	4 US-09-868-758-3	Sequence 3, App1
16	36	92.3	745	2 US-08-887-518-4	Sequence 4, App1
17	36	92.3	745	2 US-09-023-321-4	Sequence 4, App1
18	36	92.3	745	2 US-08-890-853-2	Sequence 4, App1
19	36	92.3	745	2 US-09-032-475-4	Sequence 4, App1
20	36	92.3	745	2 US-09-099-125A-2	Sequence 2, App1
21	36	92.3	745	2 US-09-099-125A-2	Sequence 2, App1
22	36	92.3	745	3 US-09-032-476-2	Sequence 2, App1
23	36	92.3	745	3 US-08-890-854-2	Sequence 2, App1
24	36	92.3	745	3 US-09-023-324-2	Sequence 15, App1
25	36	92.3	745	3 US-09-168-829-15	Sequence 9, App1
26	36	92.3	745	3 US-08-910-820-9	Sequence 9, App1
27	36	92.3	745	3 US-08-910-820-9	Sequence 9, App1

28	36	92.3	745	4 US-09-109-986-2	Sequence 2, App1
29	36	92.3	745	4 US-09-844-908-9	Sequence 9, App1
30	36	92.3	745	4 US-09-868-758-4	Sequence 4, App1
31	36	92.3	996	4 US-09-417-197-123	Sequence 123, App
32	36	92.3	997	4 US-09-417-197-121	Sequence 121, App
33	35	89.7	137	1 US-08-392-419-2	Sequence 2, App1
34	35	89.7	140	3 US-08-836-561-27	Sequence 27, App1
35	35	89.7	140	3 US-08-836-561-63	Sequence 63, App1
36	35	89.7	140	3 US-08-836-561-74	Sequence 74, App1
37	35	89.7	140	3 US-08-836-561-78	Sequence 78, App1
38	35	89.7	140	3 US-08-836-561-83	Sequence 83, App1
39	35	89.7	140	3 US-08-579-378A-4	Sequence 4, App1
40	35	89.7	140	4 US-09-434-122-27	Sequence 27, App1
41	35	89.7	140	4 US-09-434-122-63	Sequence 63, App1
42	35	89.7	140	4 US-09-434-122-74	Sequence 74, App1
43	35	89.7	140	4 US-09-434-122-78	Sequence 78, App1
44	35	89.7	140	4 US-09-434-122-83	Sequence 83, App1
45	35	89.7	140	5 PCT-US93-11612-4	Sequence 4, App1

#### ALIGNMENTS

##### RESULT 1

US-09-252-991A-28780  
; Sequence 28780, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfeld et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 28780  
; LENGTH: 454  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-28780

Query Match 100.0%; Score 39; DB 4; Length 454;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
|||||

DB 305 LEWSWL 310

US-08-887-518-3  
; Sequence 3, Application US/08887518  
; Patent No. 5843721  
; GENERAL INFORMATION:  
; APPLICANT: Roche, Mike  
; APPLICANT: Wu, Lin  
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-887-518-3

Query March 92.3% Score 36; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
DB 738 LDMSWL 743

RESULT 3  
US-09-023-321-3  
Sequence 3, Application US/09023321  
Patent No. 5844073

GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,321  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-09-023-321-3

Query Match 92.3% Score 36; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
DB 738 LDMSWL 743

RESULT 4  
US-08-890-853-4  
Sequence 4, Application US/08890853  
Patent No. 5851812

GENERAL INFORMATION:  
APPLICANT: Goedel, David V.  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-853-4

Query Match 92.3% Score 36; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
DB 738 LDMSWL 743

RESULT 5  
US-09-032-475-3  
Sequence 3, Application US/09032475  
Patent No. 5854003

GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,475  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/887,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-032-475-3

Query Match  
Best Local Similarity 92.3%; Score 36; DB 2; Length 745;  
Pred. No. 5.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
|:||||  
DB 738 LDMSWL 743

RESULT 6  
US-09-099-125A-4  
Sequence 4, Application US/09099125A  
Patent No. 5916760  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Moronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,125A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-099-125A-4

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-099-125A-4

Query Match  
Best Local Similarity 92.3%; Score 36; DB 2; Length 745;  
Pred. No. 5.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
|:||||  
DB 738 LDMSWL 743

RESULT 7  
US-09-099-124A-4  
Sequence 4, Application US/09099124A  
Patent No. 5939302  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Moronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,124A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-099-124A-4

RESULT 8  
US-09-032-476-4  
; Sequence 4, Application US/09032476  
; Patent No. 6235492  
; GENERAL INFORMATION:  
; APPLICANT: Roche, Mike  
; APPLICANT: Cao, Zhaodan  
; APPLICANT: R. Guier, Catherine  
; TITLE OF INVENTION: IKK- $\gamma$  Proteins, Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/032,476  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/890,854  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: T97-006-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 745 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-032-476-4  
Query Match 92.3%; Score 36; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LEWSWL 6  
Db 738 LDMSWL 743  
RESULT 9  
US-08-890-854-4  
; Sequence 4, Application US/08890854  
; Patent No. 6235512  
; GENERAL INFORMATION:  
; APPLICANT: Roche, Mike  
; APPLICANT: Cao, Zhaodan  
; APPLICANT: R. Guier, Catherine  
; TITLE OF INVENTION: IKK- $\gamma$  Proteins, Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/890,854  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: T97-006-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 745 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-890-854-4  
Query Match 92.3%; Score 36; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LEWSWL 6  
Db 738 LDMSWL 743  
RESULT 10  
US-09-023-324-4  
; Sequence 4, Application US/09023324  
; Patent No. 6235513  
; GENERAL INFORMATION:  
; APPLICANT: Roche, Mike  
; APPLICANT: Cao, Zhaodan  
; APPLICANT: R. Guier, Catherine  
; TITLE OF INVENTION: IKK- $\gamma$  Proteins, Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,324  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/890,854  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: T97-006-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 745 amino acids  
; TYPE: amino acid



STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-324-4

Query Match 92.3%; Score 36; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
|:||||  
Db 738 LDMSWL 743

RESULT 11  
US-09-168-629-2  
Sequence 2, Application US/09168629  
Patent No. 6242253  
GENERAL INFORMATION:  
APPLICANT: Karin, Michael  
APPLICANT: Didonato, Joseph A.  
APPLICANT: Rochwarf, David M.  
APPLICANT: Hayakawa, Makio  
APPLICANT: Zandi, Ebrahim  
TITLE OF INVENTION: Ikr kinase, Subunits Thereof, and Methods of Using Same  
FILE REFERENCE: P-UD 3295  
CURRENT APPLICATION NUMBER: US/09/168,629  
EARLIER FILING DATE: 1998-10-08  
EARLIER APPLICATION NUMBER: 60/061,470  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 745  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-168-629-2

Query Match 92.3%; Score 36; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
|:||||  
Db 738 LDMSWL 743

RESULT 12  
US-08-910-820-10  
Sequence 10, Application US/08910820  
Patent No. 6258579  
GENERAL INFORMATION:  
APPLICANT: Mercutio, Frank  
APPLICANT: Zhu, Hengyi  
APPLICANT: Barbosa, Miguel  
APPLICANT: Li, Ghan  
APPLICANT: Murray, Brian W.  
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSER: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/910,820  
FILING DATE: 12-AUG-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 860098.413C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-910-820-10

Query Match 92.3%; Score 36; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
|:||||  
Db 738 LDMSWL 743

RESULT 13  
US-08-810-131A-2  
Sequence 2, Application US/08810131A  
Patent No. 6268194  
GENERAL INFORMATION:  
APPLICANT: Karin, Michael  
APPLICANT: Didonato, Joseph A.  
APPLICANT: Rochwarf, David M.  
APPLICANT: Hayakawa, Makio  
APPLICANT: Zandi, Ebrahim  
TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/810,131A  
FILING DATE: 25-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 2408  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-810-131A-2

Query Match 92.3%; Score 36; DB 3; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.5e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LEMSWL 6  
|:||||  
Db 738 LEMSWL 743

RESULT 14  
US-09-109-986-4  
; Sequence 4, Application US/09109986  
; Patent No. 6479266  
; GENERAL INFORMATION:  
; APPLICANT: Rotne, Mike  
; APPLICANT: Cao, Zhaoan  
; APPLICANT: R. Grier, Catherine  
; TITLE OF INVENTION: IKK-1 Proteins, Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/109,986  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/890,854  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: T97-006-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 745 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-109-986-4

Query Match 92.3%; Score 36; DB 4; Length 745;  
Best Local Similarity 83.3%; Pred. NO. 5.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEMSWL 6  
|:||||  
Db 738 LEMSWL 743

RESULT 15  
US-09-844-908-10  
; Sequence 10, Application US/09844908  
; Patent No. 6576437  
; GENERAL INFORMATION:  
; APPLICANT: Mercurio, Frank  
; APPLICANT: Zhu, Hengyi  
; APPLICANT: Barbosa, Miguel  
; APPLICANT: Li, Gian  
; APPLICANT: Murray, Brian W.  
; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE  
; COMPLEX AND METHODS OF USE THEREFOR

NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/844,908  
; FILING DATE: 27-Apr-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/910,820  
; FILING DATE: 12-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Makl, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 860098.413C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 745 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
; US-09-844-908-10

Query Match 92.3%; Score 36; DB 4; Length 745;  
Best Local Similarity 83.3%; Pred. NO. 5.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LEMSWL 6  
|:||||  
Db 738 LEMSWL 743

Search completed: February 18, 2004, 14:41:47  
Job time : 7.06579 sec

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds  
(without alignments)  
89.145 Million cell updates/sec

Title: US-09-643-260-7

Perfect score: 38  
Sequence: 1 LAMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP\_RODENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*  
15: SP\_VIRINE:\*  
16: SP\_BACTERIAP:\*  
17: SP\_ARCHAEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	1033	4 Q8N3S6	Q8N3S6 homo sapien
2	36	94.7	488	10 Q9SEJ7	Q9SEJ7 lupinus alb
3	36	94.7	675	17 Q26849	Q26849 mechanact
4	35	92.1	91	16 Q98C88	Q98C88 rhizobium 1
5	35	92.1	116	2 Q68039	Q68039 rhodobacter
6	35	92.1	135	2 Q05744	Q05744 mycobacteri
7	35	92.1	145	5 Q810L0	Q810L0 drosophila
8	35	92.1	172	2 Q9KK81	Q9KK81 brevivibacter
9	35	92.1	196	16 Q50005	Q50005 mycobacteri
10	35	92.1	197	2 Q88SV7	Q88SV7 unclutured
11	35	92.1	210	16 Q86317	Q86317 mycobacteri
12	35	92.1	321	5 Q94515	Q94515 drosophila
13	35	92.1	329	5 Q9VFP8	Q9VFP8 drosophila
14	35	92.1	398	16 Q8FMH6	Q8FMH6 bruceella su
15	35	92.1	422	16 Q92NU3	Q92NU3 rhizobium m
16	35	92.1	438	16 Q8UDU6	Q8UDU6 agrobacteri

17	35	92.1	441	16 Q8YBVO	Q8YBVO bruceella me
18	35	92.1	966	11 Q8BRK2	Q8BRK2 mus musculus
19	35	92.1	1040	10 Q8GU52	Q8GU52 oryza sativ
20	35	92.1	1055	10 Q9S722	Q9S722 arabidopsis
21	35	92.1	1057	10 Q9F17	Q9F17 arabidopsis
22	35	92.1	1058	10 Q9FLR5	Q9FLR5 arabidopsis
23	34	89.5	50	2 Q4996	Q4996 mycobacteri
24	34	89.5	77	2 Q9K1K2	Q9K1K2 pseudomonas
25	34	89.5	88	12 Q88815	Q88815 easter equ
26	34	89.5	88	12 Q88810	Q88810 easter equ
27	34	89.5	88	12 Q88803	Q88803 easter equ
28	34	89.5	88	12 Q88816	Q88816 easter equ
29	34	89.5	88	12 Q88811	Q88811 easter equ
30	34	89.5	88	12 Q88817	Q88817 easter equ
31	34	89.5	88	12 Q88809	Q88809 easter equ
32	34	89.5	88	12 Q88823	Q88823 easter equ
33	34	89.5	88	12 Q88808	Q88808 easter equ
34	34	89.5	88	12 Q88818	Q88818 easter equ
35	34	89.5	88	12 Q88801	Q88801 easter equ
36	34	89.5	88	12 Q88821	Q88821 easter equ
37	34	89.5	88	12 Q88807	Q88807 easter equ
38	34	89.5	88	12 Q88804	Q88804 easter equ
39	34	89.5	88	12 Q88822	Q88822 easter equ
40	34	89.5	88	12 Q88805	Q88805 easter equ
41	34	89.5	88	12 Q88820	Q88820 easter equ
42	34	89.5	88	12 Q88813	Q88813 easter equ
43	34	89.5	88	12 Q88814	Q88814 easter equ
44	34	89.5	88	12 Q88819	Q88819 easter equ
45	34	89.5	88	12 Q88800	Q88800 easter equ

#### ALIGNMENTS

RESULT 1  
Q8N3S6 PRELIMINARY; PRT: 1033 AA.  
AC Q8N3S6; 01-OCT-2002 (TRMBLrel. 22, Created)  
DT 01-OCT-2002 (TRMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TRMBLrel. 22, Last annotation update)  
DE Hypothetical protein (Fragment).  
GN DKFZP451G02.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wamburt R., Heubner D., Mewes H.W., Well B., Wiemann S.;  
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL, AL831955; CAD38600.1; -.  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 1033 AA; 114395 MW; ED4F629A229CDB6B CRC64;  
Query Match 100.0%; Score 38; DB 4; Length 1033;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LAMSWL 6  
DB 557 LAMSWL 562  
RESULT 2  
Q9SEJ7 PRELIMINARY; PRT: 488 AA.  
AC Q9SEJ7; 01-MAY-2000 (TRMBLrel. 13, Created)  
DT 01-MAY-2000 (TRMBLrel. 13, Last sequence update)  
DT 01-OCT-2002 (TRMBLrel. 22, Last annotation update)  
DE 1-aminocyclopropane-1-carboxylate synthase 3 (EC 4.4.1.14).

GN ACS3.  
 OS Lupinus albus (white lupine).  
 OC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC euroside 1; Fabales; Fabaceae; Papilionoideae; Genistaceae; Lupinus.  
 RX NCBI\_Taxid=3870;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Ultra;  
 RX MEDLINE=20539411; PubMed=11089679;  
 RA Bekman E.P., Saito N.J., Di Cataldo A., Regalado A.P., Ricardo C.P.,  
 Rodriguez-Ponsada C.;  
 RT "Differential expression of four genes encoding 1-aminocyclopropane-1-  
 RT carboxylate synthase in *Lupinus albus* during germination, and in  
 RT response to indole-3-acetic acid and wounding.";  
 RL Planta 211:663-672(2000).  
 CC -1- COPACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC  
 CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
 CC AMINOTRANSFERASES.  
 DR EMBL: AF119413; AAF22111.1; -.  
 DR HSSP: P37821; 1B8G.  
 DR InterPro: IPR001176; ACC\_synthase.  
 DR InterPro: IPR004839; AminoTransfer/2.  
 DR InterPro: IPR004838; NitrTransf.1.  
 DR Pfam: PF00155; aminotran 1.2; 1.  
 DR PRINTS: PR00753; ACCSYNTASE.  
 DR PROSITE: PS00105; AA\_TRANSFER\_CLASS\_1; 1.  
 KW Lyase; Pyridoxal phosphate.  
 SQ SEQUENCE 488 AA; 55026 MW; 5BB0D640DD129970 CRC64;  
 Query Match 94.7%; Score 36; DB 10; Length 488;  
 Best Local Similarity 83.3%; Pred. No. 6.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
 DB 479 IAMSWL 484

RESULT 3  
 ID 026849 PRELIMINARY; PRT; 675 AA.  
 AC 026849;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Heavy-metal transporting CPX-type ATPase.  
 GN MTH755.  
 OS Methanobacterium thermoautotrophicum.  
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
 OC Methanobacteriaceae; Methanobacter.  
 RX NCBI\_Taxid=167420;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Delta H;  
 RX MEDLINE=98037514; PubMed=9371463;  
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-W., Dubois J.,  
 RA Aldredge T., Bashirzadeh R., Blakey D., Cook R., Gilbert K.,  
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pochter B., Qiu D.,  
 RA Spadatore R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,  
 RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,  
 RA McQuigley S., Shimer G., Goyal A., Pietrovski S., Church G.M.,  
 RA Daniels C.J., Mao J.-I., Rice P., Neelling J., Reeve J.N.;  
 RT "Complete genome sequence of *Methanobacterium thermoautotrophicum*  
 RT deltaH: functional analysis and comparative genomics.";  
 RL J. Bacteriol. 179:7135-7155(1997).  
 DR EMBL: AE000854; AAB85258.1; -.  
 DR InterPro: IPR006403; ATPase-IB1\_Cu.  
 DR InterPro: IPR006416; ATPase-IB\_Hvy.  
 DR InterPro: IPR001757; ATPase\_E1-E2.

DR InterPro: IPR001756; Cu ATPase.  
 DR InterPro: IPR005834; Hydrolase.  
 DR Pfam: PF00122; E1-E2 ATPase; 1.  
 DR Pfam: PF00702; Hydrolase; 1.  
 DR PRINTS: PR00119; CATRAPASE.  
 DR PRINTS: PR00943; CUATPASE.  
 DR TIGRPFAM: TIGR01511; ATPase-IB1\_Cu; 1.  
 DR TIGRPFAM: TIGR01525; ATPase-IB\_Hvy; 1.  
 DR TIGRPFAM: TIGR01494; ATPase\_P-type; 3.  
 DR PROSITE: PS00154; ATPASE\_E1-E2; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 675 AA; 72337 MW; 56A5D4C175C0CC6F CRC64;  
 Query Match 94.7%; Score 36; DB 17; Length 675;  
 Best Local Similarity 83.3%; Pred. No. 8.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
 DB 299 IAMSWL 304

RESULT 4  
 ID 098C88 PRELIMINARY; PRT; 91 AA.  
 AC 098C88;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
 DE Exopolysaccharide production repressor, ExoX.  
 GN MRS253.  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobium; Proteobacteria; Mesorhizobium.  
 RX NCBI\_Taxid=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAFF303099;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 RT *Mesorhizobium loti*.";  
 RL DNA Res. 7:331-338(2000).  
 DR EMBL: AP003006; BAB51733.1; -.  
 KW Complete proteome.  
 SQ SEQUENCE 91 AA; 9887 MW; 10F09237249B37F0 CRC64;  
 Query Match 92.1%; Score 35; DB 16; Length 91;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
 DB 18 VAMSWL 23

RESULT 5  
 ID 068039 PRELIMINARY; PRT; 116 AA.  
 AC 068039;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Hypothetical 12.6 kDa protein.  
 OS Rhodospirillum rubrum (Rhodospirillum rubrum).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;  
 OC Rhodospirillaceae; Rhodospirillum.  
 RX NCBI\_Taxid=1061;  
 RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=SB1003;  
RX MEDLINE=97404404; PubMed=9256491;  
RA Vlack C., Paces V., Maltsev N., Paces J., Haselkorn R., Feinstein M.;  
RT "Sequence of a 189-kb segment of the chromosome of Rhodospirillum rubrum";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).  
DR EMBL: AF010496; AAC16125.1;  
DR InterPro: IPR005133; Phag\_MhG\_YuF.  
DR Pfam: PF03334; Phag\_MhG\_YuF; 1.  
DR TIGRfam: TIGR01300; CPA3\_mhG\_phag; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 116 AA; 12553 MW; FPF91E726D421996 CRC64;  
  
Query Match 92.1%; Score 35; DB 2; Length 116;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 LAMSWL 6  
DB 63 LMSWML 68  
  
RESULT 6  
ID 005744 PRELIMINARY; PRT; 135 AA.  
AC 005744;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE Hypothetical 14.5 kDa protein.  
GN MLCB5.12.  
OS Mycobacterium leprae.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1769;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Badcock K., Churcher C.M.;  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
RT [2]  
RP SEQUENCE FROM N.A.  
RA Parkhill J., Barrell B.G., Rajandream M.A.;  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93188700; PubMed=8446027;  
RA Biglieri K., Honore N., Woods S.A., Caudron B., Cole S.T.;  
RT "Use of an ordered cosmid library to deduce the genomic organization  
of Mycobacterium leprae";  
RL Mol. Microbiol. 7:197-206(1993).  
DR EMBL: Z95151; CAB08408.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 135 AA; 14516 MW; E7B32E2379C4888C CRC64;  
  
Query Match 93.1%; Score 35; DB 2; Length 135;  
Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 LAMSWL 6  
DB 23 LMSWML 28  
  
RESULT 7  
ID 081010 PRELIMINARY; PRT; 145 AA.  
AC 081010;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE CG32240-PA (GH04494P).  
GN CG32240.  
  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoeklin R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Burton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers J.H., Blazey R.G., Champe M., Pfeiffer B.D.,  
RA Abail J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Bernier B.P., Bhandari D., Bolshakov S.,  
RA Borokov D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,  
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Crawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Fabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodeson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,  
RA Foster C., Gabrielian A.S., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibeagwa C.,  
RA Jalali W., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,  
RA Laeske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Mlshina N.V., Mobarry C., Morris L., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Furl V., Reese M.G.,  
RA Reimert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,  
RA Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodgett M., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster";  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Celisner S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
RA Barton J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
RA Dodeson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,  
RA Gonzalez M., Houck J., Hoskins R.A., Hoeklin D., Howard T.J.,  
RA Ibeagwa C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
RA Paclet J., Paragad V., Park S., Patel S., Pfeiffer B.,  
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
RA Stapleton M., Strong R., Svitek R., Tector C., Tyler D.,  
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
RT "Sequencing of Drosophila melanogaster genome";  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Mista S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celisner S.E.,  
RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,  
RA Seale S.M., Smith B., Shu S., Smutnick G., Whitfield B.,  
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
RT "Annotation of Drosophila melanogaster genome";

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [1]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Flybaee;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Y;  
 RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,  
 RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nuno J., Pacleb J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celinker S.;  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AEO03481; AAN11600.1; -;  
 DR EMBL; BT001386; AAN71141.1; -;  
 SQ SEQUENCE 145 AA; 17393 MW; 4EF7D500940F762A CRC64;

Query Match 92.1%; Score 35; DB 5; Length 145;  
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
 :|||||  
 Db 36 LAMSWL 41

RESULT 8  
 Q9KK81 PRELIMINARY; PRT; 172 AA.

AC Q9KK81;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Hypothetical 18.8 kDa protein.  
 GN CRTK.

OS Brevibacterium linens.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Micrococccineae; Brevibacteriaceae; Brevibacterium.  
 OX NCBI\_TaxID=1703;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=DSM 20426;  
 RX MEDLINE=20279196; PubMed=10821176;

RA Krubasik P., Sandmann G.;  
 RT "A carotenogenic gene cluster from Brevibacterium linens with novel  
 RT lysozyme cyclase genes involved in the synthesis of aromatic  
 RT carotenoids";  
 RL MOL. Gen. Genet. 263:423-432(2000).

DR EMBL; AF139916; AAF65585.1; -;  
 DR InterPro; IPR006032; Ribosomal\_S12\_23.  
 DR InterPro; IPR004307; TPO\_MBR.

DR Pfam; PF03073; TPO\_MBR; 1.  
 DR PROSITE; PS00055; RIBOSOML\_S12; 1.  
 KM Hypothetical protein.

SQ SEQUENCE 172 AA; 18808 MW; 9F6BD848B95875P5 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 172;  
 Best Local Similarity 83.3%; Pred. No. 3.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
 :|||||  
 Db 91 LAMSWL 96

RESULT 9  
 Q50005

ID Q50005 PRELIMINARY; PRT; 196 AA.

AC Q50005;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE U1764V (Hypothetical protein ML1041).

GN ML1041.  
 OS Mycobacterium leprae.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1769;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA Smith D.R., Robison K.;  
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=TN;

RX MEDLINE=21128732; PubMed=11234002;  
 RA Cole S.T., Elgimeier K., Parkhill J., James K.D., Thomson N.R.,  
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,  
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R.M., Devlin K., Duthoy S., Fellwell T., Fraser A., Hamlin N.,  
 RA Holroyd S., Hornby T., Jagels K., Lacroix C., Maclean J., Moule S.,  
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,  
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,  
 RA Squares S., Stevens K., Taylor K., Woodward S., Woodward J.R.,  
 RA Barrall B.G.;

RT "Massive gene decay in the leprosy bacillus";  
 RL Nature 409:1007-1011(2001).

DR EMBL; U15181; AAG2925.1; -;  
 DR EMBL; AL583920; CAC31422.1; -;  
 DR Lepitoma; ML1041; -;  
 KM Hypothetical protein; Complete proteome.

SQ SEQUENCE 196 AA; 21186 MW; 1SD4AF7CDF653936 CRC64;

Query Match 92.1%; Score 35; DB 16; Length 196;  
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
 :|||||  
 Db 109 LAMSWL 114

RESULT 10  
 Q8RSV7

ID Q8RSV7 PRELIMINARY; PRT; 197 AA.

AC Q8RSV7;  
 DT 01-JUN-2002 (TREMblrel. 21, Created)

DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)

DE Maturase (Fragment).  
 OS uncultured marine bacterium.

OC Bacteria; environmental samples.  
 OX NCBI\_TaxID=56765;

RN [1]

RP SEQUENCE FROM N.A.  
 RA Podar M., Mullineux L., Sogin M.L., Perlman P.S.;

RT "Bacterial group II introns in a deep sea hydrothermal vent  
 RT environment";  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF075118; AAL78689.1; -;  
 DR InterPro; IPR000477; RVTse.

DR Pfam; PF00078; RVC; 1.  
 KM RNA-directed DNA polymerase; Transferase.

FT NON TER 1  
 SQ SEQUENCE 197 AA; 24010 MW; FA76F629B32D36A CRC64;

Query Match 92.1%; Score 35; DB 2; Length 197;  
 Best Local Similarity 83.3%; Pred. No. 3.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6  
DB 172 LAWSWL 177

## RESULT 11

086317 PRELIMINARY; PRT; 210 AA.  
AC 086317  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Hypothetical protein RV2680.  
GN RV2680 OR MT2754 OR MYO10.04.  
OS Mycobacterium tuberculosis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H37RV;  
RX MEDLINE=9825987; PubMed=9634230;  
RA Cole S.T., Broese R., Parkhill J., Garnier T., Churcher C., Harris D.,  
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
RA Davies R., Devlin K., Feltham D., Gentles S., Hamlin N., Holtroyd S.,  
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
RA Sultson J.E., Taylor K., Whitehead S., Barrett B.G.;  
RT Deciphering the biology of Mycobacterium tuberculosis from the  
RT complete genome sequence.;  
RL Nature 393:537-544(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CDC 1551 / Oshkosh;  
RA Fleisemann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
RA Peterson J., Deboy R., Dodson R., Gwin M., Haft D., Hickey E.,  
RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,  
RA Baler W., Uterback T., Weidman J., Knouri H., Gill J., Mikula A.,  
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
RT laboratory strains.";  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z96072; CAB09496.1; -  
DR EMBL; AE007105; AAK47069.1; ALT\_INIT.  
DR TIGR; MT2754; -  
DR TubercuList; RV2680; -  
KM Hypothetical protein; Complete proteome.  
SQ SEQUENCE 210 AA; 22573 MW; 2D9429BF1FE0956A CRC64;

Query Match 92.1%; Score 35; DB 16; Length 210;  
Best Local Similarity 83.3%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6  
DB 123 LAWSWL 128

## RESULT 12

094515 PRELIMINARY; PRT; 321 AA.  
AC 094515  
DT 01-FEB-1997 (TREMBlrel. 02, Created)  
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE ITC protein (LD15458P) (Sphingolipid delta 4 desaturase protein DES-  
DE 11).  
GN ITC OR DES1 OR CG9078.  
OS Drosophila melanogaster (fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gecayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champs C.R., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.M., Miklos G.L.G.,  
RA Abell J.F., Agbayani A., An H.-U., Andrews-Frankoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Bendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benes P.V., Bernan B.P., Bhendari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferris S., Fleischmann W.,  
RA Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasse K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laso P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Mlehnke N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pachek J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rees M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=OREGON R;  
RX MEDLINE=97156918; PubMed=9003299;  
RA Endo K., Akiyama T., Kobayashi S., Okada M.;  
RT "Degenerative spermatocyte, a novel gene encoding a transmembrane  
RT protein required for the initiation of meiosis in Drosophila  
RT spermatogenesis.";  
RL Mol. Gen. Genet. 253:157-165(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkeley;  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Farfan D., Frisbe B., George R.,  
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Nuno J., Pacleb J., Paragas V., Park S., Pounanavong S., Wan K.,  
RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;  
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Body;  
RA Terns P., Franke S., Zaehring U., Sperling P., Heinz R.;  
RT "Identification and Characterization of a Sphingolipid Delta-4-  
RT Desaturase Family.";  
RL J. Biol. Chem. 277:10000-10006(2002).  
DR EMBL; AE003612; AAF52318.1; -  
DR EMBL; X94180; CAA63889.1; -  
DR EMBL; AY061196; AAL28744.1; -  
DR EMBL; AF466379; AAM12535.1; -

DR FlyBase; FBgn0001941; tlc.  
 DR InterPro; IPR001064; Crystallin.  
 DR InterPro; IPR005804; FA desat. fam.  
 DR InterPro; IPR006025; Zn\_Mtpeptidase.  
 DR Pfam; PF00487; FA desaturase; 1.  
 DR PROSITE; PS00225; CRYSTALLIN\_BETNGAMMA; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 DR Transmembrane.  
 SQ SEQUENCE 321 AA; 37213 MW; B8DB31961BF5F38E CRC64;

Query Match 92.1%; Score 35; DB 5; Length 321;  
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
 :|||  
 Db 64 LAMSWL 69

RESULT 13  
 Q9VFE8 PRELIMINARY; PRT; 329 AA.

AC Q9VFE8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE CG10148 protein.  
 GN CG10148.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyrygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Plannkoch C., Baldwin D.,  
 RA Ballew R.M., Baas A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Butke K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Dublin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foeller C., Gabriellian A.B., Gary N.S., Gelbart W.M., Glasser K.,  
 RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegam C.,  
 RA Jaisi M., Kalush F., Karpen G.H., Ke Z., Krenshaw J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Liao X., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier B.E., Spradling A.C., Stapleton M., Strong R., Sun B.,  
 RA Svyrkbe R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weisbrock G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195 (2000).  
 DR EMBL; AE003698; AAF54907.1; -  
 DR FlyBase; FBgn0038120; CG10148.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR003591; LRR\_Typ.  
 DR Pfam; PF00560; LRR; 4.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR SMART; SM00369; LRR\_Typ; 1.  
 DR PROSITE; PS05006; LRR\_TYPICAL; 1.  
 SQ SEQUENCE 329 AA; 37165 MW; C41063485C334DA CRC64;

Query Match 92.1%; Score 35; DB 5; Length 329;  
 Best Local Similarity 83.3%; Pred. No. 6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
 :|||  
 Db 17 LAMSWL 22

RESULT 14  
 Q8FWH6 PRELIMINARY; PRT; 398 AA.

AC Q8FWH6;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Pyridine nucleotide-diaphorase oxidoreductase family protein.  
 GN BRA0479.  
 OS Brucella suis.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Brucellaceae; Brucella.  
 OX NCBI\_TaxID=29461;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=1330 / Biovar 1;  
 RX MEDLINE=42247741; PubMed=12271122;  
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,  
 RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Bauman M.J.,  
 RA Daugherty S.C., Debroy R.T., Durkin A.S., Kolonay J.F., Madupu R.,  
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,  
 RA Redmiller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,  
 RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.,  
 RT "The Brucella suis genome reveals fundamental similarities between  
 RT animal and plant pathogens and symbionts."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).  
 DR EMBL; AE014545; AAN33671.1; -  
 DR TIGR; BRA0479; -  
 KW Complete proteome.  
 SQ SEQUENCE 398 AA; 43624 MW; 574D95CA928B8424 CRC64;

Query Match 92.1%; Score 35; DB 16; Length 398;  
 Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
 :|||  
 Db 370 VAMSWL 375

RESULT 15  
 Q92NU3 PRELIMINARY; PRT; 422 AA.

AC Q92NU3;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Putative NAH dehydrogenase transmembrane protein (BC 1.6.99.3).  
 GN NH OR R02079 OR SWC04452.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Sinorhizobium.



OX NCBI\_TaxID=382;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1021;  
RX MEDLINE=2139507; PubMed=11481430;  
RA Capela D., Barloy-Hubler F., Gouzy J., Borhe G., Ampe F., Batut J.,  
RA Boisset P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
RA Godrie T., Goffeau A., Kahn D., Kise E., Lelaure V., Masny D.,  
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,  
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;  
RT "Analysis of the chromosome sequence of the legume symbiont  
RT Sinorhizobium meliloti strain 1021.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
DR EMBL; AL591789; CAC46558.1; -;  
DR InterPro; IPR001327; PAD\_pyr\_redox.  
DR InterPro; IPR001100; Pyr\_redox.  
DR Pfam; PF00070; Pyr\_redox; 1.  
DR PRINTS; PR00368; FADPNR.  
DR PRINTS; PR00411; PNDPRPASEI.  
KW Oxidoreductase; Complete proteome.  
SQ SEQUENCE 422 AA; 46023 MW; 1490D9AC1EA517DB CRC64;

Query Match 92.1%; Score 35; DB 16; Length 422;

Best Local Similarity 83.3%; Pred. No. 7.6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LANSWL 6

DB 394 VANSWL 399

Search completed: February 18, 2004, 14:35:43  
Job time : 19.3684 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds  
(without alignment)  
35.929 Million cell updates/sec

Title: US-09-643-260-7  
Perfect score: 38  
Sequence: 1 LAMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	35	92.1	196 4 US-08-311-731A-69	Sequence 69, Appl
2	35	92.1	198 4 US-08-311-731A-319	Sequence 319, App
3	34	89.5	56 4 US-09-205-258-359	Sequence 359, App
4	34	89.5	63 4 US-08-311-731A-311	Sequence 311, App
5	34	89.5	172 4 US-09-252-991A-17325	Sequence 17325, A
6	34	89.5	260 4 US-09-252-991A-21611	Sequence 21611, A
7	34	89.5	269 4 US-09-252-991A-31792	Sequence 31792, A
8	34	89.5	280 4 US-09-634-238-334	Sequence 334, App
9	34	89.5	313 4 US-09-252-991A-28418	Sequence 28418, A
10	34	89.5	320 4 US-09-339-159B-22	Sequence 22, Appl
11	34	89.5	331 4 US-09-339-159B-12	Sequence 12, Appl
12	34	89.5	335 4 US-09-252-991A-23948	Sequence 23948, A
13	34	89.5	343 4 US-09-252-991A-26240	Sequence 26240, A
14	34	89.5	369 4 US-09-339-159B-16	Sequence 16, Appl
15	34	89.5	468 4 US-09-485-648-4	Sequence 4, Appl
16	34	89.5	468 4 US-09-503-565-4	Sequence 4, Appl
17	34	89.5	468 4 US-09-485-649-4	Sequence 4, Appl
18	34	89.5	468 4 US-09-339-159B-8	Sequence 8, Appl
19	34	89.5	476 4 US-09-339-159B-4	Sequence 4, Appl
20	34	89.5	490 4 US-09-339-159B-2	Sequence 2, Appl
21	34	89.5	493 4 US-09-485-648-2	Sequence 2, Appl
22	34	89.5	493 4 US-09-503-565-2	Sequence 2, Appl
23	34	89.5	493 4 US-09-485-649-2	Sequence 2, Appl
24	34	89.5	493 4 US-09-339-159B-6	Sequence 6, Appl
25	34	89.5	545 4 US-09-252-991A-25304	Sequence 25304, A
26	33	86.8	95 4 US-09-252-991A-19590	Sequence 19590, A
27	33	86.8	355 3 US-08-818-112-79	Sequence 79, Appl

28	33	86.8	355 4 US-08-818-111-80	Sequence 80, Appl
29	33	86.8	355 4 US-09-056-556-79	Sequence 79, Appl
30	33	86.8	355 4 US-09-072-596-80	Sequence 80, Appl
31	33	86.8	416 4 US-09-252-991A-23585	Sequence 23585, A
32	33	86.8	454 4 US-09-252-991A-28780	Sequence 28780, A
33	32	84.2	137 1 US-08-137-117D-31	Sequence 31, Appl
34	32	84.2	137 2 US-08-436-717-31	Sequence 31, Appl
35	32	84.2	187 6 5217891-4	Patent No. 5217891
36	32	84.2	193 4 US-09-252-991A-31699	Sequence 31699, A
37	32	84.2	224 4 US-09-465-901-30	Sequence 30, Appl
38	32	84.2	379 4 US-09-252-991A-26255	Sequence 26255, A
39	32	84.2	745 2 US-08-887-518-3	Sequence 3, Appl
40	32	84.2	745 2 US-09-023-321-3	Sequence 3, Appl
41	32	84.2	745 2 US-08-890-853-4	Sequence 4, Appl
42	32	84.2	745 2 US-09-032-475-3	Sequence 3, Appl
43	32	84.2	745 2 US-09-099-125A-4	Sequence 4, Appl
44	32	84.2	745 2 US-09-099-124A-4	Sequence 4, Appl
45	32	84.2	745 3 US-09-032-476-4	Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-08-311-731A-69  
Sequence 69, Application US/08311731A  
Patent No. 6583266  
GENERAL INFORMATION:  
APPLICANT: SMITH, DOUGLAS  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAMPRAE FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 411  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,731A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: GATES, EDWARD R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: C0044/7125  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/720-3500  
TELEFAX: 617/720-2441  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 196 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULAR TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: MYCOBACTERIUM LAMPRAE  
US-08-311-731A-69

Query Match 92.1%; Score 35; DB 4; Length 196;  
Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0;  
QY 1 LAMSWL 6

Db 109 VAMSWL 114

## RESULT 2

US-08-311-731A-319  
Sequence 319, Application US/08311731A  
Patent No. 6583266  
GENERAL INFORMATION:  
APPLICANT: SMITH, DOUGLAS  
APPLICANT: MOO, JEN-I  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 411  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,731A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: GATES, EDWARD R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: C0044/7125  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/720-3500  
TELEFAX: 617/720-2441  
INFORMATION FOR SEQ ID NO: 319:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 198 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Mycobacterium leprae  
US-08-311-731A-319

Query Match 92.1%; Score 35; DB 4; Length 198;  
Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
Db 111 VAMSWL 116

RESULT 3  
US-09-205-258-359  
Sequence 359, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT APPLICATION NUMBER: US/09/205,258  
CURRENT FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375

EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15

EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 1227  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 359  
; LENGTH: 56  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (56)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-205-258-359

Query Match 89.5%; Score 34; DB 4; Length 56;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5  
DB 9 LAMSW 13

RESULT 4  
US-08-311-731A-311  
; Sequence 311, Application US/08311731A  
; Patent No. 6583266  
; GENERAL INFORMATION:  
; APPLICANT: SMITH, DOUGLAS  
; APPLICANT: MAO, JEN-I  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR  
; NUMBER OF SEQUENCES: 411  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: WOLF, GREENFIELD & SACKS, P.C.  
; STREET: 600 ATLANTIC AVENUE  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/311,731A  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GATES, EDWARD R.  
; REGISTRATION NUMBER: 31,616  
; REFERENCE/DOCKET NUMBER: C0044/7125  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/720-3500  
; TELEFAX: 617/720-2441  
; INFORMATION FOR SEQ ID NO: 311:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 63 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Mycobacterium leprae  
US-08-311-731A-311

Query Match 89.5%; Score 34; DB 4; Length 63;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AMSWL 6

DB 43 AMSWL 47

RESULT 5  
US-09-252-991A-17325  
; Sequence 17325, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; SEQ ID NO 17325  
; LENGTH: 172  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-17325

Query Match 89.5%; Score 34; DB 4; Length 172;  
Best Local Similarity 100.0%; Pred. No. 2,3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5  
DB 38 LAMSW 42

RESULT 6  
US-09-252-991A-21611  
; Sequence 21611, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 21611  
; LENGTH: 260  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-21611

Query Match 89.5%; Score 34; DB 4; Length 260;  
Best Local Similarity 100.0%; Pred. No. 3,3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5  
DB 186 LAMSW 190

RESULT 7  
US-09-252-991A-31792  
; Sequence 31792, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

```

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31792
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31792

Query Match      89.5%; Score 34; DB 4; Length 269;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 LAWSWL 6
Db      232 LAWGWL 237

RESULT 8
US-09-634-238-334
; Sequence 334, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christensen, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; TITLE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.104311
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 334
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(280)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-634-238-334

Query Match      89.5%; Score 34; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAWSW 5
Db      170 LAWSW 174

RESULT 9
US-09-252-991A-28418
; Sequence 28418, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
```

```

; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28418
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28418

Query Match      89.5%; Score 34; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAWSW 5
Db      80 LAWSW 84

RESULT 10
US-09-339-159B-22
; Sequence 22, Application US/09339159B
; Patent No. 6566114
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Markus
; APPLICANT: Schuelein, Martin
; APPLICANT: Schmoor, Kirtk
; APPLICANT: Andersen, Lene
; APPLICANT: Bjornvad, Mads
; TITLE OF INVENTION: No. 6566114e1 Mannanases
; FILE REFERENCE: 5440.204-US
; CURRENT APPLICATION NUMBER: US/09/339,159B
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 22
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-339-159B-22

Query Match      89.5%; Score 34; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAWSW 5
Db      276 LAWSW 280

RESULT 11
US-09-339-159B-12
; Sequence 12, Application US/09339159B
; Patent No. 6566114
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Markus
; APPLICANT: Schuelein, Martin
; APPLICANT: Schmoor, Kirtk
; APPLICANT: Andersen, Lene
; APPLICANT: Bjornvad, Mads
; TITLE OF INVENTION: No. 6566114e1 Mannanases
; FILE REFERENCE: 5440.204-US
; CURRENT APPLICATION NUMBER: US/09/339,159B
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 331
; TYPE: PRT
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/ ORGANISM: Bacillus sp.AA12
US-09-339-159B-12

Query Match      89.5%; Score 34; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAMSW 5
        |||||
        281 LAMSW 285

RESULT 12
US-09-252-991A-23948
; Sequence 23948, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23948
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23948

Query Match      89.5%; Score 34; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ANSWL 6
        |||||
        247 ANSWL 251

RESULT 13
US-09-252-991A-26240
; Sequence 26240, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26240
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26240

Query Match      89.5%; Score 34; DB 4; Length 343;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAMSW 5
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        299 LAMSW 303
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```
RESULT 14
US-09-339-159B-16
; Sequence 16, Application US/09339159B
; Patent No. 6566114
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Markus
; APPLICANT: Schuilein, Martin
; APPLICANT: Schmoor, Kirk
; APPLICANT: Andersen, Lene
; APPLICANT: Bjornvad, Mads
; TITLE OF INVENTION: No. 6566114el Mannanases
; FILE REFERENCE: 5440.204-US
; CURRENT APPLICATION NUMBER: US/09/339,159B
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-339-159B-16

Query Match      89.5%; Score 34; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAMSW 5
        |||||
        318 LAMSW 322

RESULT 15
US-09-485-648-4
; Sequence 4, Application US/09485648
; Patent No. 6376445
; GENERAL INFORMATION:
; APPLICANT: Bettiol, Jean-Luc P.
; APPLICANT: Showell, Michael S.
; TITLE OF INVENTION: Detergent Compositions Comprising a Mannanase and a
; FILE REFERENCE: Mannanase and protease
; CURRENT APPLICATION NUMBER: US/09/485,648
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: PCT/US98/11996
; PRIOR FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-485-648-4

Query Match      89.5%; Score 34; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LAMSW 5
        |||||
        280 LAMSW 284

Search completed: February 18, 2004, 14:41:47
Job time : 8.06579 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds  
(without alignment)  
79.423 Million cell updates/sec

Title: US-09-643-260-7  
Perfect score: 38  
Sequence: 1 LAMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	89.5	338	1	GALE MYCPN
2	34	89.5	1239	1	POLS_EEBV
3	34	89.5	1240	1	POLS_EEBV
4	34	89.5	1402	1	NIGO_MOUSE
5	33	86.8	118	1	YEL6_HAEIN
6	33	86.8	685	1	RORI_DROME
7	33	86.8	1053	1	HMDH_SCHPO
8	33	86.8	1564	1	N184_SCHPO
9	32	84.2	60	1	YMRP_ECOLI
10	32	84.2	107	1	YMRP_RHILLO
11	32	84.2	136	1	Y07C_BPT4
12	32	84.2	252	1	Y410_RHISN
13	32	84.2	446	1	N14M_CERCA
14	32	84.2	471	1	MEUB_ENTAE
15	32	84.2	471	1	MEUB_KLEPV
16	32	84.2	586	1	S132_MOUSE
17	32	84.2	587	1	S132_MOUSE
18	32	84.2	592	1	S132_MOUSE
19	32	84.2	745	1	IKKA_HUMAN
20	32	84.2	745	1	IKKA_MOUSE
21	32	84.2	756	1	IKKB_HUMAN
22	32	84.2	757	1	IKKB_MOUSE
23	32	84.2	757	1	IKKB_MOUSE
24	32	84.2	842	1	AMPN_LACDL
25	32	84.2	981	1	RRPO_AHNNV
26	32	84.2	982	1	RRPO_GNNV
27	31	81.6	51	1	LHB2_ECTHA
28	31	81.6	53	1	LHB1_ECTHA
29	31	81.6	54	1	LHB6_RHOAC
30	31	81.6	54	1	LHB7_RHOAC
31	31	81.6	247	1	Y0B3_YEAST
32	31	81.6	255	1	UNG_HSV2
33	31	81.6	262	1	CTE2_MOUSE

34	31	81.6	278	1	CVST_SYNF7
35	31	81.6	300	1	Y223_HAEIN
36	31	81.6	326	1	N1JM_ASTER
37	31	81.6	343	1	YSC2_THERM
38	31	81.6	367	1	NODX_RHILV
39	31	81.6	443	1	PD6C_BRANA
40	31	81.6	447	1	PD6C_SPIOL
41	31	81.6	448	1	PD6C_ARATH
42	31	81.6	467	1	S1L5_MOUSE
43	31	81.6	483	1	VE2_HPV14
44	31	81.6	493	1	VE2_HPV19
45	31	81.6	497	1	VE2_HPV20

## ALIGNMENTS

## RESULT 1

GALE\_MYCPN STANDARD, PRT, 338 AA.  
AC P75517;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE UDP-glucose 4-epimerase (EC 5.1.3.2) (Galactosyltransferase) (UDP-galactose 4-epimerase).  
GN GALE OR MPN257 OR MP576.  
OS Mycoplasma pneumoniae.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
OX NCBI\_TaxID=2104;

RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 29342 / M129;  
RX MEDLINE=97105885; PubMed=8948633;  
RA Himmelfreuch R., Hilbert H., Piagens H., Pirkl E., Li B.-C., Herrmann R.;

RT "Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae";  
RL Nucleic Acids Res. 24:4420-4449(1996).  
CC -1- CATALYTIC ACTIVITY: UDP-glucose = UDP-galactose.  
CC -1- COFACTOR: NAD.

CC -1- PATHWAY: Galactose metabolism; third step.  
CC -1- SUBUNIT: Homodimer (By similarity).  
CC -1- SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY.

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CC -----  
DR EMBL; AE000056; AAB96224.1; -  
DR PIR; S73902; S73902.  
DR HSSP; P09147; IRVS.  
DR InterPro; IPR001509; Epimerase\_Dh.  
DR InterPro; IPR005886; GALE.  
DR Pfam; PF01370; Epimerase; 1.  
DR TIGRfam; TIGR01179; gale; 1.  
KW Isomerase; NAD; Galactose metabolism; Complete proteome.  
KW NP\_BIND  
FT NAD (POTENTIAL).  
SQ SEQUENCE 338 AA; 38132 MW; 9C50FF3B5E68C03 CRC64;

Query Match 89.5%; Score 34; DB 1; Length 338;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
DB 244 LAMSWL 249

RESULT 2  
ID POLS\_EEEV STANDARD; PRT; 1239 AA.  
AC P08768;  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 01-NOV-1988 (Rel. 40, Last annotation update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Structural polypeptide (P130) [contains: Coat protein C (EC 3.4.21.-)  
DE (Capid protein C); Spike glycoprotein E3; Spike glycoprotein E2;  
DE 6 kDa peptide; Spike glycoprotein E1].  
OS Eastern equine encephalitis virus (Eastern equine encephalomyelitis  
OS virus).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
OC Alphavirus.  
OX NCBI\_Taxid=11021;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=82V-2137;  
RX MEDLINE=87282265; PubMed=2886548;  
RA Chang G.-J.J., Trent D.W.;  
RT "Nucleotide sequence of the genome region encoding the 26S mRNA of  
RT eastern equine encephalomyelitis virus and the deduced amino acid  
RT sequence of the viral structural proteins.";  
RL J. Gen. Virol. 68:2129-2142(1987).  
CC -1- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.  
CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.  
CC -1- MISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL  
CC SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL  
CC HEMAGGLUTININ.  
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.  
CC -----  
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CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL: X05816; CAA29261.1; -  
CC PIR: A26816; VHWVEE.  
CC HSSP: P03315; 1VCP.  
CC DR MEROPS; S03.001; -  
CC DR InterPro; IPR002548; Alpha\_E1\_glycop.  
CC DR InterPro; IPR000936; Alpha\_E2\_glycop.  
CC DR InterPro; IPR002533; Alpha\_E3\_glycop.  
CC DR InterPro; IPR000930; Togavirin.  
CC DR Pfam; PF00944; Alpha\_core; 1.  
CC DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
CC DR Pfam; PF00943; Alpha\_E2\_glycop; 1.  
CC DR Pfam; PF01563; Alpha\_E3\_glycop; 1.  
CC DR PRINTS; PR00798; TOGAVIRIN.  
CC KM Coat protein; Polypeptide; Transmembrane; Glycoprotein; Hydrolase;  
CC Serine protease.  
CC -----  
CC CHAIN 1 259 COAT PROTEIN C.  
CC FT CHAIN 260 322 SPIKE GLYCOPROTEIN E3.  
CC FT CHAIN 323 742 SPIKE GLYCOPROTEIN E2.  
CC FT CHAIN 743 798 6 kDa PEPTIDE.  
CC FT CHAIN 799 1239 SPIKE GLYCOPROTEIN E1.  
CC FT ACT\_SITE 136 136 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC FT ACT\_SITE 142 142 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC FT ACT\_SITE 210 210 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC FT TRANSMEM 261 277 POTENTIAL.  
CC FT TRANSMEM 684 701 POTENTIAL.  
CC FT TRANSMEM 727 737 POTENTIAL.  
CC FT TRANSMEM 777 798 POTENTIAL.  
CC FT TRANSMEM 1211 1235 POTENTIAL.  
CC FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC FT CARBOHYD 932 932 N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC SEQUENCE 1239 AA; 137431 MW; 8C764A405D2D41C CRC64;  
Query Match 89.54; Score 34; DB 1; Length 1239;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 2 AWSML 6  
Db 1205 AWSML 1209  
RESULT 3  
ID POLS\_EEEV STANDARD; PRT; 1240 AA.  
AC P27284;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Structural polypeptide (P130) [contains: Coat protein C (EC 3.4.21.-)  
DE (Capid protein C); Spike glycoprotein E3; Spike glycoprotein E2;  
DE 6 kDa peptide; Spike glycoprotein E1].  
OS Eastern equine encephalitis virus (strain VA31ten broeck) (Eastern  
OS equine encephalomyelitis virus).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
OC Alphavirus.  
OX NCBI\_Taxid=11022;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91220727; PubMed=2024496;  
RA Weaver S.C., Scott T.W., Rico-Hesse R.;  
RT "Molecular evolution of eastern equine encephalomyelitis virus in  
RT North America.";  
RL Virology 182:774-784(1991).  
CC -1- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.  
CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.  
CC -1- MISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL  
CC SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL  
CC HEMAGGLUTININ.  
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.  
CC -----  
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CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL: M69094; AAA42980.1; -  
CC PIR: A39992; VHWVEV.  
CC HSSP: P03315; 1VCP.  
CC DR MEROPS; S03.001; -  
CC DR InterPro; IPR002548; Alpha\_E1\_glycop.  
CC DR InterPro; IPR000936; Alpha\_E2\_glycop.  
CC DR InterPro; IPR002533; Alpha\_E3\_glycop.  
CC DR InterPro; IPR000930; Togavirin.  
CC DR Pfam; PF00944; Alpha\_core; 1.  
CC DR Pfam; PF01589; Alpha\_E1\_glycop; 1.  
CC DR Pfam; PF00943; Alpha\_E2\_glycop; 1.  
CC DR Pfam; PF01563; Alpha\_E3\_glycop; 1.  
CC DR PRINTS; PR00798; TOGAVIRIN.  
CC KM Coat protein; Polypeptide; Transmembrane; Glycoprotein; Hydrolase;  
CC Serine protease.  
CC -----  
CC CHAIN 1 260 COAT PROTEIN C.  
CC FT CHAIN 261 323 SPIKE GLYCOPROTEIN E3.  
CC FT CHAIN 324 743 SPIKE GLYCOPROTEIN E2.  
CC FT CHAIN 744 799 6 kDa PEPTIDE.  
CC FT CHAIN 800 1240 SPIKE GLYCOPROTEIN E1.  
CC FT ACT\_SITE 137 137 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC FT ACT\_SITE 143 143 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC FT ACT\_SITE 211 211 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC FT TRANSMEM 259 276 POTENTIAL.  
CC FT TRANSMEM 695 712 POTENTIAL.  
CC FT TRANSMEM 722 738 POTENTIAL.  
CC FT TRANSMEM 781 799 POTENTIAL.  
CC TRANSMEM 1212 1236 POTENTIAL.



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FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 638 638 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 834 834 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 933 933 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1240 AA; 137290 MW; ABBE81599D083045 CRC64;

Query Match
Best Local Similarity 89.5%; Score 34; DB 1; Length 1240;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AWSWL 6
DB 1206 AWSWL 1210

RESULT 4
N160_MOUSE
ID N160_MOUSE STANDARD; PRT; 1402 AA.
AC 0920M3; 09CZD9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Nuclear pore complex protein Nup160 (Nucleoporin Nup160) (160 kDa
DE nucleoporin) (Gene trap locus N160) (GTL-13).
GN NUP160 OR GTL-13 OR KIA0197.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Van de Putte T., Cozijnsen M., Dewulf N., Tydzanowski P., Lemny O.,
RA Huybrecock D.;
RT KIA0197 gene (D8J781), complete cds.; similar to human
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

[2]
SEQUENCE OF 1151-1402 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Niemi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gasteirland T., Glassl C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldi M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hall D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hasehizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).

[3]
IDENTIFICATION, SUBUNIT, AND SUBCELLULAR LOCATION.
RX MEDLINE=21448620; PubMed=11564755;
RA Belagere N., Rabut G., Bai S.W., van Overbeek M., Beaudouin J.,
RA Elieberg J., Zaccagna O.V., Pasteau F., Labas V., Fromont-Racine M.,
RA "An evolutionarily conserved NPC subcomplex, which redistributes in
RT part to kinetochores in mammalian cells.";
RL J. Cell Biol. 154:1147-1160(2001).

[4]
IDENTIFICATION, FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
RX MEDLINE=21541555; PubMed=11584705;

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RA Vasu S., Shah S., Orjalo A., Park M., Fischer W.H., Forbes D.J.;
RT "Novel vertebrate nucleoporins Nup133 and Nup160 play a role in mRNA
RT export.";
RL J. Cell Biol. 155:339-354(2001).
CC -1- SUBUNIT: Involved in poly(A)+ RNA transport.
CC -1- SUBUNIT: Forms part of the Nup160 subcomplex in the nuclear pore
CC which is composed of Nup160, Nup133, Nup107 and Nup96. This
CC complex plays a role in RNA export and in tethering Nup8 and
CC Nup153 to the nucleus.
CC -1- SUBCELLULAR LOCATION: Nuclear pore complex.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to a
CC frameshift in position 1157 and a stop codon in position 1396.
CC -----
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CC -----
DR EMBL; AF104415; AAD17922.2;
DR EMBL; AK012715; BAB28429.1; ALT_FRAME.
DR MGI; MGI:1926227; Nup160.
DR GO; GO:0005643; C:nuclear pore; IDA.
DR GO; GO:0005487; F:nucleocytoplasmic transporter activity; IDA.
DR GO; GO:0006406; P:mRNA-nucleus export; IDA.
KW Nuclear protein; Transport.
FT CONFLICT 1156 1156 A -> T (IN REF. 2).
FT CONFLICT 1314 1314 E -> G (IN REF. 2).
FT CONFLICT 1368 1368 N -> D (IN REF. 2).
SQ SEQUENCE 1402 AA; 158230 MW; 3BF5D9F057D28772 CRC64;

Query Match
Best Local Similarity 89.5%; Score 34; DB 1; Length 1402;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AWSWL 6
DB 1230 AWSWL 1234

RESULT 5
YE16_HAEIN
ID YE16_HAEIN STANDARD; PRT; 118 AA.
AC P4418;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein H11416 precursor.
GN H11416.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxId=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KM20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fletschmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Wierick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fielde C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Pine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Frazer C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RL Rd.";
RL Science 269:496-512(1995).

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CC -----  
 CC EMBL; U34821; AAC23067.1; -  
 CC DR PIR; I64028; I64028.  
 CC DR TIGR; H1416; -  
 CC DR InterPro; IPR006481; holin\_lambda.  
 CC DR Pfam; PF05106; Phage\_holin\_3\_1.  
 CC DR TIGR/Pfam; TIGR01594; holin\_lambda; 1.  
 CC KW Hypothetical protein; Signal; Complete proteome.  
 CC FT SIGNAL 1 27 POTENTIAL.  
 CC FT CHAIN 28 118 HYPOTHETICAL PROTEIN H1416.  
 CC SQ SEQUENCE 118 AA; 13516 MW; 96CE5D469D8E2B CRC64;

Query Match 86.8%; Score 33; DB 1; Length 118;  
 Best Local Similarity 83.3%; Pred. No. 63;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAWSWL 6  
 Db 11 LINSWL 16

RESULT 6  
 ID ROR1 DROME STANDARD; PRT; 685 AA.  
 AC Q24486;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase transmembrane receptor Ror precursor  
 DE (EC 2.7.1.112) (drom).  
 GN ROR OR CG4926.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.  
 RC STRAIN=Canton-S; TISSUE=Larval brain;  
 RX MEDLINE=9334822; PubMed=8394009;  
 RA Wilson C., Goeberghen D.C.I., Steller H.;  
 RT "Ror, a potential neurotrophic receptor gene, encodes a Drosophila  
 RT homolog of the vertebrate Ror family of Trk-related receptor tyrosine  
 RT kinases.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7109-7113(1993).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams W.D., Celikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.C., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Peiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Anli J.F., Agbayani A., An H.-U., Andrews-Plannoch C., Baldwin D.,  
 RA Bailly R.M., Baau L.E., Bakendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Borchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis J.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke S., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fierliera S., Fleischmann W.,  
 RA Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heitman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jajali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Jialali B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laspo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mikhina N.V., Mobarry C., Morris J., Mohtrefi A.,  
 RA Mount S.M., Koy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paclet J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,  
 RA Svitckas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RA "The genome sequence of Drosophila melanogaster.";  
 RA Science 287:2185-2195(2000).  
 RL [3]  
 RP SEQUENCE OF 545-597 FROM N.A.  
 RX MEDLINE=98401146; PubMed=9731193;  
 RA Oates A.C., Kollberg P., Achen M.G., Wilks A.F.;  
 RT "Sampling the genomic pool of protein tyrosine kinase genes using the  
 RT polymerase chain reaction with genomic DNA."  
 RL Biochem. Biophys. Res. Commun. 249:660-667(1998).  
 CC CC -1- FUNCTION: Tyrosine-protein kinase receptor that functions during  
 CC early stages of neuronal development.  
 CC CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein.  
 CC CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC CC -1- TISSUE SPECIFICITY: Expressed in neurons of the developing nervous  
 CC system.  
 CC CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. ROR  
 CC SUPRAMITY.  
 CC CC -1- SIMILARITY: Contains 1 frizzled (FZ) domain.  
 CC CC -1- SIMILARITY: Contains 1 kringle domain.  
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CC -----  
 CC EMBL; I20297; AAA28860.1; -  
 CC EMBL; AE003626; AAF52885.1; -  
 CC EMBL; AJ002908; CAA05743.1; -  
 CC DR PIR; A48289; A48289.  
 CC DR HSSP; P11362; 1FGK.  
 CC DR FLYBASE; FBgn0010407; Ror.  
 CC GO; GO:0016023; C:integral to membrane; NAS.  
 CC DR GO; GO:0004713; P:protein tyrosine kinase activity; NAS.  
 CC DR GO; GO:0007417; P:central nervous system development; IEP.  
 CC DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.  
 CC DR InterPro; IPR000024; Pz domain.  
 CC DR InterPro; IPR000001; Kringle.  
 CC DR InterPro; IPR000719; Prot kinase.  
 CC DR InterPro; IPR002011; RTKinaseII.  
 CC DR InterPro; IPR001245; Tyr\_kinase.  
 CC DR Pfam; PF00051; kringle; 1.  
 CC DR Pfam; PF00069; pkinase; 1.  
 CC DR PRINTS; PR00018; KRINGLE.  
 CC DR PRINTS; PR00109; TYRKINASE.  
 CC DR PRODOM; PD000395; TyKingle; 1.  
 CC DR PRODOM; PD000001; Prot\_kinase; 1.  
 CC DR SMART; SM00130; KR; 1.  
 CC DR SMART; SM00139; TYRK; 1.  
 CC DR PROSITE; PS50038; FZ; 1.  
 CC DR PROSITE; PS50021; KRINGLE\_1; 1.  
 CC DR PROSITE; PS50070; KRINGLE\_2; 1.

DR	PROSITE; PS00107;	PROTEIN_KINASE_ATP; 1.
DR	PROSITE; P550011;	PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00109;	PROTEIN_KINASE_TYR; 1.
DR	PROSITE; PS00239;	RECEPTOR_TYR_KIN_II; 1.
KM	Transferrase; Kinase;	Tyrosine-protein kinase; ATP-binding; Receptor
KM	Transmembrane; Signal;	Glycoprotein; Kringles; Phosphorylation;
KM	Developmental protein.	
FT	SIGNAL	1 24
FT	CHAIN	25 685
FT	POTENTIAL.	
FT	TYROSINE-PROTEIN KINASE TRANSMEMBRANE RECEPTOR FOR EXTRACELLULAR POTENTIAL.	
FT	POTENTIAL.	
FT	CYTOSOLASMIC (POTENTIAL) . P.	
FT	KRINGLE.	
FT	PROTEIN KINASE.	
FT	ATP (BY SIMILARITY) .	
FT	ATP (BY SIMILARITY) .	
FT	BY SIMILARITY.	
FT	PHOSPHORYLATION (AUTO-) (BY SIMILARITY)	
FT	MOD_RES	565 565
FT	MOD_RES	569 569
FT	MOD_RES	570 570
FT	MOD_RES	570 570
FT	CARBOHYD	45 45
FT	CARBOHYD	63 63
FT	CARBOHYD	129 129
FT	CARBOHYD	144 144
FT	CARBOHYD	250 250
SO	SEQUENCE	685 AA; 78142 MM; 526162D27D5FD7C7 CRC64;

Query Match	86.8%	Score 33	DB 1	Length 685
Best Local Similarity	83.3%	Pred. No. 3.1e+02		
Matches	5	Conservative	0	Mismatches 1
			Indels	0
			Gaps	0

QY	1	LAWSWL	6
Db	259	LRMSWL	264

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RESULT 7
HMDH_SCHPO
ID _HMDH_SCHPO STANDARD; PRT; 1053 AA.
AC Q10283; 074425;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34) (HMG-CoA reductase).
GN HMG1 OR SPCCL162.09C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RM
RX MEDLINE FROM N.A.
RX MEDLINE=97051601; Pubmed=88962278;
RA Lam P. Y., Edwards S., Wright R.;
RT "Molecular, functional and evolutionary characterization of the gene encoding HMG-CoA reductase in the fission yeast, Schizosaccharomyces pombe." ;
RT Yeast 12:1107-1124(1996).
RL [2]
RN
RM
RX MEDLINE FROM N.A.
RX STRAIN=972;
RA MEDLINE=21848401; Pubmed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Scourse J., Peat N., Hayles J., Baker S., Baeham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

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Holroyd S., Hornaby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
RA James J., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
RA Oliver K., O'Neill S., Pearson S., Saunders D., Quail M.A., Rabinowitsch E.,  
RA Rathford K., Rutter S., Sanders D., Seeger K., Sharp S.,  
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
RA Woodward J., Voickert G., Art R., Robben J., Gymnopoulos B.,  
RA Meltons I., Vansteete E., Rieser W., Schaefer M., Mueller-Auer S.,  
RA Gabel C., Fuchs M., Filicz C., Holzer E., Moselt D., Hilbert H.,  
RA Bozaym K., Langner I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
RA Egger P., Zimmermann W., Wedler H., Wambut R., Purnelle B.,  
RA Goifeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S.,  
RA Gallibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Lucas M., Roche M., Gallardin C., Tallada V.A., Garzon A., Thode G.,  
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,  
RA Cerutti L., Lowe T., McCormie W.R., Paulsen I., Potashkin J.,  
RA Shipakovski G.V., Usery D., Barrett B.G., Nurse P.;  
RT "The genome sequence of *Schistosaccharomyces pombe*.";  
RL Nature 415:871-880(2002).  
CC -I- FUNCTION: INVOLVED IN THE CONTROL OF CHOLESTEROL BIOSYNTHESIS. IT  
IS THE RATE-LIMITING ENZYME OF THE STEROL BIOSYNTHESIS.  
CC -I- CATALYTIC ACTIVITY: (R)-mevalonate + CoA + 2 NADP(+) = (S)-3-  
hydroxy-3-methylglutaryl-CoA + 2 NADPH.  
CC CC -I- PATHWAY: Cholesterol biosynthesis.  
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
reticulum.  
CC  
CC -I- SIMILARITY: BELONGS TO THE HMG-COA REDUCTASE FAMILY.  
-----  
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DR EMBL; AL76979; BAB32977.1; -.  
DR EMBL; U702360; CAB19589.1; -.  
DR PIR; S72194; S72194.  
DR GeneDB Spombe; SPCC162.09c; -.  
DR InterPro; IPRO042202; HMGC\_COA\_red.  
DR InterPro; IPRO04554; HMGC\_COA\_R\_NADP.  
DR InterPro; IPRO00731; SSD\_5TM.  
DR Pfam; PF00368; HMGC\_COA\_red; 1.  
DR PRINTS; PR00071; HMGCOARDPASE.  
DR TIGRFAMs; TIGR00533; HMGC\_COA\_R\_NADP; 1.  
DR PROSITE; PS00066; HMGC\_COA\_REDUCTASE\_1; 1.  
DR PROSITE; PS00318; HMGC\_COA\_REDUCTASE\_2; 1.  
DR PROSITE; PS01192; HMGC\_COA\_REDUCTASE\_3; FALSE\_NEG.  
DR PROSITE; PS50065; HMGC\_COA\_REDUCTASE\_4; 1.  
DR PROSITE; PS50156; SSD; 1.  
CM Oxidoreductase; Glycoprotein; Endoplasmic reticulum; Transmembrane;  
CW cholesterol biosynthesis; NADP.  
FT DOMAIN 1 547 MEMBRANE-BOUND.  
FT DOMAIN 2 548  
FT DOMAIN 3 615  
FT DOMAIN 4 616  
FT TRANSMEM 9 1053 POTENTIAL.  
FT TRANSMEM 204 224 POTENTIAL.  
FT TRANSMEM 253 253 POTENTIAL.  
FT TRANSMEM 259 279 POTENTIAL.  
FT TRANSMEM 321 341 POTENTIAL.  
FT TRANSMEM 342 362 POTENTIAL.  
FT TRANSMEM 418 438 POTENTIAL.  
FT TRANSMEM 527 547 POTENTIAL.  
FT ACT\_SITE 712 712 BY SIMILARITY.  
FT ACT\_SITE 922 922 BY SIMILARITY.  
FT ACT\_SITE 1018 1018 GENERAL BASE (BY SIMILARITY).  
FT CARBOHYD 137 137 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 339 339 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 518 518 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 578 578 N-LINKED (GLCNAC... ) (POTENTIAL).

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FT CARBOHYD 776 776 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1022 1022 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 751 751 N -> D (IN REF. 1).
SQ SEQUENCE 1053 AA; 114876 MW; 335EC2365222D238 CRC64;

Query Match
Best Local Similarity 86.8%; Score 33; DB 1; Length 1053;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
DB 177 ISMSWL 182

RESULT 8
ID N184 SCHPO STANDARD; PRT; 1564 AA.
AC 09P7M6; 09Y6G4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nucleoporin nup184 (Nuclear pore protein nup184).
GN NUP184 OR SPAP27G11.10C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
RC STRAIN=972;
RC MEDLINE=99318821; PubMed=10388805;
RT "Regulation of mRNA export by nutritional status in fission yeast.";
RL Genes 152:827-838(1999).

[2]
RN SEQUENCE FROM N.A.
RC STRAIN=972;
RC MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Scoufou J., Peat N., Hayles J., Baker S., Baaham D., Bowman S.,
RA Brooke K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Frazer A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jasele K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rablinoiwisch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Snelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Voicikert G., Aert R., Robben J., Gymnopoulos B.,
RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritsch C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehman H., Reinhard R., Pohl T.M.,
RA Beyer P., Zimmermann W., Wedler R., Wambut R., Burnell B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,
RA Galliard F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rocher M., Galliard C., Tallada V.A., Garzon A., Thode J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
RA Sgarbi L., Lowe T., McCombie M.R., Paulsen I., Pochanin J.,
RA Sgarbi L., Lowe T., McCombie M.R., Paulsen I., Pochanin J.,
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).

-1- FUNCTION: INTERACTS WITH POM152 IN THE CORE STRUCTURE OF THE
NUCLEAR PORE COMPLEX (NPC). INVOLVED IN THE EXPORT OF MRNA.

-1- SUBCELLULAR LOCATION: Nuclear pore complex.

-1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 1560
ONWARD AND IS LONGER (1628 AA) DUE TO A FRAMESHIFT.

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CC -----
DR EMBL; AF055035; AAD3830.1; ALT_FRAME.
DR EMBL; AL157917; CAB76031.1; -.
DR GeneDB Spombe; SPAP27G11.10C; -.
KW Nuclear protein; Transport.
FT CONFLICT 1219 1219
SQ SEQUENCE 1564 AA; 176962 MW; 248F3A5F338C30B7 CRC64;

Query Match
Best Local Similarity 86.8%; Score 33; DB 1; Length 1564;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6
DB 6 LMSWI 11

RESULT 9
ID YMR_ECOLI STANDARD; PRT; 60 AA.
AC P75979;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ymr.
GN YMR OR B1150.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RC MEDLINE=97426617; PubMed=9278503;
RA Blatney F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirtpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.,
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).

[2]
RN SEQUENCE FROM N.A.
RC STRAIN=K12;
RC MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sano G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horichi T.,
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map."
RL DNA Res. 3:137-155(1996).

-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

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CC -----
DR EMBL; AE000214; AAC74234.1; -.
DR EMBL; D90749; BAA35976.1; -.
DR EMBL; D90750; BAA35988.1; -.
DR PIR; C64860; C64860.
DR EcoGene; BGI4336; ymr.

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KM Hypothetical protein; Transmembrane; Complete proteome.  
 PT TRANSMEM 5 25 POTENTIAL.  
 DT 26 46  
 SQ SEQUENCE 60 AA; 6381 MW; A41487AAFEED364A CRC64;  
 Query Match 84.2%; Score 32; DB 1; Length 60;  
 Best Local Similarity 83.3%; Pred. No. 47;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
 DB 39 LFWSWL 44

RESULT 10  
 ID YNFA\_RH1LO STANDARD; PRT; 107 AA.  
 AC 0984U2;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical protein ml17841.  
 GN ML17841.  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Mesorhizobium.  
 OK NCBI\_TaxID=381;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAFP303099;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneo T., Nakamura Y., Sato S., Asami T., Sasaki S.,  
 RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,  
 RA Takuchi C., Yamada M., Tabata S.;  
 RA "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 Mesorhizobium loti";  
 RT DNA Res. 7:331-338(2000).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE UPF0060 FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; APO03012; BAB54221.1; -;  
 DR HAMAP; MF\_00010; -; 1.  
 DR InterPro; IPR003844; UPF0060.  
 DR Pfam; PF02694; UPF0060; 1.  
 DR ProDom; PD015609; UPF0060; 1.  
 KW Hypothetical protein; Transmembrane; Complete proteome.  
 FT TRANSMEM 4 24 POTENTIAL.  
 FT TRANSMEM 30 50 POTENTIAL.  
 FT TRANSMEM 60 80 POTENTIAL.  
 FT TRANSMEM 87 107 POTENTIAL.  
 SQ SEQUENCE 107 AA; 11591 MW; 0C666D5221C16C3 CRC64;

Query Match 84.2%; Score 32; DB 1; Length 107;  
 Best Local Similarity 83.3%; Pred. No. 80;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
 DB 71 LAMWML 76

RESULT 11  
 Y07C\_BPT4

ID Y07C\_BPT4 STANDARD; PRT; 136 AA.  
 AC P13323;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical 16.0 kDa protein in segB-1pt intergenic region (ORF3).  
 GN Y07C ORF1-2 OR TRNA3.  
 OS Bacteriophage T4.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
 OC T4-like viruses.  
 OK NCBI\_TaxID=10665;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86037230; PubMed=4057254;  
 RA Broda J., Abelson J.;  
 RT "Sequence organization and control of transcription in the  
 RT bacteriophage T4 RNA region";  
 RL J. Mol. Biol. 185:545-563(1985).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RA Kuter E., Aizawa F., Kunitawa T., Tugita A., Mosig G.,  
 RA Mesyanzhinov V., Ruger W., Stidham T., Thomas E.;  
 RT "Bacteriophage T4 genome analysis";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 CC -----  
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 CC -----  
 CC EMBL; X03016; CAA26805.1; -;  
 DR EMBL; AF158101; AAP42681.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 136 AA; 16034 MW; 02ED3B4D6D274D9A CRC64;

Query Match 84.2%; Score 32; DB 1; Length 136;  
 Best Local Similarity 80.0%; Pred. No. 1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AMSWL 6  
 DB 35 AMSWL 39

RESULT 12  
 ID Y410\_RH1SN STANDARD; PRT; 252 AA.  
 AC P55498;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Hypothetical 28.6 kDa protein Y410.  
 GN Y410.  
 OS Rhizobium sp. (strain NGR234).  
 OG Plasmid sym pNGR234a.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.  
 OK NCBI\_TaxID=394;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97305956; PubMed=9163424;  
 RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,  
 RA Perret X.;  
 RT "Molecular basis of symbiosis between Rhizobium and legumes";  
 RL Nature 387:394-401(1997).  
 CC -1- SIMILARITY: LOW SIMILARITY TO THE IS111A/IS128/IS153 FAMILY OF  
 CC TRANSPOSASES.  
 CC -1- SIMILARITY: HIGH TO F13; SOME, TO Y4PF/Y4SB AND Y4QE.  
 CC -----  
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 CC -----  
 DR EMBL; A500079; AAB91710.1; -;  
 DR InterPro; IPR003346; Transposase\_20;  
 DR Pfam; PF02371; Transposase\_20; 1;  
 KM Hypothetical protein, Plasmid.  
 SO SEQUENCE 252 AA; 28552 MW; D993C7DA03E15190 CRC64;

Query Match 84.2%; Score 32; DB 1; Length 252;  
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAWSWL 6  
 DB 190 LAWSWL 195

## RESULT 13

NTM\_CERCA STANDARD; PRT; 446 AA.  
 ID NTM\_CERCA  
 AC Q34048; Q34053;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).  
 GN ND4.  
 OS Ceratitidis capitata (Mediterranean fruit fly).  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Tephritidae; Tephritidae; Ceratitidis.  
 OK NCBI\_TaxId=7213;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Gatcemala laboratory colony, and Hawaii laboratory colony;  
 RX MEDLINE=95261546; PubMed=7742977;  
 RA Gasparich G.E., Sheppard W.S., Han H.Y., McPherson B.A., Steck G.J.;  
 RT "Analysis of mitochondrial DNA and development of PCR-based  
 RT diagnostic molecular markers for Mediterranean fruit fly (Ceratitidis  
 RT capitata) populations.";  
 RL Insect Mol. Biol. 4:61-67(1995).  
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
 CC -----  
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 CC -----  
 DR EMBL; U12925; AAA85797.1; -;  
 DR EMBL; U12924; AAA85796.1; -;  
 DR InterPro; IPR003918; NADH-ub oxred4.  
 DR InterPro; IPR001750; Oxidored\_g1.  
 DR InterPro; IPR000260; Oxidored\_g5\_N.  
 DR Pfam; PF00361; oxidored\_g1; 1.  
 DR Pfam; PF01059; oxidored\_g5\_N; 1.  
 KM PRINTS; PR01437; NUOXDRDTRASE4.  
 KM Oxidoreductase; NAD; Ubiquinone; Mitochondrion.  
 SO SEQUENCE 446 AA; 50967 MW; E9AAAC06796897FD CRC64;

Query Match 84.2%; Score 32; DB 1; Length 446;  
 Best Local Similarity 66.7%; Pred. No. 2.9e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LAWSWL 6  
 DB 190 LAWSWL 195

DB 374 VSWSWL 379

## RESULT 14

MEIB\_ENTAB STANDARD; PRT; 471 AA.  
 ID MEIB\_ENTAB  
 AC 007366;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Melibiose carrier protein (Thiomethylgalactoside permease II)  
 DE (Melibiose permease) (Na+ (Li+)/melibiose symporter) (Melibiose  
 DE transporter).  
 GN MEIB.  
 OS Enterobacter aerogenes (Aerobacter aerogenes).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Enterobacter.  
 OK NCBI\_TaxId=546;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97332569; PubMed=9188803;  
 RA Okazaki N., Kuroda M., Shimamoto T., Tsuchiya T.;  
 RT "Characteristics of the melibiose transporter and its primary  
 RT structure in Enterobacter aerogenes.";  
 RL Biochim. Biophys. Acta 1326:83-91(1997).  
 CC -1- FUNCTION: PROTEIN RESPONSIBLE FOR MELIBIOSE TRANSPORT. IT IS  
 CC CAPABLE OF USING HYDROGEN AND LITHIUM CATIONS AS COUPLING CATIONS  
 CC FOR CO-TRANSPORT, DEPENDENT ON THE PARTICULAR SUGAR TRANSPORTED  
 CC (SYMPORT SYSTEM).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.  
 CC -1- SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY  
 CC (SGP).  
 CC -----

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 CC -----

DR EMBL; D86576; BAA20461.1; -;  
 DR InterPro; IPR001927; Na/Gal\_symport.  
 DR TIGRFAMs; TIGR00792; gph; 1.  
 KM PROSITE; PS00872; NA GALACTOSIDE SYMP; 1.  
 DR TRANSFOS; Sugar transport; Transmembrane; Inner membrane; Symport.  
 FT DOMAIN 1 11  
 FT TRANSMEM 12 32  
 FT DOMAIN 33 36  
 FT TRANSMEM 37 57  
 FT DOMAIN 58 79  
 FT TRANSMEM 80 100  
 FT DOMAIN 101 106  
 FT TRANSMEM 107 127  
 FT DOMAIN 128 149  
 FT TRANSMEM 150 170  
 FT DOMAIN 171 175  
 FT TRANSMEM 176 196  
 FT DOMAIN 197 234  
 FT TRANSMEM 235 255  
 FT DOMAIN 256 266  
 FT TRANSMEM 267 287  
 FT DOMAIN 288 296  
 FT TRANSMEM 297 317  
 FT DOMAIN 318 323  
 FT TRANSMEM 324 344  
 FT DOMAIN 345 373  
 FT TRANSMEM 374 394  
 FT DOMAIN 395 411  
 FT TRANSMEM 412 432  
 FT DOMAIN 433 471  
 SO SEQUENCE 471 AA; 52214 MW; 9755D85D91828106 CRC64;

Query Match 84.2%; Score 32; DB 1; Length 471;  
 Best Local Similarity 83.3%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LAMSWL 6  
 ||| ||  
 Db 106 LAMWVL 111

RESULT 15  
 MELB\_KLEPN STANDARD; PRT; 471 AA.

AC 002581;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Melibiose carrier protein (Thiomethylgalactoside permease II)  
 DE (Melibiose permease) (Na+ (Li+)/melibiose symporter) (Melibiose transporter).  
 GN MELB.  
 OS Klebsiella pneumoniae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Klebsiella.  
 OX NCBI\_TaxId=573;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=2002;  
 RX MEDLINE=92406738; PubMed=1339436;  
 RA Hama H., Wilson T.H.;  
 RT "Primary structure and characteristics of the melibiose carrier of  
 Klebsiella pneumoniae";  
 RL J. Biol. Chem. 267:18371-18376(1992).  
 CC -1- FUNCTION: PROTEIN RESPONSIBLE FOR MELIBIOSE TRANSPORT. IT IS  
 CAPABLE OF USING HYDROGEN AND LITHIUM CATIONS AS COUPLING CATIONS  
 FOR CORTRANSPORT, DEPENDING ON THE PARTICULAR SUGAR TRANSPORTED  
 (SYMPORT SYSTEM). IT CATALYZES HYDROGEN CATION-MELIBIOSE, LITHIUM  
 CATION-LACTOSE, & HYDROGEN/LITHIUM CATIONS-METHYL-1-THIO-BETA-D-  
 GALACTOPYRANOSIDE (TMG) CORTRANSPORT. THIS PROTEIN SEEMS TO BE  
 LACKING THE ABILITY TO RECOGNIZE SODIUM CATIONS.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.  
 CC -1- SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY  
 (SGP).  
 CC -----  
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 CC -----  
 DR EMBL; M97257; AAA25067.1; -.  
 DR PIR; B44166; B44166.  
 DR InterPro; IPR001927; Na/Gal\_symport.  
 DR TIGRFBMS; TIGR00792; gph; 1.  
 DR PROSITE; PS00872; NA\_GALACTOSIDE\_SYM; 1.  
 KW Transport; Sugar transport; Transmembrane; Inner membrane; Symport.  
 FT DOMAIN 1 11  
 FT TRANSMEM 12 32 POTENTIAL.  
 FT DOMAIN 33 36 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 37 57 POTENTIAL.  
 FT DOMAIN 58 79 POTENTIAL.  
 FT TRANSMEM 80 100 POTENTIAL.  
 FT DOMAIN 101 106 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 107 127 PERIPLASMIC (POTENTIAL).  
 FT DOMAIN 128 149 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 150 170 POTENTIAL.  
 FT DOMAIN 171 175 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 176 196 POTENTIAL.  
 FT DOMAIN 197 234 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 235 255 POTENTIAL.  
 FT DOMAIN 256 266 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 267 287 POTENTIAL.

FT DOMAIN 288 296 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 297 317 POTENTIAL.  
 FT DOMAIN 318 323 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 324 344 POTENTIAL.  
 FT DOMAIN 345 373 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 374 394 POTENTIAL.  
 FT DOMAIN 395 411 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 412 432 POTENTIAL.  
 FT DOMAIN 433 471 CYTOPLASMIC (POTENTIAL).  
 SQ SEQUENCE 471 AA; 52329 MW; 6D373D098F4BAEC7 CRC64;

Query Match 84.2%; Score 32; DB 1; Length 471;  
 Best Local Similarity 83.3%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LAMSWL 6  
 ||| ||  
 Db 106 LAMWVL 111

Search completed: February 18, 2004, 14:28:05  
 Job time : 4.55263 secs

GenCore version 5.1.6  
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# OM protein - protein search, using ew model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds  
(without alignments)  
87.531 Million cell updates/sec

Title: US-09-643-260-7

Perfect score: 38  
Sequence: 1 LAMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	94.7	675	2 H69200	heavy-metal transp
2	35	92.1	116	2 T03472	conserved hypothet
3	35	92.1	172	2 T51122	crck protein limpo
4	35	92.1	196	2 C87039	conserved hypothet
5	35	92.1	210	2 C70528	hypothetical prote
6	35	92.1	421	2 A12824	NADH dehydrogenase
7	35	92.1	438	2 H97602	probable NADH deny
8	35	92.1	441	2 A13607	NADH2 dehydrogenas
9	34	89.5	136	2 A10124	probable prepillin
10	34	89.5	151	2 AE2249	hypothetical prote
11	34	89.5	162	2 B81635	conserved hypothet
12	34	89.5	207	2 A48608	El glycoprotein -
13	34	89.5	224	2 C48652	transfer protein s
14	34	89.5	264	2 H83224	phosphonate transp
15	34	89.5	266	2 C83602	proliporotein dia
16	34	89.5	296	2 E83292	conserved hypothet
17	34	89.5	338	2 S73902	UDP-glucose 4-epim
18	34	89.5	357	2 C97564	hypothetical prote
19	34	89.5	446	2 A83355	hypothetical prote
20	34	89.5	516	2 J80134	mannan endo-1,4-de
21	34	89.5	709	2 F75584	hypothetical prote
22	34	89.5	1147	2 T35781	hypothetical prote
23	34	89.5	1239	1 VHWYBE	structural polypro
24	34	89.5	1240	1 VHWYEV	structural polypro
25	34	89.5	1241	1 S26373	genome polyprotein
26	34	89.5	1242	2 S72350	structural polypro
27	34	89.5	1242	2 A56605	structural polypro
28	34	89.5	1315	2 T05300	hypothetical prote
29	34	89.5	1411	2 T48529	hypothetical prote

30	34	89.5	4924	2 T50176	probable peptide s
31	33	86.8	65	2 E83492	hypothetical prote
32	33	86.8	72	2 AD2464	hypothetical prote
33	33	86.8	118	2 I64028	hypothetical prote
34	33	86.8	306	2 G82256	conserved hypothet
35	33	86.8	311	2 A83169	hypothetical prote
36	33	86.8	355	2 F70983	hypothetical prote
37	33	86.8	420	2 E72357	probable serine pr
38	33	86.8	433	2 E70968	sugar ABC transpor
39	33	86.8	440	2 D87076	hypothetical prote
40	33	86.8	661	2 F83342	probable conserved
41	33	86.8	685	1 A48289	probable cation-tr
42	33	86.8	919	2 T37062	neurotrophic recep
43	33	86.8	1053	2 S72194	probable transcrip
44	33	86.8	1628	2 T43682	hydroxymethylgluta
45	33	86.8	2121	2 T27406	nucleoporin - fls
					hypothetical prote

## ALIGNMENTS

RESULT 1  
Heavy-metal transporting Cpx-type ATPase - Methanobacterium thermoautotrophicum (strain  
C/Species: Methanobacterium thermoautotrophicum  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999  
C/Accession: H69200  
R/Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
Oliv, D.; Spadefora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, I.  
K.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func  
A/Reference number: A69000; MUID:98037514; PMID:9371463  
A/Accession: H69200  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-675 <MTN>  
A/Cross-References: GB:A600854; GB:A600666; NID:G2621839; PIDN:AAB85258.1; PID:G26218  
A/Experimental source: strain Delta H  
C/Genetics:  
A/Genes: MTH755  
C/Superfamily: Enterococcus copper-transporting ATPase cobP; ATPase nucleotide-binding  
F/76-413/Domain: ATPase transduction domain homology <ATP>  
F/484-626/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 94.7% Score 36; DB 2; Length 675;  
Best Local Similarity 83.3% Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
DB 299 IAMSWL 304

RESULT 2  
T03472  
conserved hypothetical protein - Rhodobacter capsulatus  
C/Species: Rhodobacter capsulatus  
C/Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 08-Oct-1999  
C/Accession: T03472  
R/Vlack, C.; Paces, V.; Malcev, N.; Paces, J.; Haselkorn, R.; Forststein, M.  
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997  
A/Title: Sequence of a 189-Kb segment of the chromosome of Rhodobacter capsulatus SB10C  
A/Reference number: Z14955; MUID:97404404; PMID:9256491  
A/Accession: T03472  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-116 <VLV>  
A/Cross-References: EMBL:AF010496; NID:G3128256; PIDN:AA016125.1; PID:G3128273  
C/Genetics:  
A/Map position: 1

Query Match 92.1% Score 35; DB 2; Length 116;



Best Local Similarity 83.3%; Pred. No. 57;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LAMSWL 6  
:|||||  
Db 63 LAMSWL 68

RESULT 3  
T51122  
crkC protein [imported] - Brevibacterium linens  
C/Species: Brevibacterium linens  
C/Date: 28-Jul-2000 #sequence\_revision 28-Jul-2000 #text\_change 28-Jul-2000  
C/Accession: T51122  
R/Authors: P. J. Sandmann, G.  
Mol. Gen. Genet. 263, 423-432, 2000  
A/Title: A carotenogenic gene cluster from Brevibacterium linens with novel lycopen cyc  
A/Reference number: Z55303; MUID:20279196; PMID:10821176  
A/Accession: T51122  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-172 <KRU>  
A/Cross-references: EMBL:AF139916; PDB:APF5585.1  
A/Experimental source: DSM 20426; ATCC9175  
C/Genetics:  
A/Gene: crkC

Query Match 92.1%; Score 35; DB 2; Length 172;  
Best Local Similarity 83.3%; Pred. No. 83;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
:|||||  
Db 91 VAMSWL 96

RESULT 4  
C87039  
conserved hypothetical protein ML1041 [imported] - Mycobacterium leprae  
C/Species: Mycobacterium leprae  
C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
C/Accession: C87039  
R/Authors: S. T. Eigmeier, K. J. Parkhill, J. J. James, K. D. Thomson, N. R. Wheeler, P. R. H.  
C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
A/Title: Massive gene decay in the leprosy bacillus.  
A/Reference number: A86909; MUID:21128732; PMID:11234002  
A/Accession: C87039  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-196 <STO>  
A/Cross-references: GB:AL450380; NID:G13093055; PDB:CAC31422.1; GSPDB:GN00147  
C/Genetics:  
A/Gene: ML1041  
C/Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2680

Query Match 92.1%; Score 35; DB 2; Length 196;  
Best Local Similarity 83.3%; Pred. No. 93;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
:|||||  
Db 109 VAMSWL 114

RESULT 5  
C70528  
hypothetical protein Rv2680 - Mycobacterium tuberculosis (strain H37RV)  
C/Species: Mycobacterium tuberculosis  
C/Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 15-Sep-2000  
C/Accession: C70528

R/Authors: S. T. Eigmeier, K. J. Parkhill, J. J. James, K. D. Thomson, N. R. Wheeler, P. R. H.  
C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
A/Title: Massive gene decay in the leprosy bacillus.  
A/Reference number: A86909; MUID:21128732; PMID:11234002  
A/Accession: C87039  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-196 <STO>  
A/Cross-references: GB:AL450380; NID:G13093055; PDB:CAC31422.1; GSPDB:GN00147  
C/Genetics:  
A/Gene: ML1041  
C/Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2680

Query Match 92.1%; Score 35; DB 2; Length 210;  
Best Local Similarity 83.3%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
:|||||  
Db 123 VAMSWL 128

RESULT 6  
A12824  
NADH dehydrogenase ndh [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C/Species: Agrobacterium tumefaciens  
C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C/Accession: A12824  
R/Authors: D. W. Setubal, J. C. J. Kaul, R. J. Monks, D. J. Chen, L. J. Wood, G. E. Chen, Y. J. Mo.  
Ergen, G. J. Gillet, W. J. Grant, C. J. Genthner, D. J. Kutayvin, T. J. Levy, R. J. Li, M. J. McCle  
; Karp, P. J. Romero, P. J. Zhang, S.  
Science 294, 2317-2323, 2001  
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm  
ster, E. W.  
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A/Reference number: AB2577; MUID:21608550; PMID:11743193  
A/Accession: A12824  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-421 <KIR>  
A/Cross-references: GB:AE008688; PDB:AA143015.1; PDB:G17740478; GSPDB:GN00186  
A/Experimental source: strain C58 (Dupont)  
C/Genetics:  
A/Gene: ndh  
A/Map position: circular chromosome  
C/Superfamily: NADH dehydrogenase

Query Match 92.1%; Score 35; DB 2; Length 421;  
Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
:|||||  
Db 393 VAMSWL 398

RESULT 7  
H97602  
probable NADH dehydrogenase (Y09899) [imported] - Agrobacterium tumefaciens (strain C5)  
C/Species: Agrobacterium tumefaciens  
C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002  
C/Accession: H97602  
R/Authors: B. J. Hinkle, G. J. Gattung, S. J. Miller, N. J. Blanchard, M. J. Qurollo, B. J. Goldma  
A. J. Liu, F. J. Wollam, C. J. Allinger, M. J. Doughty, D. J. Scott, C. J. Lappas, C. J. Matkeiz, B  
Science 294, 2323-2328, 2001  
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium ti  
A/Reference number: A97559; MUID:21608551; PMID:11743194  
A/Accession: H97602  
A/Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-438 <KUR>  
A:Cross-references: GB:AE007869; PIDN:AA87777.1; PID:g15157148; GSPDB:GN00169  
C:Genetics:  
A:Gene: AGR\_C\_3667  
A:Map position: circular chromosome  
C:Superfamily: NADH dehydrogenase

Query Match 92.1%; Score 35; DB 2; Length 438;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
DB 410 VAMSWL 415

## RESULT 8

A:13607  
NADH2 dehydrogenase (EC 1.6.99.3) [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis  
C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 03-Jun-2002

C:Accession: A13607  
R:DelVecchio, V.G.; Kaparat, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: A0252; PMID:11756688

A:Accession: A13607  
A:Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-441 <KUR>

A:Cross-references: GB:AE008918; PIDN:AL54028.1; PID:g17964981; GSPDB:GN00191

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BME10786

A:Map position: 11

C:Superfamily: NADH dehydrogenase

C:Keywords: oxidoreductase

Query Match 92.1%; Score 35; DB 2; Length 441;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
DB 413 VAMSWL 418

RESULT 9  
A:10124  
probable prepillin peptidase dependent protein YPO1017 [imported] - Yersinia pestis (stra

C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001

C:Accession: A10124  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tittball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: A10124

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-136 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC89860.1; PID:g15979085; GSPDB:GN00175

C:Genetics:

A:Gene: YPO1017

Query Match 89.5%; Score 34; DB 2; Length 136;

Best Local Similarity 100.0%; Pred. No. 94;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAMSWL 6  
DB 68 LAMSWL 72

## RESULT 10

A:AE2249  
hypothetical protein alr3548 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002

C:Accession: AE2249

R:Kaneko, T.; Nakamura, Y.; Waki, C.P.; Kurita, T.; Sasamoto, S.; Watanabe, A.; Iriuchi

Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ar

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AE2249

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-151 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA875247.1; PID:g17132681; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr3548

Query Match 89.5%; Score 34; DB 2; Length 151;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSW 5  
DB 18 LAMSW 22

## RESULT 11

A:B83635  
conserved hypothetical protein PA0085 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: B83635

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; E

adman, S.; Yun, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lapidis, K.; Lin

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path

A:Reference number: AB2950; MUID:20437337; PMID:10984043

A:Accession: B83635

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-162 <STO>

A:Cross-references: GB:AE004447; GB:AE004091; NID:g9945902; PIDN:AA03475.1; GSPDB:GN0C

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA0085

Query Match 89.5%; Score 34; DB 2; Length 162;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSW 5  
DB 28 LAMSW 32

## RESULT 12

A:A48608  
B1 glycoprotein - eastern equine encephalomyelitis virus (fragment)

C:Species: eastern equine encephalomyelitis virus

C:Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 26-Aug-1999

C:Accession: A48608

R:Weaver, S.C.; Bellett, L.A.; Goussat, L.; Repik, P.M.; Scott, T.W.; Holland, J.J.

Virology 195, 700-709, 1993

A>Title: Diversity within natural populations of eastern equine encephalomyelitis virus.  
 A/Reference number: A48608; MUID:9331728; PMID:8101674  
 A/Contents: 215-85; MD5B  
 A/Accession: A48608  
 A/Status: preliminary  
 A/Molecule type: nucleic acid  
 A/Residues: 1-207 <MEA>  
 A/Cross-references: GB:563996; NID:9400551; PIDN:AA827576.1; PID:9400552  
 A/Note: sequence extracted from NCBI backbone (NCBIN:135481, NCBI:P:135482)  
 C/Superfamily: togavirus structural polyprotein  
 C/Keywords: glycoprotein

Query Match 89.5%; Score 34; DB 2; Length 207;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAMSW 6  
 DB 173 LAMSW 177

## RESULT 13

C48652 transfer protein epdA - Streptomyces ambofaciens plasmid pSAM2  
 C/Species: Streptomyces ambofaciens  
 C/Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 22-Oct-1999  
 C/Accession: C48652; S33428  
 R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; I  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam,  
 ; Lory, S.; Olson, M.V.  
 A/Title: Transfer functions of the conjugative integrating element pSAM2 from Streptomy  
 A/Reference number: A48652; MUID:93374848; PMID:8366038  
 A/Accession: C48652  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-224 <HAG>  
 A/Cross-references: EMBL:Z19593; NID:9298051; PIDN:CAA7641.1; PID:9298054  
 C/Genetics:  
 A/Genome: plasmid

Query Match 89.5%; Score 34; DB 2; Length 224;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5  
 DB 66 LAMSW 70

## RESULT 14

H83224 phosphonate transport protein phnB PA3382 [Imported] - Pseudomonas aeruginosa (strain PA  
 C/Species: Pseudomonas aeruginosa  
 C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C/Accession: H83224  
 R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; I  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam,  
 ; Lory, S.; Olson, M.V.  
 A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
 A/Reference number: A82950; MUID:20437337; PMID:10984043  
 A/Accession: H83224  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-264 <STO>  
 A/Cross-references: GB:AE004759; GB:AE004091; NID:99949500; PIDN:AA606770.1; GSPDB:GN001  
 A/Experimental source: strain PA01  
 C/Genetics:  
 A/Gene: phnB; PA3382  
 C/Superfamily: phnB protein

Query Match 89.5%; Score 34; DB 2; Length 264;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5  
 DB 31 LAMSW 35

## RESULT 15

C83602 prolipoprotein diacylglycerol transferase PA0341 [Imported] - Pseudomonas aeruginosa (s  
 C/Species: Pseudomonas aeruginosa  
 C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C/Accession: C83602  
 R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; I  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; La  
 ; Lory, S.; Olson, M.V.  
 A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat  
 A/Reference number: A82950; MUID:20437337; PMID:10984043  
 A/Accession: C83602  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-266 <STO>  
 A/Cross-references: GB:AE004472; GB:AE004091; NID:99946188; PIDN:AA603730.1; GSPDB:GN0  
 A/Experimental source: strain PA01  
 C/Genetics:  
 A/Gene: lgt; PA0341  
 C/Superfamily: prolipoprotein diacylglycerol transferase

Query Match 89.5%; Score 34; DB 2; Length 266;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSW 6  
 DB 229 LAMSW 234

Search completed: February 18, 2004, 14:38:40  
 Job time : 7.5921 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds  
(without alignments)  
89.145 Million cell updates/sec

Title: US-09-643-260-6  
Perfect score: 40  
Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriophage:\*
- 17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	236	3 Q8NUT9	Q8NUT9 Bionectria
2	37	92.5	274	16 Q8G659	Q8G659 Bifidobacter
3	37	92.5	437	16 Q92K30	Q92K30 Rhizobium m
4	37	92.5	548	16 Q92M15	Q92M15 Rhizobium m
5	37	92.5	581	5 Q8MSH3	Q8MSH3 diosaphila
6	37	92.5	597	5 Q9VGP2	Q9VGP2 diosaphila
7	37	92.5	610	16 Q86712	Q86712 streptomyc
8	37	92.5	885	16 Q91389	Q91389 pseudomonas
9	36	90.0	205	16 Q9ACR5	Q9ACR5 streptomyc
10	36	90.0	227	4 Q8IKX8	Q8IKX8 homo sapien
11	36	90.0	242	12 Q919K8	Q919K8 culicx nigrit
12	36	90.0	355	11 Q8B1T9	Q8B1T9 mus musculu
13	36	90.0	358	10 Q50002	Q50002 prunus arme
14	36	90.0	374	16 Q9HZ10	Q9HZ10 pseudomonas
15	36	90.0	433	16 Q8P4A1	Q8P4A1 xanthomonas
16	36	90.0	438	16 Q8PFT8	Q8PFT8 xanthomonas

17	36	90.0	452	4 Q96AB7	Q96AB7 homo sapien
18	36	90.0	463	5 Q8MWJ0	Q8MWJ0 apis cerana
19	36	90.0	477	11 Q9CYT6	Q9CYT6 mus musculu
20	36	90.0	484	4 Q8BTV6	Q8BTV6 homo sapien
21	36	90.0	686	16 Q8FQ29	Q8FQ29 corynebacte
22	36	90.0	889	16 Q9AAZ6	Q9AAZ6 caulobacter
23	36	90.0	1005	10 Q9XGZ2	Q9XGZ2 arabidopsis
24	36	90.0	5435	2 Q9LXK2	Q9LXK2 streptomyc
25	34	85.0	166	4 Q8NBW1	Q8NBW1 homo sapien
26	34	85.0	273	10 Q94JN4	Q94JN4 arabidopsis
27	34	85.0	273	10 Q94JN4	Q94JN4 arabidopsis
28	34	85.0	275	10 Q65710	Q65710 arabidopsis
29	34	85.0	376	3 Q9UVL4	Q9UVL4 penicillium
30	34	85.0	617	10 P93050	P93050 arabidopsis
31	34	85.0	1074	16 Q8PJ70	Q8PJ70 xanthomonas
32	34	85.0	1842	3 Q96WT6	Q96WT6 schizosacch
33	34	85.0	1842	3 Q96WT7	Q96WT7 schizosacch
34	34	85.0	1842	3 Q96WT8	Q96WT8 schizosacch
35	33	82.5	49	6 Q8VBA5	Q8VBA5 equus caball
36	33	82.5	98	5 Q9VBA5	Q9VBA5 diosaphila
37	33	82.5	136	2 Q8KZ39	Q8KZ39 uncultured
38	33	82.5	154	11 Q8BGD2	Q8BGD2 mus musculu
39	33	82.5	161	6 Q8MUT3	Q8MUT3 oryctolagus
40	33	82.5	161	11 Q9Z1P9	Q9Z1P9 rattus norv
41	33	82.5	198	16 Q9PAB4	Q9PAB4 xylenella fas
42	33	82.5	213	12 Q9B1I7	Q9B1I7 melaleucid h
43	33	82.5	213	12 Q9DPT1	Q9DPT1 melaleucid h
44	33	82.5	234	3 Q8NUT6	Q8NUT6 hyocera bc
45	33	82.5	234	3 Q00095	Q00095 trichoderma

## ALIGNMENTS

### RESULT 1

Q8NUT9 PRELIMINARY; PRT; 236 AA.  
AC Q8NUT9  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Endoglucanase.  
GN CEL12C.  
OS Bionectria ochroleuca.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
CC Hypocreales; Bionectriaceae; Bionectria.  
OX NCBI\_TaxID=29856;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22067395; PubMed=12073090;  
RA Goedegebuur F., Fowler T., Phillips J., van der Kleij P.,  
van Solingen P., Dankmeyer L., Power S.D.,  
RT "Cloning and relational analysis of 15 novel fungal endoglucanases  
from family 12 glycosyl hydrolase."  
RL Curr. Genet. 41:89-98(2002).  
DR EMBL; AF435065; AAM7708.1; -  
DR InterPro; IPR002594; Glyco\_hydro\_12.  
DR Pfam; PF01670; Glyco\_hydro\_12; 1.  
DR ProDom; PD004316; Glyco\_hydro\_12; 1.  
SQ SEQUENCE 236 AA; 26024 MW; C3D8A7E33F0C41D8 CRC64;

Query Match 92.5%; Score 37; DB 3; Length 236;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
DB 63 ADMSWA 68

### RESULT 2

Q8G659 PRELIMINARY; PRT; 274 AA.

AC Q8659; 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Probable dihydroorotate dehydrogenase electron transfer subunit.  
 GN PRK OR BL0790.  
 OS Bifidobacterium longum.  
 OC Bacteri; Actinobacteria; Actinobacteridae; Bifidobacteriales;  
 OC Bifidobacteriaceae; Bifidobacterium.  
 OX NCBI\_TaxID=216816;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCC 2705;  
 RX MEDLINE=22294977; PubMed=12381787;  
 RA Schell M.A., Karimanzou M., Snel B., Vilanova D., Berger B.,  
 RA Paesi G., Zwaalen M.-C., Desiere F., Bork P., Delley M.,  
 RA Pridmore R.D., Arisong F.; Bifidobacterium longum reflects its adaptation  
 RT to the human gastrointestinal tract."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).  
 DR EMBL; AEO14701; FAN24605.1; -  
 KM Complete proteome.  
 SQ SEQUENCE 274 AA; 29978 MW; 971E016E79636DB CRC64;

Query Match 92.5%; Score 37; DB 16; Length 274;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
 DB 171 ADMSWS 176

RESULT 3  
 ID Q92K30 PRELIMINARY; PRT; 437 AA.

AC Q92K30; 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Hypothetical protein R02283.  
 GN R02283 OR SMC01671.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteri; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1021;  
 RX MEDLINE=21396507; PubMed=11481430;  
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
 RA Boistard P., Becker A., Boutry M., Cadieu B., Dreano S., Gloux S.,  
 RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaire V., Masuy D.,  
 RA Pohl T., Portetelle D., Puhler A., Purnelle B., Rampersingh U.,  
 RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;  
 RT "Analysis of the chromosome sequence of the legume symbiont  
 RT Sinorhizobium meliloti strain 1021."  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
 DR EMBL; AL591790; CAC46862.1; -  
 KM Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 437 AA; 48372 MW; 950E0B3D966CE78 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 437;  
 Best Local Similarity 83.3%; Pred. No. 3.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
 DB 157 ADMSWA 162

RESULT 4  
 Q92M15

ID Q92M15 PRELIMINARY; PRT; 548 AA.

AC Q92M15; 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Putative fatty-acid-CoA ligase protein (EC 6.-.-.-).  
 GN R02631 OR SMC00741.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteri; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1021;  
 RX MEDLINE=21396507; PubMed=11481430;  
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
 RA Boistard P., Becker A., Boutry M., Cadieu B., Dreano S., Gloux S.,  
 RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaire V., Masuy D.,  
 RA Pohl T., Portetelle D., Puhler A., Purnelle B., Rampersingh U.,  
 RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;  
 RT "Analysis of the chromosome sequence of the legume symbiont  
 RT Sinorhizobium meliloti strain 1021."  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
 DR EMBL; AL591791; CAC47210.1; -  
 KM Ligase; Complete proteome.  
 SQ SEQUENCE 548 AA; 59383 MW; 659A68C546EA953B CRC64;

Query Match 92.5%; Score 37; DB 16; Length 548;  
 Best Local Similarity 83.3%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
 DB 235 ADMSWA 240

RESULT 5  
 ID Q8MSH3 PRELIMINARY; PRT; 581 AA.

AC Q8MSH3; 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE GH24640p.  
 GN CG6728.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkely;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Fries B.,  
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.U., Nuno U., Paclid J., Parag V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celniker S.;  
 RT Submitter (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AV118818; AAM50678.1; -  
 DR EMBL; FBgn0037896; CG6728.  
 KM FlyBase; FBgn0037896; CG6728.  
 DR InterPro; IPR000172; GMC\_oxred.  
 DR InterPro; IPR000169; SHProt\_acetate.  
 DR Pfam; PF00732; GMC\_oxred; 3.  
 DR PROSITE; PS00639; THIOLE PROTEASE HIS; 1.  
 SQ SEQUENCE 581 AA; 63475 MW; A2F13BBBC58A96D CRC64;

Query Match 92.5%; Score 37; DB 16; Length 548;  
 Best Local Similarity 83.3%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match 92.5%; Score 37; DB 5; Length 581;  
 Best Local Similarity 83.3%; Pred. No. 4.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 :|||||  
 Db 158 SDMSWA 163

RESULT 6  
 Q9VGP2 PRELIMINARY; PRT; 597 AA.  
 AC Q9VGP2; 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE CG6728 protein.  
 GN CG6728  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxId=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RC MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amaratunga P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA Sutcliffe M.J., Smith R.L., Peterson D., Miller L., Brown J.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milto G.L.G.,  
 RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benise P.V., Bereman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A.L., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hovstern D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M.B., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laeok P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pacible J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Pui V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier B.C., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Maasman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 DB EMBL; AEO03691; AAF54634.1; -;  
 DR FlyBase; FBgn0037896; CG6728.  
 DR InterPro; IPR001172; GMC\_oxred.  
 DR InterPro; IPR00169; SHPOT\_acetate.  
 DR Pfam; PFO0732; GMC\_oxred.1.  
 DR PROSITE; PS00624; GMC\_oxred.2; 1.  
 DR PROSITE; PS00639; THIOL\_PROTEASE\_HIS; 1.  
 SQ SEQUENCE 597 AA; 65274 MW; 8C4C362AFPA0902A CRC64;

Query Match 92.5%; Score 37; DB 5; Length 597;  
 Best Local Similarity 83.3%; Pred. No. 4.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 :|||||  
 Db 158 SDMSWA 163

RESULT 7  
 O86712 PRELIMINARY; PRT; 610 AA.  
 AC O86712; 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein SC06530.  
 GN SC06530 OR SC5C7.15.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycinae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxId=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2) / M145;  
 RC MEDLINE=2196410; PubMed=12000953;  
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Chellis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleier H.,  
 RA Harper D., Bateman A., Brown S., Chandra S., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 RA Huang C.-H., Kleier T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K.E., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete Streptomyces  
 coelicolor A3(2).";  
 RL Nature 417:141-147(2002).  
 DR EMBL; AL939128; CAA20627.1; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 610 AA; 67368 MW; 053CBA90DB589021 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 610;  
 Best Local Similarity 83.3%; Pred. No. 4.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 :|||||  
 Db 83 ADMWA 88

RESULT 8  
 Q91389 PRELIMINARY; PRT; 885 AA.  
 AC Q91389; 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Two-component sensor KdpD.  
 GN KDPD OR PA1636.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxId=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 15692 / PAO1;  
 RC MEDLINE=20437337; PubMed=10984043;  
 RA Stever C.R., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltz L., Tolentino B., Westbrook-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laidig K., Lam R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,  
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an  
 RT opportunistic pathogen."  
 RL Nature 406:959-964(2000).  
 CC -1- SIMILARITY: TO PROKARYOTE SENSOR TRANSDUCTION PROTEINS.  
 DR EMBL: AE004591; MAG5025.1; -.  
 DR HSSP: P02933; IJOY.  
 DR InterPro: IPR003594; ATPbind\_ATPase.  
 DR InterPro: IPR004358; Bact\_sens\_pr\_C.  
 DR InterPro: IPR003018; GAF.  
 DR InterPro: IPR003661; His\_kinase.  
 DR InterPro: IPR005467; His\_kinase.  
 DR InterPro: IPR003852; KdpD.  
 DR Pfam: PF02518; HATPase\_c; 1.  
 DR Pfam: PF00512; HsKKA; 1.  
 DR Pfam: PF02702; KdpD; 1.  
 DR PRINTS: PR00344; BCTRLSENSOR.  
 DR SMART: SM00065; GAF; 1.  
 DR SMART: SM00387; HATPase\_c; 1.  
 DR SMART: SM00388; HsKKA; 1.  
 DR PROSITE: PS50109; HIS\_KIN; 1.  
 KM Kinase; Phosphorylation; Sensory transduction; Transferase;  
 KW Complete proteome.  
 SQ SEQUENCE 885 AA; 97019 MW; 20FC8E2B2AB876C0 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 885;  
 Best Local Similarity 83.3%; Pred. No. 6.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 DB 563 ADMAWA 568

RESULT 9  
 ID Q9ACR5 PRELIMINARY; PRT; 205 AA.  
 AC Q9ACR5;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Hypothetical protein SCP1.253.  
 GN SCP1.253.  
 OS Streptomyces coelicolor.  
 OG Bacteri; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AS(2);  
 RX MEDLINE=21956410; PubMed=12000953;  
 RA Bertley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleeer H.,  
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Frazer A., Gobie A., Hidalgo J., Hornsby T., Howarth S.,  
 RA Huang C.-H., Kleiser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.,  
 RT "Complete genome sequence of the model actinomycete *Streptomyces*  
 RT *coelicolor* AS(2)."  
 RL Nature 417:141-147(2002).  
 DR EMBL: AL590464; CAC36779.1; -.  
 KM Hypothetical protein; Plasmid; Complete proteome.  
 SQ SEQUENCE 205 AA; 23051 MW; 6602396CF93F2D9 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 205;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
 DB 10 ADMSW 14

RESULT 10  
 ID Q8IXK8 PRELIMINARY; PRT; 227 AA.  
 AC Q8IXK8;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Similar to hypothetical protein BC017335.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC040173; AA040173.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 227 AA; 25487 MW; F1A71EA57062A05 CRC64;

Query Match 90.0%; Score 36; DB 4; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
 DB 113 ADMSW 117

RESULT 11  
 ID Q919X8 PRELIMINARY; PRT; 242 AA.  
 AC Q919X8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE CUN068 hypothetical protein.  
 GN CUN068.  
 OS *Culex nigripalpus* baculovirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.  
 OX NCBI\_TaxID=130556;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Florida1997;  
 RX MEDLINE=2148685; PubMed=11602755;  
 RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,  
 RA Becnel J.J., Rock D.L., Kutish G.F.,  
 RT "Genome Sequence of a Baculovirus Pathogenic for *Culex nigripalpus*,"  
 RT J. Virol. 75:11157-11165(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Florida1997;  
 RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,  
 RA Becnel J.J., Rock D.L., Kutish G.F.,  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF403738; AA094146.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 242 AA; 27222 MW; 6014967531110B52 CRC64;

Query Match 90.0%; Score 36; DB 12; Length 242;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
 DB 80 DMSWA 84

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RESULT 12
ID 08BIT9 PRELIMINARY; PRT; 355 AA.
AC 08BIT9;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Mitochondrial ribosomal protein L41 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
RA The PANOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RT Nature 420:563-573 (2002).
DR EMBL; AK087998; BAC40084.1;
SO SEQUENCE 355 AA; 40183 MW; PEF8546127402D58 CRC64;

Query Match 90.0%; Score 36; DB 11; Length 355;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 215 ADMSW 219

RESULT 13
ID 050002 PRELIMINARY; PRT; 358 AA.
AC 050002;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Cysteine protease.
OS Prunus armeniaca (Apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside 1; Rosales; Rosaceae; Amygdaloidae; Prunus.
OX NCBI_Taxid=36596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bergeon; TISSUE=Mesocarp, and Exocarp;
RA Mbegule-A-Mbegule D., Gomez R.-M., Fils-Lycaon B.;
RT "Sequence of APTPI, a Cysteine Proteinase From Apricot Fruit
RT (Accession No. U93166). Gene Expression During Fruit Ripening. (PGR97-
RT 179)."
RL Plant Physiol. 115:1730-1730(1997).
DR EMBL; U93166; AAB97142.1;
DR HSRP; P07711; ICDL.
DR MEROPS; C01.041; -.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR000169; SHPoc_acetate.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPA1N.
DR SMART; SM00645; Pept_C1; 1.
DR SMART; SM00645; Pept_C1; 1.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
KW Hydroxylase; Protease; Thiol protease.
SQ SEQUENCE 358 AA; 39309 MW; C98F78793B002554 CRC64;

Query Match 90.0%; Score 36; DB 10; Length 358;

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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 108 ADMSW 112

RESULT 14
ID 09H210 PRELIMINARY; PRT; 374 AA.
AC 09H210;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Hypothetical protein PA3230.
GN PA3230.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_Taxid=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
MEDLINE=20437337; PubMed=10984043;
RX Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.D., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino B., Westbrock-Adams S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lathig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RT Nature 406:959-964(2000).
DR EMBL; AE004746; AAC06618.1;
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 374 AA; 42269 MW; 31EF185C4F683884 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
DB 81 DMSWA 85

RESULT 15
ID 08P4A1 PRELIMINARY; PRT; 433 AA.
AC 08P4A1;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Cationic amino acid transporter.
GN XCC3809.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_Taxid=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Augusto R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
RA Canavotte G., Canavan F., Cardozo U., Chambergro F., Clapina L.P.,
RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Doroty H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Fomiglieri E.F., Franco M.C., Greggio C.C., Guber A.,
RA Katsuyama A.M., Kishii L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

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RA Martins E.C., Meléndez J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,  
RA Spindola L.A.F., Takita M.A., Tamura R.B., Teixeira B.C., Tezza R.I.D.,  
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,  
RA Secubal J.C., Kitajima J.P.,  
RT "Comparison of the genomes of two Xanthomonas pathogens with differing  
RT host specificities."  
RL Nature 417:459-463(2002).  
DR EMBL: AE012502; AMW43483.1; -  
DR InterPro: IPR002293; AA/rel\_permease1.  
DR InterPro: IPR004841; Permease.  
DR Pfam: PF00324; aa\_permeases; 1.  
KW Complete proteome.  
SQ SEQUENCE 433 AA; 45128 MW; EF217D2A7C516533 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 433;  
Best Local Similarity 100.0%; Pred.No. 4.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
|||||

DB 181 DMSWA 185

Search completed: February 18, 2004, 14:35:41  
Job time : 18.3684 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds

(Without alignments)  
/9.423 Million cell updates/sec

Title: US-09-643-260-6  
Sequence: 1 ADMSMA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	90.0	470	1 NRAM_IADBU	Q07570 Influenza a
2	36	90.0	470	1 NRAM_IADCH	Q07571 Influenza a
3	36	90.0	470	1 NRAM_IADH2	Q07572 Influenza a
4	36	90.0	470	1 NRAM_IADJ2	Q07573 Influenza a
5	36	90.0	470	1 NRAM_IADJ3	Q07599 Influenza a
6	36	90.0	470	1 NRAM_IACRN	Q07574 Influenza a
7	36	90.0	470	1 NRAM_IAGHD	Q07577 Influenza a
8	36	90.0	470	1 NRAM_IAMH1	Q07578 Influenza a
9	36	90.0	470	1 NRAM_IAMAE	Q07583 Influenza a
10	36	90.0	470	1 NRAM_IATKL	Q07585 Influenza a
11	36	90.0	598	1 MRJ5_APIRE	Q97432 apis mellif
12	34	85.0	376	1 PGLR_PENGR	O93883 penicillium
13	34	85.0	1842	1 PAS2_SCHPO	Q10289 s fatty aci
14	33	82.5	99	1 NOS3_SHEEP	P79209 ovls arles
15	33	82.5	220	1 Y132_METUA	Q57596 methanococ
16	33	82.5	232	1 C1B2_SHEEP	P80943 ovls arles
17	33	82.5	333	1 C1B2_SHEEP	Q29422 ovls arles
18	33	82.5	410	1 Y801_DEIRA	Q97468 delinococcus
19	33	82.5	421	1 PNKL_SCHPO	O13911 echizosacch
20	33	82.5	470	1 NRAM_IAGIT	Q07581 Influenza a
21	33	82.5	479	1 BGIA_BACSU	P42973 bacillus su
22	33	82.5	492	1 AERA_AERTR	P09166 aeromonas t
23	33	82.5	529	1 YCQ0_METUA	P46810 mycobacteri
24	33	82.5	578	1 YC12_KLEBN	O58617 methanococ
25	33	82.5	579	1 YC12_KLEBN	Q48458 klebsiella
26	33	82.5	817	1 PHK_STRCO	Q8CK51 streptomyce
27	33	82.5	914	1 PUX2_CLOSR	P50900 clostridium
28	33	82.5	1201	1 NOS3_MOUSE	P70313 mus musculu
29	33	82.5	1202	1 NOS3_HUMAN	P29474 mus sapien
30	33	82.5	1204	1 NOS3_BOVIN	P29472 bos taurus
31	33	82.5	1204	1 NOS3_PIG	Q28869 sus scrofa
32	32	80.0	100	1 NOS3_CANVO	P97270 canis porce
33	32	80.0	107	1 STEL_RHIVE	P00302 rhus vernic

34	32	80.0	125	1 VG61_BPMO2	O64253 mycobacteri
35	32	80.0	272	1 C7L1_RHORI	P23135 rhodospirill
36	32	80.0	282	1 3MG2_ECOLI	P04395 escherichia
37	32	80.0	295	1 X7G9_HUMAN	O99871 homo sapien
38	32	80.0	339	1 YXGB_ECOLI	P27250 escherichia
39	32	80.0	360	1 WNT2_ECOLI	P34889 caenorhabdi
40	32	80.0	362	1 DCUP_YEAST	P32347 saccharomyc
41	32	80.0	375	1 H1S7_XANCP	P58882 xanthomonas
42	32	80.0	411	1 POLC_BUCAI	P57265 buchiera ap
43	32	80.0	418	1 HLT_VIRBA	O99289 vibrio para
44	32	80.0	453	1 NRAM_IAMIL	P03470 influenza a
45	32	80.0	454	1 NRAM_IAPUE	P03468 influenza a

## ALIGNMENTS

ID	NRAM_IADBU	STANDARD	PRT	470 AA.
AC	Q07570;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Neuraminidase (EC 3.2.1.18).			
GN	NA.			
OS	Influenza A virus (strain A/Duck/Burjacta/652/88).			
OC	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;			
OC	Influenza A viruses; Influenzavirus A.			
OX	NCBI_Taxid=38956;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93212520; PubMed=8460490;			
RA	Salto T., Kawacka Y., Webster R.G.;			
RT	"Phylogenetic analysis of the N8 neuraminidase gene of Influenza A			
RT	viruses."			
RL	Virology 193:868-876(1993).			
CC	-1- FUNCTION: Removes the terminal sialic acid from carbohydrate side			
CC	chains of the host cell surface proteins and from the viral			
CC	envelope. Such a reaction prevents self-aggregation and facilitates			
CC	the mobility of the virus to and from the site of infection.			
CC	-1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,			
CC	alpha-(2-8)-glycosidic linkages of terminal sialic residues in			
CC	oligosaccharides, glycoproteins, glycolipids, colominic acid and			
CC	synthetic substrates.			
CC	-1- SUBUNIT: Homotrimer.			
CC	-1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED			
CC	SPIKE ON THE SURFACE OF THE VIRION.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.			
CC	-----			
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL; L06572; AAA3365.1; -.			
DR	HSSP; P06820; 2BAT.			
DR	InterPro; IPR001860; Glyco_hydro_34.			
DR	Pfam; PF00064; neur; 1.			
DR	ProDom; PD000431; Glyco_hydro_34; 1.			
KW	Hydrolase; Glycosidase; Glycoprotein; Transmembrane.			
FT	TRANSMEM	7	38	ANCHOR (BY SIMILARITY).
FT	DOMAIN	39	88	HYPERVARIABLE STALK REGION.
FT	DOMAIN	89	470	HEAD OF NEURAMINIDASE.
FT	ACT_SITE	273	273	BY SIMILARITY.
FT	ACT_SITE	275	275	BY SIMILARITY.
FT	CARBOHYD	46	46	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	54	54	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	144	144	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	293	293	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 398 398 N-LINKED (GLCNAC.. ) (POTENTIAL).  
SQ SEQUENCE 470 AA; 51989 MW; DIA6F07460F6F8AD CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;  
Best Local Similarity 100.0%; Pred. No. 62;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
DB 453 ADMSW 457

## RESULT 2

NRAM\_IADCH STANDARD; PRT; 470 AA.  
ID NRAM\_IADCH  
AC 007571;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuraminidase (EC 3.2.1.18).  
GN NA.  
OS Influenza A virus (strain A/Duck/Chabarovsk/1610/72).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza A viruses; Influenzavirus A.  
OX NCBI\_TaxID=39571;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93212520; PubMed=8460490;  
RA Saito T., Kawasaka Y., Webster R.G.;

RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A  
viruses."

RL Virology 193:868-876(1993).

CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side  
chains of the host cell surface proteins and from the viral  
envelope. Such a reaction prevents self-aggregation and facilitate  
the mobility of the virus to and from the site of infection.  
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,  
alpha-(2-8)-glycosidic linkages of terminal sialic residues in  
oligosaccharides, glycoproteins, glycolipids, colominic acid and  
synthetic substrates.  
CC -1- SUBUNIT: Homotrimer.  
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED  
SPIKE ON THE SURFACE OF THE VIRION.

CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.

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CC EMBL: L06573; AAA43367.1; -.

DR HSSP; P06820; 2BAT.

DR InterPro; IPR001860; Glyco\_hydro\_34.

DR Pfam; PF00064; neur; 1.

DR ProDom; PD000431; Glyco\_hydro\_34; 1.

KM Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.

FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).

FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.

FT ACT\_SITE 89 470 HEAD OF NEURAMINIDASE.

FT ACT\_SITE 273 273 BY SIMILARITY.

FT CARBOHYD 46 46 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 54 54 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 84 84 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 144 144 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 293 293 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 398 398 N-LINKED (GLCNAC.. ) (POTENTIAL).

SQ SEQUENCE 470 AA; 52070 MW; 169AB89FB8E8006DC CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;

Best Local Similarity 100.0%; Pred. No. 62;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
DB 453 ADMSW 457

## RESULT 3

NRAM\_IADH2 STANDARD; PRT; 470 AA.  
ID NRAM\_IADH2  
AC 007572;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuraminidase (EC 3.2.1.18).  
GN NA.  
OS Influenza A virus (strain A/Duck/Hokkaido/8/80).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza A viruses; Influenzavirus A.  
OX NCBI\_TaxID=11358;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93212520; PubMed=8460490;  
RA Saito T., Kawasaka Y., Webster R.G.;

RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A  
viruses."

RL Virology 193:868-876(1993).

CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side  
chains of the host cell surface proteins and from the viral  
envelope. Such a reaction prevents self-aggregation and facilitate  
the mobility of the virus to and from the site of infection.  
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,  
alpha-(2-8)-glycosidic linkages of terminal sialic residues in  
oligosaccharides, glycoproteins, glycolipids, colominic acid and  
synthetic substrates.  
CC -1- SUBUNIT: Homotrimer.  
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED  
SPIKE ON THE SURFACE OF THE VIRION.

CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.

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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: L06574; AAA43372.1; -.

DR HSSP; P06820; 2BAT.

DR InterPro; IPR001860; Glyco\_hydro\_34.

DR Pfam; PF00064; neur; 1.

DR ProDom; PD000431; Glyco\_hydro\_34; 1.

KM Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.

FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).

FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.

FT ACT\_SITE 89 470 HEAD OF NEURAMINIDASE.

FT ACT\_SITE 273 273 BY SIMILARITY.

FT CARBOHYD 46 46 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 54 54 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 84 84 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 144 144 N-LINKED (GLCNAC.. ) (POTENTIAL).

FT CARBOHYD 293 293 N-LINKED (GLCNAC.. ) (POTENTIAL).

SQ SEQUENCE 470 AA; 52015 MW; B1C1D3B2C650B93C CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;

Best Local Similarity 100.0%; Pred. No. 62;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5

DB 453 ADMSW 457

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|||||
RESULT 4
NRAM_IADW2 STANDARD; PRT; 470 AA.
ID NRAM_IADW2 007573;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Memphis/928/74).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OC NCBI_TaxId=11357;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
RT viruses."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L06575; AAA3404.1; -.
DR HSP: P06820; 2BAT.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur; 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
KM Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38
FT DOMAIN 39 88
FT ACT SITE 273 273
FT ACT SITE 275 275
FT CARBOHYD 46 46
FT CARBOHYD 54 54
FT CARBOHYD 84 84
FT CARBOHYD 144 144
FT CARBOHYD 293 293
FT CARBOHYD 398 398
SQ SEQUENCE 470 AA; 52146 MW; 30F5F9FE364C1F49 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADMSW 5
DB 453 ADMSW 457

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RESULT 5
NRAM_IADW3 STANDARD; PRT; 470 AA.
ID NRAM_IADW3 007599;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Ukraine/1/63).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OC NCBI_TaxId=11374;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
RT viruses."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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CC -----
DR EMBL: L06576; AAA16234.1; -.
DR HSP: P06820; 2BAT.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur; 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
KM Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 37
FT DOMAIN 38 88
FT ACT SITE 273 273
FT ACT SITE 275 275
FT CARBOHYD 46 46
FT CARBOHYD 54 54
FT CARBOHYD 84 84
FT CARBOHYD 144 144
FT CARBOHYD 398 398
SQ SEQUENCE 470 AA; 51960 MW; B46D54A03AC8C8 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 6
NRAM_IAGFN STANDARD; PRT; 470 AA.
ID NRAM_IAGFN 007574;
AC 007574;
DT 01-FEB-1995 (Rel. 31, Created)

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DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Guinea fowl/New York/4-3587/84).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38963;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
RT viruses."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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CC -----
DR EMBL, L06584; AAA3428.1; -.
DR HSSP, P06820; 2BAT.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur. 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
KM Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52348 MW; D3BD2AAC0159F866 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADM5W 5
DB 453 ADM5W 457

RESULT 7
ID NRAM_IAGHD STANDARD; PRT; 470 AA.
AC Q07577;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.

```

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OS Influenza A virus (strain A/Herring gull/DE/67/88).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38964;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
RT viruses."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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CC -----
DR EMBL, L06585; AAA3368.1; -.
DR HSSP, P06820; 2BAT.
DR InterPro: IPR001860; Glyco_hydro_34.
DR ProDom: PD000431; Glyco_hydro_34; 1.
KM Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52265 MW; 2BAF0B75B80539B7 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADM5W 5
DB 453 ADM5W 457

RESULT 8
ID NRAM_IAGHI STANDARD; PRT; 470 AA.
AC Q07578;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Egypt/511/89).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11401;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RT Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT viruses."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
DR EMBL, L06579; AAA43374.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur; 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
DR HydroLase; Glycosidase; Glycoprotein; Transmembrane.
KW DOMAIN 39 88 ANCHOR (BY SIMILARITY).
FT TRANSMEM 7 38 HYPERVARIABLE STALK REGION.
FT DOMAIN 39 88 HEAD OF NEURAMINIDASE.
FT ACT SITE 273 273 BY SIMILARITY.
FT ACT SITE 273 273 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52234 MW; C50B21050A37668 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 9
NRAM_IATKL STANDARD; PRT; 470 AA.
AC 007583;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Mallard/Edmonton/220/90).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38965;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RT Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT viruses."
RL Virology 193:868-876(1993).

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RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT viruses."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
DR EMBL, L06586; AAA43369.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur; 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
DR HydroLase; Glycosidase; Glycoprotein; Transmembrane.
KW DOMAIN 39 88 ANCHOR (BY SIMILARITY).
FT TRANSMEM 7 38 HYPERVARIABLE STALK REGION.
FT DOMAIN 39 88 HEAD OF NEURAMINIDASE.
FT ACT SITE 273 273 BY SIMILARITY.
FT ACT SITE 273 273 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52070 MW; 557630C3B11P2765 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 10
NRAM_IATKL STANDARD; PRT; 470 AA.
AC 007583;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Turkey/Minesota/501/78).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38984;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RT Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RT viruses."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side

```

CC chains of the host cell surface proteins and from the viral  
 CC envelope. Such a reaction prevents self-aggregation and facilitate  
 CC the mobility of the virus to and from the site of infection.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,  
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in  
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and  
 CC synthetic substrates.  
 CC -1- SUBUNIT: Homotrimer.  
 CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED  
 CC SPIKE ON THE SURFACE OF THE VIRION.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.  
 CC -----  
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 CC -----  
 CC DR EMBL; L06588; AAA43410.1; -.  
 CC DR HSRP; P06820; 2BAT.  
 CC DR InterPro: IPR001860; Glyco\_hydro\_34.  
 CC DR Pfam; PF00064; neur; 1.  
 CC DR ProDom; PD000431; Glyco\_hydro\_34; 1.  
 CC KM Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.  
 CC FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).  
 CC FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.  
 CC FT ACT\_SITE 273 273 BY SIMILARITY.  
 CC FT ACT\_SITE 275 275 BY SIMILARITY.  
 CC FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC SQ SEQUENCE 470 AA; 52352 MW; DE573742ABF1E6B CRC64;  
 CC -----  
 CC Query Match 90.0%; Score 36; DB 1; Length 470;  
 CC Best Local Similarity 100.0%; Pred. No. 62;  
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC -----  
 CC QY 1 ADMSW 5  
 CC DB 453 ADMSW 457  
 CC -----  
 CC RESULT 11  
 CC MRJ5\_APTME STANDARD; PRT; 598 AA.  
 CC AC 097432;  
 CC DT 28-FEB-2003 (Rel. 41, Created)  
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 CC DE Major royal jelly protein 5 precursor (MRJP-5) (See-milk protein).  
 CC GN MRJP5.  
 CC OS Apis mellifera (Honeybee).  
 CC OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygora;  
 CC OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
 CC OC Apidae; Apis.  
 CC OX NCBI\_TaxID=7460;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE=Head;  
 CC RA MEDLINE=99373663; PubMed=10441680;  
 CC RT "Albert S., Bhattacharya D., Kauding J., Schmitzova J., Simuth J.;  
 CC "The family of major royal jelly proteins and its evolution.";  
 CC J. Mol. Evol. 49:290-297(1999).  
 CC RL -1- PUNCTION: MAY PLAY AN IMPORTANT ROLE IN HONEYBEE NUTRITION. IT IS  
 CC FOUND IN THE ROYAL JELLY WHICH IS THE FOOD OF THE QUEEN HONEY BEE  
 CC LARVA. THE ROYAL JELLY DETERMINES THE DEVELOPMENT OF THE YOUNG  
 CC LARVAE AND IS RESPONSIBLE FOR THE HIGH REPRODUCTIVE ABILITY OF THE

CC HONEYBEE QUEEN.  
 CC -1- SUBCELLULAR LOCATION: Extracellular.  
 CC -1- TISSUE SPECIFICITY: HYPOPHARYNGEAL GLANDS OF NURSE HONEY BEES.  
 CC -1- DEVELOPMENTAL STAGE: PRODUCED BY THE CERVICAL GLANDULAR SYSTEM OF  
 CC THE NURSE HONEY BEE.  
 CC -1- SIMILARITY: BELONGS TO THE MAJOR ROYAL JELLY PROTEIN FAMILY.  
 CC -----  
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 CC -----  
 CC DR EMBL; AF004842; AAD01205.1; -.  
 CC DR InterPro: IPR003534; Royaljelly.  
 CC DR Pfam; PF03022; MRJP, 2.  
 CC DR PRINTS; PR01366; ROYALJELLY.  
 CC KM Signal; Repeat; Glycoprotein.  
 CC FT SIGNAL 1 17 POTENTIAL.  
 CC FT CHAIN 18 598 MAJOR ROYAL JELLY PROTEIN 5.  
 CC FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC SQ SEQUENCE 598 AA; 70236 MW; 2C603C7B7ACDF63 CRC64;  
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 CC Query Match 90.0%; Score 36; DB 1; Length 598;  
 CC Best Local Similarity 100.0%; Pred. No. 77;  
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC -----  
 CC QY 2 DMSWA 6  
 CC DB 113 DMSWA 117  
 CC -----  
 CC RESULT 12  
 CC PGLR\_PENGR STANDARD; PRT; 376 AA.  
 CC AC 093883;  
 CC DT 30-MAY-2000 (Rel. 39, Created)  
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 CC DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 CC DE Polygalacturonase precursor (EC 3.2.1.15) (Pg) (Pectinase).  
 CC GN PGL.  
 CC OS Penicillium griseoforme.  
 CC OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 CC OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.  
 CC OX NCBI\_TaxID=84562;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC STRAIN=CCT 6421;  
 CC RA Ribon A.B., Coelho J.L.C., Barros B.G., Araujo E.F.;  
 CC "Cloning and characterization of a gene encoding the  
 CC RT endopolygalacturonase of Penicillium griseoforme.";  
 CC Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 CC RL -1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-  
 CC galactosiduronic linkages in pectate and other galacturonans.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES  
 CC (POLYGALACTURONASES).  
 CC -----  
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 CC -----  
 CC DR EMBL; AF085238; AAC83692.1; -.  
 CC DR InterPro: IPR000743; Glyco\_hydro\_28.  
 CC DR InterPro: IPR006626; PbnL.

DR Pfam; PF00295; Glyco\_hydro\_28; 1.  
 DR SMART; SM00710; Pfh1; 5.  
 DR PROSITE; PS00502; POLYGALACTURONASE; 1.  
 KM Hydrolase; Glycosidase; Cell wall; Signal.  
 FT SIGNAL; 1 20 POTENTIAL.  
 FT CHAIN; 21 376 POLYGALACTURONASE.  
 SO SEQUENCE 376 AA; 38068 MW; 1ED1EC56ED56528 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 376;  
 Best Local Similarity 66.7%; Pred. No. 1e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 DB 349 SDMSWS 354

RESULT 13  
 ID FAS2\_SCHPO STANDARD; PRT; 1842 AA.  
 AC Q10289; O14163; P78973;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Fatty acid synthase subunit alpha (BC 2.3.1.96) [includes:  
 DE Acyl carrier; 3-oxoacyl-[acyl-carrier protein] reductase  
 DE (EC 1.1.1.100) (Beta-ketoacyl-[acyl-carrier protein] reductase); 3-oxoacyl-[acyl-carrier  
 DE protein] synthase (EC 2.3.1.41) (Beta-ketoacyl synthase)].  
 DE FAS2 OR LSD1 OR SPAC4A8.11C.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxId=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96354912; PubMed=8769419;  
 RA Saitoh S., Takahashi K., Nabeeshima K., Yamashita Y., Nakaseko Y.,  
 RA Hiraoka A., Yanagida M.;  
 RT "Aberrant mitosis in fission yeast mutants defective in fatty acid  
 RT synthetase and acetyl CoA carboxylase.";  
 RL J. Cell Biol. 134:949-961(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21363051; PubMed=11470243;  
 RA Yokoyama K., Saitoh S., Ishida M., Yamakawa Y., Nakamura K., Inoue K.,  
 RA Teguuchi R., Tokumura A., Nishijima M., Yanagida M., Seraka M.;  
 RT "Very long-chain fatty-acid-containing phospholipids accumulate in  
 RT fatty acid synthase temperature-sensitive mutant strains of the  
 RT fission yeast Schizosaccharomyces pombe fag2/lcd1.";  
 RL Biochim. Biophys. Acta 1532:223-233(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Brooks K., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Scouras J., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor A., Cronin A., Davis P., Fellwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hildalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Voicakeert G., Aert R., Robben J., Grynoprez B.,  
 RA Welbels I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gebel C., Fuchs M., Fitz C., Holzer E., Moesli D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Medler H., Wandt R., Pirmale B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakowski G.V., Ussery D., Barrett B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe.";  
 RN Nature 415:871-880(2002).  
 RN [4]  
 RP SEQUENCE OF 1-215 FROM N.A.  
 RA Koken M.H.M., de Rooij J.;  
 RL Submitted (Feb-1997) to the EMBL/GenBank/DBJ database.  
 RN [5]  
 RP SEQUENCE OF 1-20.  
 RX MEDLINE=94245730; PubMed=8188691;  
 RA Kaeslin E., Heyer W.-D.;  
 RT "Schizosaccharomyces pombe fatty acid synthase mediates DNA strand  
 RT exchange in vitro.";  
 RL J. Biol. Chem. 269:14103-14110(1994).  
 CC -1- FUNCTION: FATTY ACID SYNTHETASE. CATALYZES THE FORMATION OF  
 CC LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH.  
 CC THE ALPHA SUBUNIT CONTAINS DOMAINS FOR: ACYL CARRIER PROTEIN,  
 CC 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE, AND 3-OXOACYL-[ACYL-  
 CC CARRIER-PROTEIN] SYNTHASE. THIS SUBUNIT COORDINATES THE BINDING  
 CC OF THE SIX BETA SUBUNITS TO THE ENZYME COMPLEX.  
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + N malonyl-CoA + 2N NADPH = a  
 CC long-chain acyl-CoA + N CoA + N CO(2) + 2N NADP(+).  
 CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-[acyl-  
 CC carrier protein] = 3-oxoacyl-[acyl-carrier protein] + CO(2) +  
 CC [acyl-carrier protein].  
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.  
 CC -1- SUBUNIT: [Alpha(6)beta(6)] hexamers of two multifunctional  
 CC subunits (alpha and beta).  
 CC -1- SIMILARITY: TO THE FATTY ACID SYNTHETASE, SUBUNIT ALPHA FROM  
 CC OTHER FUNGI.  
 CC -----  
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 CC -----  
 CC EMBL; D83412; BAA11913.1; -;  
 CC EMBL; AB013747; BAB62029.1; -;  
 CC EMBL; Z88762; CAB11481.1; -;  
 CC EMBL; U82216; AAB39943.1; -;  
 CC DR PIR; A54083; A54083.  
 CC DR PIR; T38781; T38781.  
 CC DR PIR; T43409; T43409.  
 CC GenDB; Spombe; SPAC4A8.11C; -;  
 CC InterPro; IPR002582; ACPS.  
 CC InterPro; IPR000794; Ketoacyl-synt.  
 CC InterPro; IPR004568; Pantechm\_tm.  
 CC InterPro; IPR006162; Pantane\_attach.  
 CC DR Pfam; PF01648; ACPS; 1.  
 CC Pfam; PF02801; ketoacyl-synt\_C; 1.  
 CC Pfam; PF02801; ketoacyl-synt\_C; 1.  
 CC ProDom; PD004282; ACPS; 1.  
 CC TIGRfams; TIGR00556; pantechm\_tm; 1.  
 CC PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.  
 CC PROSITE; PS00606; B\_KETOACYL\_SYNTHASE; 1.  
 KM Fatty acid biosynthesis; Multifunctional enzyme; Oxidoreductase;  
 KM Transferrase; NADP; Phosphopantetheine.  
 FT DOMAIN 1 ?  
 FT DOMAIN 1 ?  
 FT BINDING 180 ? 1842 BETA-KETOACYL REDUCTASE.  
 FT BINDING 180 180 PHOSPHOPANTHETHEINE (BY SIMILARITY).  
 FT ACT SITE 1262 1262 BETA-KETOACYL SYNTHASE (BY SIMILARITY).  
 FT ACT SITE 107 107 S -> A (IN REF. 4).  
 FT CONFLICT 422 422 K -> R (IN REF. 1).



SQ SEQUENCE 1842 AA; 202168 MW; E4019F2D133EB571 CRC64;  
 Query Match 85.0%; Score 34; DB 1; Length 1842;  
 Best Local Similarity 66.7%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 :||:|  
 DB 400 SDWNWA 405

RESULT 14  
 NOS3\_SHEEP STANDARD; PRT; 99 AA.  
 AC P79209;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type II) (NOSIII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS) (Fragment).  
 GN NOS3 OR NOS.  
 OS Ovis aries (Sheep).  
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.  
 OC NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Endothelial cells;  
 RA Aguan K., Weiner C.P.;  
 RT "Effect of hypoxia on the microvasculature of developing fetal brain of sheep: a studies on the expression pattern of constitutive forms of nitric oxide synthase."  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A cAMP-MEDIATED SIGNAL TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline + nitric oxide + N NADP(+).  
 CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF THE ENZYME (BY SIMILARITY).  
 CC -1- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN (BY SIMILARITY).  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: U76738; AAB40705.1; -.  
 DR HSSP; P29473; IDOC.  
 DR InterPro; IPR004030; NO\_synthase.  
 DR Pfam; PF02898; NO\_synthase; 1.  
 DR PROSITE; PS60001; NOS; PARTIAL.  
 KM Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Calcium-binding; Heme; Multigene family.  
 FT NON\_TER 1  
 FT NON\_TER 99  
 SQ SEQUENCE 99 AA; 11034 MW; 82C3C765557031DA CRC64;

Query Match 82.5%; Score 33; DB 1; Length 99;  
 Best Local Similarity 80.0%; Pred. No. 43;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
 :||:|  
 DB 65 ADMAW 69

RESULT 15  
 Y132\_METUA STANDARD; PRT; 220 AA.  
 ID Y132\_METUA  
 AC 057596;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein Mj0132.  
 GN Mj0132.  
 OS Methanococcus jannaschii.  
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.  
 OC NCBI\_TaxID=2190;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;  
 RX MEDLINE=96337999; PubMed=8688087;  
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weissbrock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghegan N.S.M., Feldman J.F., Fuhrmann J.L., Nguyen D., Uliaszek T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Rasmussen M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Frazer C.W., Smith H.O., Woese C.R., Venter J.C.;  
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";  
 RL Science 273:1058-1073 (1996).  
 CC -1- SIMILARITY: TO M. JANNASCHII MJ1220 AND MJEC142.  
 CC -1- SIMILARITY: WITH TYPE I RESTRICTION SYSTEM ADENINE METHYLASES (M SUBUNIT).  
 CC -----  
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 CC -----  
 CC EMBL: U67470; AAB98113.1; -.  
 DR PIR; D64316; D64316.  
 DR TIGR; Mj0132; -.  
 DR InterPro; IPR003356; N6\_DNA\_Mtase.  
 DR Pfam; PF02384; N6\_Mtase; 1.  
 KM Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 220 AA; 25766 MW; 710DDA84C7A47954 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 220;  
 Best Local Similarity 80.0%; Pred. No. 88;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
 :||:|  
 DB 33 ADMAW 37

Search completed: February 18, 2004, 14:28:04  
 Job time : 3.55263 secs

GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 / Search time 6.5921 Seconds  
(without alignment)

87.531 Million cell updates/sec

Title: US-09-643-260-6

Perfect score: 40

Sequence: 1 ADMSNA 6

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	610	2	T35222
2	37	92.5	885	2	C83441
3	36	90.0	374	2	B83241
4	36	90.0	889	2	B87304
5	34	85.0	275	2	T05822
6	34	85.0	617	2	C84922
7	34	85.0	1842	2	T33409
8	34	85.0	1842	2	T38781
9	33	82.5	132	2	S65785
10	33	82.5	198	2	B82531
11	33	82.5	220	2	D64316
12	33	82.5	232	2	S58353
13	33	82.5	239	2	D90470
14	33	82.5	257	2	D87152
15	33	82.5	276	2	B75337
16	33	82.5	304	2	F63632
17	33	82.5	310	2	JC7853
18	33	82.5	324	2	AB3548
19	33	82.5	328	2	E72424
20	33	82.5	333	2	S47246
21	33	82.5	350	2	S71923
22	33	82.5	368	2	H90998
23	33	82.5	410	2	D75475
24	33	82.5	415	2	AB1844
25	33	82.5	418	2	AB1460
26	33	82.5	421	2	AF1097
27	33	82.5	433	2	T31511
28	33	82.5	433	2	T31511
29	33	82.5	467	2	G82697

30	33	82.5	478	2	B89790	6-phospho-beta-glu
31	33	82.5	479	2	I39953	6-phospho-beta-glu
32	33	82.5	492	2	S03098	acetylarginine precu
33	33	82.5	529	2	C86958	probable GMP synth
34	33	82.5	539	2	T15256	hypothetical prote
35	33	82.5	578	2	C64452	restriction modifi
36	33	82.5	590	2	S72813	GMP synthase (glut
37	33	82.5	616	2	C69226	type I restriction
38	33	82.5	623	2	E75221	type I restriction
39	33	82.5	765	2	S76795	hypothetical prote
40	33	82.5	836	2	D82177	conserved hypochet
41	33	82.5	1202	2	S71424	nitric-oxide synth
42	33	82.5	1203	1	A47501	nitric-oxide synth
43	33	82.5	1205	1	A38943	nitric-oxide synth
44	33	82.5	1329	2	D87226	conserved hypochet
45	33	82.5	1409	2	S74916	alkaline phosphata

#### ALIGNMENTS

RESULT 1  
T35222  
hypothetical protein SC5C7.15 SC5C7.15 - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 05-Nov-1999  
C:Accession: T35222  
R:Seeger, K.V.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, September 1998  
A:Reference number: Z21572  
A:Accession: T35222  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-610 <SEE>  
A:Cross-references: EMBL:AL031515; PIDN:CAA20627.1; GSPDB:GN00070; SCODEB:SC5C7.15  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: SCODEB:SC5C7.15

Query Match 92.5%, Score 37, DB 2, Length 610;  
Best Local Similarity 83.3%, Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSNA 6  
DB 83 ADMSNA 88

#### RESULT 2

C83441  
two-component sensor KdpD PA1636 [imported] - Pseudomonas aeruginosa (strain PAO1)

C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: C83441

R:Stover, C.K.; Phan, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warener, P.; Hickey, M.J.; E  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lardig, K.; Lin

.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path

A:Reference number: AB2950; MUID:2043737; PMID:10984043

A:Accession: C83441

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1885 <STO>

A:Cross-references: GB:AB004591; GB:AE004091; NID:G9947599; PIDN:AA05025.1; GSPDB:GNOC

A:Experimental source: strain PAO1

C:Genetics:  
A:Gene: kdpD; PA1636

Query Match 92.5%, Score 37, DB 2, Length 885;  
Best Local Similarity 83.3%, Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMGMA 6  
|||||  
563 ADMGMA 568

## RESULT 3

B83241  
conserved hypothetical protein PA3230 [imported] - Pseudomonas aeruginosa (strain PAO1)  
C/Species: Pseudomonas aeruginosa  
C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C/Accession: B83241  
R/Stover, C.K.; Plam, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidig, K.; Lim,  
.; Loy, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A/Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho  
gen  
A/Reference number: A82950; MUID:2043737; PMID:10964043  
A/Accession: B83241  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-374 <STO>  
A/Cross-references: GB:AE004746; GB:AE004091; NID:g9949350; PIDN:AG06618.1; GSPDB:GN001  
C/Experimental source: strain PAO1  
C/Genetics:  
A/Genes: PA3230

Query Match 90.0%; Score 36; DB 2; Length 374;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
|||||  
DB 61 DMSWA 85

## RESULT 4

E87304  
Tomb-dependent receptor [imported] - Caulobacter crescentus  
C/Species: Caulobacter crescentus  
C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001  
C/Accession: E87304  
R/Nierman, W.C.; Poldylyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eilen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A/Title: Complete Genome Sequence of Caulobacter crescentus.  
A/Reference number: A87249; MUID:21173698; PMID:11259647  
A/Accession: E87304  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-889 <STO>  
A/Cross-references: GB:AE005673; NID:g13421615; PIDN:AAK22433.1; GSPDB:GN00148  
C/Genetics:  
A/Genes: CC0446

Query Match 90.0%; Score 36; DB 2; Length 889;  
Best Local Similarity 100.0%; Pred. No. 2,2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
|||||  
DB 618 ADMSW 622

## RESULT 5

T05822  
hypothetical protein TSK18.170 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 13-Aug-1999  
C/Accession: T05822  
R/Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Be  
submitted to the Protein Sequence Database, April 1998  
A/Reference number: Z15453

A/Accession: T05822  
A/Molecule type: DNA  
A/Residues: 1-275 <BEV>  
A/Cross-references: EMBL:AL022580  
A/Experimental source: cultivar Columbia; BAC clone TSK18  
C/Genetics:  
A/Map position: 4  
A/Intons: 103/3; 141/3; 169/1; 206/3  
A/Note: TSK18.170

Query Match 85.0%; Score 34; DB 2; Length 275;  
Best Local Similarity 66.7%; Pred. No. 1,4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMGMA 6  
|||||  
DB 57 DMSWS 62

## RESULT 6

C84922  
probable protein kinase [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C/Accession: C84922  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Talion, I  
eues, D.; Nierman, W.C.; White, O.; Eilen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-617 <STO>  
A/Cross-references: GB:AE002093; NID:g44249408; PIDN:AMD13705.1; GSPDB:GN00139  
C/Genetics:  
A/Genes: AT2g48010  
A/Map position: 2

Query Match 85.0%; Score 34; DB 2; Length 617;  
Best Local Similarity 66.7%; Pred. No. 3,1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMGMA 6  
|||||  
DB 500 ADMGMA 505

## RESULT 7

T43409  
probable fatty-acid synthase (EC 2.3.1.85) alpha chain - fission yeast (Schizosaccharo  
myces pombe)  
N/Alternate names: fatty acid synthetase alpha subunit  
C/Species: Schizosaccharomyces pombe  
C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
C/Accession: T43409  
R/Satoh, S.; Takahashi, K.; Nabeshima, K.; Yamashita, Y.; Nakaseko, Y.; Hitate, A.; Yi  
J.; Cell Biol. 134, 949-961, 1996  
A/Title: Aberrant mitosis in fission yeast mutants defective in fatty acid synthetase  
A/Reference number: Z2493; MUID:96354912; PMID:8769419  
A/Accession: T43409  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1842 <SAI>  
A/Cross-references: EMBL:D83412; NID:g1199959; PIDN:BA11913.1; PID:g1199960  
C/Genetics:  
A/Note: Isd1+

Query Match 85.0%; Score 34; DB 2; Length 1842;  
Best Local Similarity 66.7%; Pred. No. 9,4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
DB 400 SDMNWA 405

## RESULT 8

T88781  
fatty acid synthase, subunit alpha - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jan-2000  
C:Accession: T88781  
R:Skellton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
Submitted to the EMBL Data Library, August 1997  
A:Reference number: 221751  
A:Accession: T88781  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1842 <SKP>  
A:Cross-references: EMBL:298762; PIDN:CA11481.1; GSPDB:GN00066; SPDB:SPAC4A8.11c  
A:Experimental source: strain 972h-; cosmid C4A8  
C:Genetics:  
A:Gene: SPDB:SPAC4A8.11c  
A:Map position: 1  
C:Superfamily: yeast fatty-acid synthase

Query Match 85.0%; Score 34; DB 2; Length 1842;  
Best Local Similarity 66.7%; Pred. No. 9.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
DB 400 SDMNWA 405

## RESULT 9

S65785  
mel-13a protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 26-Aug-1999  
C:Accession: S65785  
R:Teru, O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.  
Biochim. Biophys. Acta 1305, 109-112, 1996  
A:Title: Cloning and characterization of two transcripts generated from the mel-13 gene  
A:Reference number: S65785; MUID:96180310; PMID:8597592  
A:Accession: S65785  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-132 <TET>  
A:Cross-references: EMBL:U35309  
C:Genetics:  
A:Gene: mel-13  
C:Superfamily: mouse mel-13a protein  
C:Keywords: alternative splicing

Query Match 82.5%; Score 33; DB 2; Length 132;  
Best Local Similarity 80.0%; Pred. No. 96;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
DB 57 SDMSW 61

## RESULT 10

B82531  
conserved hypothetical protein XF2666 [imported] - Xylella fastidiosa (strain 9asc)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 17-Nov-2000  
C:Accession: B82531  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347  
A>Note: for a complete list of authors see reference number A59328 below  
A:Accession: B82531  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-198 <SIM>

A:Cross-references: GB:AE004072; GB:AE003849; NID:99107884; PIDN:AAE85463.1; GSPDB:GN01  
A:Experimental source: strain 9asc  
R:Simson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;  
Brienes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre,  
as-Neto, E.; Docena, C.; El-Dorzy, H.; Facinani, A.P.; Ferreira, A.J.S.  
Submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Frega, J.S.; Franca, S.C.; Franco, M.C.; Frol  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laiz  
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins,  
A:Authors: Martins, E.M.P.; Matukuma, A.C.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmiter, D.  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa, V.E.; de Sa, R.G.; Santelli, R.V.; Sawa  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva  
M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF2666  
C:Superfamily: conserved hypothetical protein M1677

Query Match 82.5%; Score 33; DB 2; Length 198;  
Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
DB 135 DMNWA 139

## RESULT 11

D64316  
restriction modification enzyme subunit M1 homolog - Methanococcus jannaschii  
C:Species: Methanococcus jannaschii  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Aug-2002  
C:Accession: D64316  
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,  
R.; Reich, C.T.; Overbeek, R.; Kikunas, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.  
xon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
Science 273, 1058-1073, 1996  
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,  
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii  
A:Reference number: A64300; MUID:96337999; PMID:8688087  
A:Accession: D64316  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-220 <BDL>  
A:Cross-references: GB:U67470; GB:L77117; NID:92826247; PIDN:AAE8113.1; PID:91592267;  
C:Genetics:  
A:Map position: REV127472-126810  
A:Start codon: TTG  
C:Superfamily: type I site-specific deoxyribonuclease chain hsdM (associate member)

Query Match 82.5%; Score 33; DB 2; Length 220;  
Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
DB 33 ADMAW 37

## RESULT 12

S58353  
C01b protein - sheep (fragment)  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 14-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 21-Jan-2000  
C:Accession: S58353

R:Ferguson, E.D.; Dutle, B.M.; Hein, W.; Hopkins, J.  
submitted to the EMBL Data Library, July 1995  
A:Description: The ovine CD1 gene family contains at least four CD1B homologues.  
A:Reference number: 559353  
A:Accession: S59353

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-232 <FER>  
A:Cross-references: EMBL:X90567; NID:g945010; PIDN:CA62187.1; PID:g945011  
A:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F:115-180/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 33; DB 2; Length 232;  
Best Local Similarity 80.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
|||:|  
Db 156 ADMTW 160

RESULT 13  
D90470  
hypothetical protein cySH [imported] - Sulfolobus solfataricus  
C:Species: Sulfolobus solfataricus  
C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 15-Jun-2001  
A:Accession: D90470  
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyer, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.  
arrett, R.A.; Ragan, M.A.; Sersen, C.W.; Van der Oost, J.  
submitted to Genbank, April 2001  
A:Description: Sulfolobus solfataricus complete genome.  
A:Reference number: A99139  
A:Accession: D90470  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-239 <RUR>  
A:Cross-references: GB:AE006641; NID:g13816282; PIDN:AAK43019.1; GSPDB:GN00155  
C:Genetics:  
A:Gene: cySH  
C:Superfamily: 3'-phosphoadenosine 5'-phosphosulfate reductase

Query Match 82.5%; Score 33; DB 2; Length 233;  
Best Local Similarity 80.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
|||:|  
Db 172 ADMTW 176

RESULT 14  
D87152  
conserved hypothetical protein ML1945 [imported] - Mycobacterium leprae  
C:Species: Mycobacterium leprae  
C>Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
A:Accession: D87152  
R:Coile, S.T.; Eiglmeyer, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho-  
eam, M.A.; Rutherford, K.M.  
Nature 409, 1007-1011, 2001  
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq  
A:Title: Massive gene decay in the leprosy bacillus.  
A:Reference number: A86909; PMID:21128732; PMID:11234002  
A:Accession: D87152  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-257 <STO>  
A:Cross-references: GB:AL450380; NID:g13093601; PIDN:CAC30900.1; GSPDB:GN00147  
C:Genetics:  
A:Gene: ML1945  
C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1100

Query Match 82.5%; Score 33; DB 2; Length 257;  
Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||:|  
Db 11 ADMSWA 16

RESULT 15  
B75337  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
A:Accession: B75337  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uckerback, T.; Zalewski, C.; I  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; PMID:20036896; PMID:10567266  
A:Accession: B75337  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-276 <WHI>  
A:Cross-references: GB:AE002032; GB:AE000513; NID:g6459715; PIDN:AAF11479.1; PID:g6459.  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DR1923  
A:Map position: 1

Query Match 82.5%; Score 33; DB 2; Length 276;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
|||:|  
Db 84 ADMAW 88

Search completed: February 18, 2004, 14:38:39  
Job time : 7.5921 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds  
(without alignments)  
35.929 Million cell updates/sec

Title: US-09-643-260-6  
Perfect score: 40  
Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	938	4 US-09-252-991A-23882	Sequence 23882, A
2	36	90.0	68	4 US-09-252-991A-18367	Sequence 18367, A
3	36	90.0	142	4 US-09-252-991A-31533	Sequence 31533, A
4	36	90.0	174	4 US-09-325-932A-163	Sequence 163, App
5	36	90.0	225	4 US-09-325-932A-162	Sequence 162, App
6	36	90.0	242	4 US-09-345-936B-3	Sequence 3, App1
7	36	90.0	378	4 US-09-325-932A-158	Sequence 158, App
8	36	90.0	445	4 US-09-252-991A-22368	Sequence 22368, A
9	36	90.0	462	4 US-09-252-991A-21704	Sequence 21704, A
10	34	85.0	44	3 US-08-905-223-274	Sequence 274, App
11	33	82.5	74	1 US-08-379-538-2	Sequence 2, App1
12	33	82.5	136	2 US-08-774-065-2	Sequence 2, App1
13	33	82.5	164	4 US-09-252-991A-23817	Sequence 23817, A
14	33	82.5	218	1 US-08-032-848C-10	Sequence 10, App1
15	33	82.5	218	1 US-08-438-870-10	Sequence 10, App1
16	33	82.5	218	1 US-08-159-948B-34	Sequence 34, App1
17	33	82.5	218	2 US-08-448-873-34	Sequence 34, App1
18	33	82.5	218	3 US-08-362-452D-34	Sequence 34, App1
19	33	82.5	218	3 US-09-216-295-1	Sequence 18, App1
20	33	82.5	218	4 US-08-507-362A-18	Sequence 18, App1
21	33	82.5	232	3 US-09-146-770-1	Sequence 1, App1
22	33	82.5	232	4 US-09-633-084-1	Sequence 1, App1
23	33	82.5	232	4 US-10-075-872-1	Sequence 1, App1
24	33	82.5	232	4 US-10-261-997-1	Sequence 1, App1
25	33	82.5	234	1 US-08-032-848C-9	Sequence 9, App1
26	33	82.5	234	1 US-08-438-870-9	Sequence 9, App1
27	33	82.5	234	3 US-09-146-770-3	Sequence 3, App1

28	33	82.5	234	3 US-09-146-770-4	Sequence 4, App1
29	33	82.5	234	3 US-09-216-295-3	Sequence 3, App1
30	33	82.5	234	3 US-09-216-295-4	Sequence 4, App1
31	33	82.5	234	4 US-09-633-084-3	Sequence 3, App1
32	33	82.5	234	4 US-09-633-084-4	Sequence 4, App1
33	33	82.5	234	4 US-10-075-872-3	Sequence 3, App1
34	33	82.5	234	4 US-10-075-872-4	Sequence 4, App1
35	33	82.5	234	4 US-10-261-997-3	Sequence 3, App1
36	33	82.5	234	4 US-10-261-997-4	Sequence 4, App1
37	33	82.5	239	4 US-09-216-295-15	Sequence 15, App1
38	33	82.5	316	4 US-09-252-991A-17312	Sequence 17312, A
39	33	82.5	467	1 US-08-140-104A-2	Sequence 2, App1
40	33	82.5	670	4 US-09-252-991A-22079	Sequence 22079, A
41	33	82.5	1205	1 US-07-908-245-2	Sequence 2, App1
42	33	82.5	1205	2 US-08-319-866-10	Sequence 10, App1
43	33	82.5	1205	3 US-09-123-708-6	Sequence 6, App1
44	33	82.5	1205	3 US-09-123-624-6	Sequence 6, App1
45	32	80.0	5	6 5217869-75	Patent No. 5217869

## ALIGNMENTS

RESULT 1  
US-09-252-991A-23882  
Sequence 23882, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 23882  
LENGTH: 938  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23882  
Query Match  
Best Local Similarity 92.5%; Score 37; DB 4; Length 938;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
CY 1 ADMSWA 6  
DB 581 ADMSWA 586  
RESULT 2  
US-09-252-991A-18367  
Sequence 18367, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 18367  
LENGTH: 68  
TYPE: PRT

ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18367

Query Match 90.0%; Score 36; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
DB 2 DMSWA 6

RESULT 3  
US-09-252-991A-31533  
Sequence 31533, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 31533  
LENGTH: 142  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-31533

Query Match 90.0%; Score 36; DB 4; Length 142;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
DB 94 ADMSW 98

RESULT 4  
US-09-325-932A-163  
Sequence 163, Application US/09325932A  
Patent No. 6451604  
GENERAL INFORMATION:

APPLICANT: Plim, Barry  
APPLICANT: Laabam, Annette  
TITLE OF INVENTION: Compositions affecting programmed cell  
FILE REFERENCE: 1022  
CURRENT APPLICATION NUMBER: US/09/325,932A  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 206  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 163  
LENGTH: 174  
TYPE: PRT  
ORGANISM: Bucalypus grandis  
US-09-325-932A-163

Query Match 90.0%; Score 36; DB 4; Length 174;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
DB 109 ADMSW 113

RESULT 5

US-09-325-932A-162  
Sequence 162, Application US/09325932A  
Patent No. 6451604  
GENERAL INFORMATION:

APPLICANT: Plim, Barry  
APPLICANT: Laabam, Annette  
TITLE OF INVENTION: Compositions affecting programmed cell  
FILE REFERENCE: 1022  
CURRENT APPLICATION NUMBER: US/09/325,932A  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 206  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 162  
LENGTH: 225  
TYPE: PRT  
ORGANISM: Bucalypus grandis  
US-09-325-932A-162

Query Match 90.0%; Score 36; DB 4; Length 225;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
DB 100 ADMSW 104

RESULT 6  
US-09-345-236B-3  
Sequence 3, Application US/09345236B  
Patent No. 6521454  
GENERAL INFORMATION:

APPLICANT: Becnel, James J.  
APPLICANT: Tuku, Fukuda  
APPLICANT: Moser, Bettina  
APPLICANT: Cockburn, Andrew  
APPLICANT: White, Susan R.  
APPLICANT: Undeen, Albert H.  
TITLE OF INVENTION: No. 6521454e1 Baculoviruses, Insecticidal  
FILE REFERENCE: 21042.0004  
CURRENT APPLICATION NUMBER: US/09/345,236B  
CURRENT FILING DATE: 1999-06-30  
NUMBER OF SEQ ID NOS: 148  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 242  
TYPE: PRT  
ORGANISM: mosquito baculovirus  
US-09-345-236B-3

Query Match 90.0%; Score 36; DB 4; Length 242;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
DB 80 DMSWA 84

RESULT 7  
US-09-325-932A-158  
Sequence 158, Application US/09325932A  
Patent No. 6451604  
GENERAL INFORMATION:

APPLICANT: Plim, Barry  
APPLICANT: Laabam, Annette  
TITLE OF INVENTION: Compositions affecting programmed cell  
FILE REFERENCE: 1022  
CURRENT APPLICATION NUMBER: US/09/325,932A  
CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 206  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 158  
LENGTH: 378  
TYPE: PRT  
ORGANISM: Eucalyptus grandis  
US-09-325-932A-158

Query Match 90.0%; Score 36; DB 4; Length 378;  
Best Local Similarity: 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
Db 128 ADMSW 132

RESULT 8  
US-09-252-991A-22368  
Sequence 22368, Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22368

LENGTH: 445

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-22368

Query Match 90.0%; Score 36; DB 4; Length 445;  
Best Local Similarity: 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
Db 304 DMSWA 308

RESULT 9

US-09-252-991A-21704

Sequence 21704, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 21704

LENGTH: 462

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21704

Query Match 90.0%; Score 36; DB 4; Length 462;  
Best Local Similarity: 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
Db 169 DMSWA 173

RESULT 10

US-08-905-223-274

Sequence 274, Application US/08905223

Patent No. 6222029

GENERAL INFORMATION:

APPLICANT: Edwards, Jean-Baptiste D.

APPLICANT: Lacroix, Bruno

TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS

NUMBER OF SEQUENCES: 503

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear

STREET: 501 West Broadway

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-3505

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Win95

SOFTWARE: Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/905,223

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Israel, Ned A.

REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550

TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 274:

SEQUENCE CHARACTERISTICS:

LENGTH: 44 amino acids

TYPE: AMINO ACID

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

ORIGINAL SOURCE:

ORGANISM: Homo Sapiens

TISSUE TYPE: Brain

FEATURE:

NAME/KEY: sig\_peptide

LOCATION: -26...-1

IDENTIFICATION METHOD: Von Heljne matrix

OTHER INFORMATION: score 9.6

US-08-905-223-274

Query Match 85.0%; Score 34; DB 3; Length 44;  
Best Local Similarity: 83.3%; Pred. No. 41;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSW 6  
Db 19 ADMSW 24

RESULT 11

US-08-379-538-2

Sequence 2, Application US/08379538

Patent No. 5804554

GENERAL INFORMATION:

APPLICANT: Volkman, Robert A.

APPLICANT: Saccomano, Nicholas A.

APPLICANT: Nason II, Deane M.



APPLICANT: Heck, Steven D.  
APPLICANT: Ronau, Robert T.  
TITLE OF INVENTION: CALCIUM CHANNEL BLOCKING POLYPEPTIDES  
TITLE OF INVENTION: FROM FILISTATA HIBERNALIS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pfizer Inc  
STREET: 235 East 42nd Street  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/379,538  
FILING DATE: 3-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/887073  
FILING DATE: 21-MAY-1992  
APPLICATION NUMBER: PCT/US93/03921  
FILING DATE: 30-APRIL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ziehlnekt, Bryan  
REGISTRATION NUMBER: 34,462  
REFERENCE/DOCKET NUMBER: PC8175A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 573-4585  
TELEFAX: (212) 573-1939  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 74 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Filistata hibernalis  
TISSUE TYPE: venom  
US-08-379-538-2

Query Match 82.5%; Score 33; DB 1; Length 74;  
Best Local Similarity 80.0%; Pred. No. 95;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSMA 6  
DB 52 DMSWS 56

RESULT 12  
US-08-774-065-2  
Sequence 2, Application US/08774065  
GENERAL INFORMATION:  
APPLICANT: Bower, Benjamin  
APPLICANT: Clarkson, Kathleen  
APPLICANT: Latenay, Edmund  
APPLICANT: Ward, Michael  
TITLE OF INVENTION: NOVEL OVERSIZED CELLULASE COMPOSITIONS  
TITLE OF INVENTION: FOR USE IN DETERGENT COMPOSITIONS AND  
TITLE OF INVENTION: IN THE TREATMENT OF TEXTILES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENENCOR INTERNATIONAL  
STREET: 925 PAGE MILL ROAD  
CITY: PALO ALTO

STATE: CALIFORNIA  
COUNTRY: UNITED STATES  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Fastseq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/774,065  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Glasster, Debra J.  
REGISTRATION NUMBER: 33,888  
REFERENCE/DOCKET NUMBER: GC368  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-846-7620  
TELEFAX: 415-845-6504  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 136 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-774-065-2

Query Match 82.5%; Score 33; DB 2; Length 136;  
Best Local Similarity 66.7%; Pred. No. 1,76+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSMA 6  
DB 62 ADMOMS 67

RESULT 13  
US-09-252-991A-23817  
Sequence 23817, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 23817  
LENGTH: 164  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23817

Query Match 82.5%; Score 33; DB 4; Length 164;  
Best Local Similarity 83.3%; Pred. No. 2,16+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSMA 6  
DB 132 AGMSMA 137

RESULT 14  
US-08-032-848C-10  
Sequence 10, Application US/08032848C  
Patent No. 5475101

GENERAL INFORMATION:  
APPLICANT: Ward, Michael  
APPLICANT: Clarkson, Kathleen A.  
APPLICANT: Weiss, Geoffrey L.  
APPLICANT: Larens, Edward  
APPLICANT: Lorch, Jeffrey D.  
TITLE OF INVENTION: Purification and Molecular Cloning of  
TITLE OF INVENTION: EG III Cellulase  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genencor International  
STREET: 180 Kimball Way  
CITY: South San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/032,848C  
FILING DATE: MAR 17 1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Horn, Margaret A.  
REGISTRATION NUMBER: 33,401  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415 742-7356  
TELEFAX: 415 742-7217  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 218 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-032-848C-10

Query Match 82.5%; Score 33; DB 1; Length 218;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||  
: 46 ADWQMS 51

Db

RESULT 15  
US-08-438-870-10  
Sequence 10, Application US/08438870  
Patent No. 5753484  
GENERAL INFORMATION:  
APPLICANT: Ward, Michael  
APPLICANT: Clarkson, Kathleen A.  
APPLICANT: Weiss, Geoffrey L.  
APPLICANT: Larens, Edward  
APPLICANT: Lorch, Jeffrey D.  
TITLE OF INVENTION: Purification and Molecular Cloning of EG  
TITLE OF INVENTION: III Cellulase  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genencor International  
STREET: 180 Kimball Way  
CITY: South San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438,870  
FILING DATE: May 10, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Christopher L. Stone  
REGISTRATION NUMBER: 35,696  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415 742-7555  
TELEFAX: 415 742-7217  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 218 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-438-870-10

Query Match 82.5%; Score 33; DB 1; Length 218;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
|||  
: 46 ADWQMS 51

Db

Search completed: February 18, 2004, 14:41:46  
Job time : 7.06579 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds  
(without alignments)  
79.423 Million cell updates/sec

Title: US-09-643-260-5

Perfect score: 40

Sequence: 1 LDMSWA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	90.0	362	1 DCUP_YEAST	P32347 baccharomyc
2	36	90.0	598	1 MRJ5_APIME	O97432 apis mellif
3	36	90.0	745	1 IKKA_HUMAN	O15111 h inhibitor
4	36	90.0	745	1 IKKA_MOUSE	O60880 m inhibitor
5	36	90.0	756	1 IKKB_HUMAN	O14920 homo sapien
6	36	90.0	757	1 IKKB_MOUSE	O08351 mus musculu
7	36	90.0	757	1 IKKB_RAT	O94778 rattus norv
8	36	90.0	983	1 EPA3_CHICK	P29318 gallus gall
9	36	90.0	983	1 EPA3_HUMAN	P29320 homo sapien
10	36	90.0	983	1 EPA3_MOUSE	P29319 mus musculu
11	36	90.0	984	1 EPA3_RAT	O08680 rattus norv
12	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
13	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
14	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
15	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
16	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
17	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
18	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
19	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
20	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
21	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
22	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
23	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
24	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
25	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
26	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
27	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
28	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
29	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
30	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
31	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
32	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu
33	36	90.0	984	1 EPA3_MOUSE	P29319 mus musculu

34	32	80.0	470	1	NRAM_IADBU	O07570 influenza a
35	32	80.0	470	1	NRAM_IADCH	O07571 influenza a
36	32	80.0	470	1	NRAM_IADH2	O07572 influenza a
37	32	80.0	470	1	NRAM_IADW2	O07573 influenza a
38	32	80.0	470	1	NRAM_IADU3	O07574 influenza a
39	32	80.0	470	1	NRAM_IADGN	O07575 influenza a
40	32	80.0	470	1	NRAM_IADGD	O07576 influenza a
41	32	80.0	470	1	NRAM_IADCT	O07577 influenza a
42	32	80.0	470	1	NRAM_IADAE	O07578 influenza a
43	32	80.0	470	1	NRAM_IADTL	O07585 influenza a
44	32	80.0	479	1	BGLA_BACSU	P42973 bacillus su
45	32	80.0	500	1	PROP_ECOLI	P30848 escherichia

## ALIGNMENTS

RESULT 1  
ID DCUP\_YEAST STANDARD, PRT, 362 AA.  
AC P32347,  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UDP).  
GN HEM12 OR HEM6 OR POP3 OR YD9609.03.  
OS Saccharomycetes cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92249304; PubMed=1576986;  
RA Garey J.R., Labbe-Bois R., Chelcowska A., Rycka J., Harrison L.,  
RA Kushner J., Labbe P.;  
RT "Uroporphyrinogen decarboxylase in Saccharomycetes cerevisiae, HEM12  
RT gene sequence and evidence for two conserved glycines essential for  
RT enzymatic activity.";  
RL Eur. J. Biochem. 205:1011-1016(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93348774; PubMed=8346678;  
RA Diflumer C., Larocque R., Keng T.;  
RT "Molecular analysis of HEM6 (HEM12) in Saccharomycetes cerevisiae, the  
RT gene for uroporphyrinogen decarboxylase.";  
RL Yeast 9:613-623(1993).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX STRAIN=8286C / AB972;  
RA Hunt S., Bowman S., Harris D., Barrell B.G., Rajandream M.A.;  
RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP MEDLINE=93111946; PubMed=1471989;  
RA Chelcowska A., Zoedek T., Garey J.R., Kushner J., Rycka J.,  
RA Labbe-Bois R.;  
RT "Identification of amino acid changes affecting yeast  
RT uroporphyrinogen decarboxylase activity by sequence analysis of hem12  
RT mutant alleles.";  
RL Biochem. J. 288:753-757(1992).  
RN [5]  
RP CARALYTIC ACTIVITY: Uroporphyrinogen-III = coproporphyrinogen + 4  
CO(2).  
CC -1- PATHWAY: Porphyrin and heme biosynthesis.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: BELONGS TO THE UROPORPHYRINOGEN DECARBOXYLASE FAMILY.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
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CC EMBL; X63721; CAA45253.1; -  
 DR EMBL; Z19089; CAA79514.1; -  
 DR EMBL; Z49209; CAA89078.1; -  
 DR PIR; S23471; S23471.  
 DR HSSP; P06133; IURO.  
 DR SGD; S0002454; HEM12.  
 DR GO; GO:0004853; F:uroporphyrinogen decarboxylase activity; IMP.  
 DR GO; GO:0006783; P:heme biosynthesis; IMP.  
 DR InterPro; IPR006361; Heme.  
 DR InterPro; IPR000257; Uro\_decboxyls.  
 DR Pfam; PF01208; URO-D; 1.  
 DR ProDom; PD003225; Uro\_decboxyls; 1.  
 DR TIGRfam; TIGR01464; Heme; 1.  
 DR PROSITE; PS00906; UROD\_1; 1.  
 DR PROSITE; PS00907; UROD\_2; 1.  
 DR Lyase; Decarboxylase; Forphyrin biosynthesis; Heme biosynthesis.  
 FT VARIANT 59 59 S -> F (IN HEM12-6 AND HEM12-12).  
 FT VARIANT 62 62 T -> I (IN HEM12-14).  
 FT VARIANT 107 107 L -> S (IN HEM12-3 AND HEM12-13).  
 FT VARIANT 215 215 S -> N (IN HEM12-2 AND HEM12-11).  
 FT MUTAGEN 33 G -> D: INACTIVATION.  
 FT MUTAGEN 300 G -> D: INACTIVATION.  
 SQ SEQUENCE 362 AA; 41349 MW; E9CB3A48E62BC277 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDMSW 5  
 Db 279 LDMSW 283

RESULT 2  
 MRJ5 APIME STANDARD; PRT; 598 AA.  
 ID MRJ5 APIME STANDARD; PRT; 598 AA.  
 AC 09743;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Major royal jelly protein 5 precursor (MRJP-5) (See-milk protein).  
 GN MRJP5.  
 OS Apis mellifera (Honeybee).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
 OC Apidae; Apis.  
 OC NCBI\_Taxid=7460;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Head;  
 RX MEDLINE=99373663; PubMed=10441680;  
 RA Albert S., Bhattacharya D., Kluding J., Schmitzova J., Simuth J.;  
 RT "The family of major royal jelly proteins and its evolution.";  
 RL J. Mol. Evol. 49:290-297(1999).  
 CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN HONEYBEE NUTRITION. IT IS  
 CC FOUND IN THE ROYAL JELLY WHICH IS THE FOOD OF THE QUEEN HONEY BEE  
 CC LARVA. THE ROYAL JELLY DETERMINES THE DEVELOPMENT OF THE YOUNG  
 CC LARVA AND IS RESPONSIBLE FOR THE HIGH REPRODUCTIVE ABILITY OF THE  
 CC HONEYBEE QUEEN.  
 CC -1- SUBCELLULAR LOCATION: Extracellular.  
 CC -1- TISSUE SPECIFICITY: HYPOPHARYNGEAL GLANDS OF NURSE HONEY BEES.  
 CC -1- DEVELOPMENTAL STAGE: PRODUCED BY THE CEPHALIC GLANDULAR SYSTEM OF  
 CC THE NURSE HONEY BEE.  
 CC -1- SIMILARITY: BELONGS TO THE MAJOR ROYAL JELLY PROTEIN FAMILY.  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

CC EMBL; AF048442; AAD01205.1; -  
 DR InterPro; IPR003534; RoyalJelly.  
 DR Pfam; PF03022; MRJP\_2.  
 DR PRINTS; P01366; ROYALJELLY.  
 KW Signal; Repeat; Glycoprotein.  
 FT SIGNAL 1 17 POTENTIAL.  
 FT CHAIN 18 598 MAJOR ROYAL JELLY PROTEIN 5.  
 FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 598 AA; 70236 MW; 2C603C7B7ACDF63 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 75;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 DMSWA 6  
 Db 113 DMSWA 117

RESULT 3  
 IKKA HUMAN STANDARD; PRT; 745 AA.  
 ID IKKA HUMAN STANDARD; PRT; 745 AA.  
 AC 01511; 014666; Q13132; Q92467;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Inhibitor of nuclear factor kappa-B kinase subunit (IC 2.7.1.1-)  
 DE (I kappa-B kinase alpha) (IKBA) (IKK-alpha) (IKK-A) (Ikkappa kinase)  
 DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous  
 DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).  
 GN CHUK OR IKKA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.  
 RC TISSUE=T-cell;  
 RX MEDLINE=97386461; PubMed=9244310;  
 RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Roche M.;  
 RT Identification and characterization of an Ikkappa kinase.";  
 RL Cell 90:373-383(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=97394468; PubMed=9252186;  
 RA Didonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;  
 RT "A cytokine-responsive Ikkappa kinase that activates the transcription  
 RT factor NF-kappaB.";  
 RL Nature 388:548-554(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND  
 RP SER-176.  
 RX MEDLINE=98008813; PubMed=9346484;  
 RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,  
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;  
 RT "IKK-1 and IKK-2: cytokine-activated Ikkappa kinases essential for  
 RT NF-kappaB activation.";  
 RL Science 278:860-866(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RX MEDLINE=99032998; PubMed=9813230;  
 RA Hu M.C.-T., Wang Y.-P.;  
 RT "Ikkappa kinase-alpha and -beta genes are coexpressed in adult and  
 RT embryonic tissues but localized to different human chromosomes.";  
 RL Gene 222:31-40(1998).  
 RN [5]  
 RP SEQUENCE OF 32-745 FROM N.A.

RC TISSUE-cervical carcinoma;  
 RX MEDLINE=96258427; PubMed8777433;  
 RA Connolly M.A., Marcu K.B.;  
 RT "CHK1, a new member of the helix-loop-helix and leucine zipper  
 RT families of interacting proteins, contains a serine-threonine kinase  
 RT catalytic domain";  
 RL Cell. Biol. Res. 41:537-549 (1995).  
 RN [6]  
 RP PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179  
 RP AND SER-180.  
 RX MEDLINE=98188283; PubMed9520446;  
 RA Ling L., Cao Z., Goeddel D.V.;  
 RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of  
 RT Ser-176";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797 (1998).  
 RN [7]  
 RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.  
 RX MEDLINE=99413720; PubMed10485710;  
 RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeiffer S.R., Pfeiffer L.M.,  
 RA Donner D.B.;  
 RT "NF-kappaB activation by tumour necrosis factor requires the Akt  
 RT serine-threonine kinase";  
 RL Nature 401:82-85 (1999).  
 RN [8]  
 RP IKKA-BINDING.  
 RX MEDLINE=99212141; PubMed10195894;  
 RA Delnase M., Hayakawa M., Chen Y., Karin M.;  
 RT "Positive and negative regulation of IkappaB kinase activity through  
 RT IKKbeta subunit phosphorylation";  
 RL Science 284:309-313 (1999).  
 RN [9]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed9819420;  
 RA Nemoto S., Didonato J.A., Iin A.;  
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase";  
 RL Mol. Cell. Biol. 18:7336-7343 (1998).  
 RN [10]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 RT inflammation and protection";  
 RL Am. J. Physiol. 278:C451-C462 (2000).  
 RN [11]  
 RP SUBUNIT OF A COMPLEX CONTAINING CREBBP, NCOA2, NCOA3, IKKB AND IKKGA.  
 RX MEDLINE=21968797; PubMed11971985;  
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,  
 RA O'Malley B.W.;  
 RT "Regulation of SRC-3 (pCTP/ACTR/ATB-1/RAC-3/TRAM-1) coactivator  
 RT activity by I kappa B kinase";  
 RL Mol. Cell. Biol. 22:3549-3561 (2002).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 CC the dissociation of the inhibitor/NF-kappa-B complex and  
 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3.  
 CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated  
 CC when dephosphorylated.  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but  
 CC also as an homodimer. Directly interacts with IKK-GAMMA/MEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MAP3K14/NIK, MEK1, IKAP and IKB-alpha-P55-50  
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of  
 CC a complex composed of NCOA2, NCOA3, IKKB, IKKG and CREBBP.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Widely expressed.  
 CC -1- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by  
 CC MEK1, and dephosphorylated by PP2A. Autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPPAB KINASE SUBFAMILY.  
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 CC -----  
 DR EMBL, AF012890; AAC51662.1; -  
 DR EMBL, AF009225; AAC51671.1; -  
 DR EMBL, AF080157; AAD08996.1; -  
 DR EMBL, U22512; AAC50713.1; -  
 DR HSSP; Q63450; 1A06.  
 DR Genew: HGNC:1974; CHK1.  
 DR MIM; 600664;  
 DR GO; GO:0005737; C:cytoplasm; TAS.  
 DR GO; GO:0008384; P:IkappaB kinase activity; TAS.  
 DR GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.  
 DR GO; GO:0007252; P:I-kappaB phosphorylation; TAS.  
 DR GO; GO:0006955; P:immune response; TAS.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR Prodom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00220; S\_TKc\_1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP\_1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST\_1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM\_1.  
 DR Trasnferase; Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation.  
 FT DOMAIN 15 302  
 FT DOMAIN 455 476  
 FT DOMAIN 738 743  
 FT NP\_BIND 21 29  
 FT BINDING 44 44  
 FT ACT\_SITE 144 144  
 FT MOD\_RES 23 23  
 FT MOD\_RES 176 176  
 FT MOD\_RES 23 23  
 FT MUTAGEN 176 176  
 FT MUTAGEN 44 44  
 FT MUTAGEN 44 44  
 FT MUTAGEN 176 176  
 FT MUTAGEN 176 176  
 FT MUTAGEN 179 179  
 FT MUTAGEN 180 180  
 FT CONFLICT 543 543  
 FT CONFLICT 604 604  
 FT CONFLICT 679 680  
 FT CONFLICT 684 684  
 FT CONFLICT 686 687  
 FT SEQUENCE 745 AA; 84653 MM; 79A08B9BC98A56C2 C6C64;  
 Query Match 90.0%; Score 36; DB 1; Length 745;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LDMSW 5  
 Db 738 LDMSW 742  
 RESULT 4  
 ID IKKA\_MOUSE STANDARD; PRT; 745 AA.  
 AC Q60680; Q6D2X3;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)  
 DE (I kappa-B kinase alpha) (IKK-A) (Ikappab kinase)  
 DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous

DE Kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFkBIA).  
 GN CHUK OR IKK.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 GN NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=BALB/c;  
 RX MEDLINE=9604444; PubMed=7558004;  
 RA Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.;  
 RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human  
 RT chromosome 10 and mouse chromosome 19.";  
 RL Genomics 27:348-351(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=BALB/c;  
 RX MEDLINE=96258427; PubMed=8777433;  
 RA Connolly M.A., Marcu K.B.;  
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper  
 RT families of interacting proteins, contains a serine-threonine kinase  
 RT catalytic domain.";  
 RL Cell. Mol. Biol. Res. 41:537-549(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RC STRAIN=C57BL/6J; TISSUE=Colon;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kanakawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nakai I., Peele G., Quackenbush J.,  
 RA Schiraldi L.M., Staab J., Suzuki R., Tomita M., Wagner L., Mashio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barh G.,  
 RA Blake J., Botfield D., Boljuna N., Carninci P., de Bonaldo M.P.,  
 RA Brownstein M.J., But C., Fletcher C., Fujita M., Gaitanari M.,  
 RA Gattung S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaurts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Konturki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [4]  
 RP ALTERNATIVE SPLICING.  
 RX MEDLINE=20198447; PubMed=10735566;  
 RA McKenzie P.R., Connolly M.A., Balzarano D., Mueller J.R.,  
 RA Gelezunas R., Marcu K.B.;  
 RT "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking  
 RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and  
 RT IKKbeta have different activation requirements.";  
 RL Mol. Cell. Biol. 20:2635-2649(2000).  
 RN [5]  
 RP PHOSPHORYLATION BY MAPK14/NIK.  
 RX MEDLINE=96188238; PubMed=5520401;  
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Minara M., Yagita H.,  
 RA Okumura K.;  
 RT "Differential regulation of IkappaB kinase alpha and beta by two  
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated  
 RT protein kinase/ERK kinase-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).  
 RN [6]  
 RP IKK-1/KB BINDING.  
 RX MEDLINE=99212141; PubMed=10195894;  
 RA Delhaese M., Hayakawa M., Chen Y., Karin M.;  
 RT "Positive and negative regulation of IkappaB kinase activity through  
 RT IKKbeta subunit phosphorylation.";  
 RL Science 284:309-313(1999).  
 RN [7]

RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., Didonato J.A., Lin A.;  
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [8]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The Ikappa B/NF-kappa B system: a key determinant of mucosal  
 RT inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 CC the dissociation of the inhibitor/NF-kappa-B complex and  
 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3.  
 CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated  
 CC when dephosphorylated.  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but  
 CC also as an homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MAPK14/NIK, MEK1, IKAP and IKK-alpha-P65-P50  
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of  
 CC a complex composed of NCOA2, NCOA3, IKKs, IKKs and CREBBP (by  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1;  
 CC IsoId=Q60680-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Delta LH;  
 CC IsoId=Q60680-2; Sequence=VSP\_004866; VSP\_004867;  
 CC Name=3; Synonyms=Delta H;  
 CC IsoId=Q60680-3; Sequence=VSP\_004868; VSP\_004869;  
 CC -1- TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and  
 CC 3 are expressed predominantly in brain and T-lymphocytes.  
 CC -1- DEVELOPMENTAL STAGES: Maximally expressed at E7 day followed by  
 CC E11, E15 and E17 days. In the limb development, its expression  
 CC predominates in the limb buds at E12.5 day.  
 CC -1- PTM: Phosphorylated by MAPK14/NIK, AKT and to a lesser extent by  
 CC MEK1, and dephosphorylated by PP2A. Autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPPAB KINASE SUBFAMILY.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: U12473; AAC52589.1; -  
 CC EMBL: AK018671; BAB31335.1; -  
 CC ETR: I49101; I49101.  
 CC HSSP: Q63450; I406.  
 CC MGD: MG1:99484; Chuk.  
 CC InterPro: IPR000719; Prot. Kinase.  
 CC InterPro: IPR002290; Ser Thr kinase.  
 CC InterPro: IPR001245; Tyr\_kinase.  
 CC Pfam: PF00069; pkinase; 1.  
 CC PRINTS: PR00109; TYRKINASE.  
 CC PRODOM: PD000001; Prot. Kinase; 1.  
 CC PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
 CC PROSITE: PS00108; PROTEIN KINASE ST; 1.  
 CC PROSITE: PS00011; PROTEIN KINASE DOW; 1.  
 CC Transferrase; Serine/threonine-protein kinase; ATP-binding;  
 CC Phosphorylation; Alternative splicing.  
 CC FT DOMAIN 15 300  
 CC FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).  
 CC FT DOMAIN 738 743 NEMO-BINDING.  
 CC FT NP\_BIND 21 29 ATP (BY SIMILARITY).  
 CC FT

[illegible]

RA Cytogetic. Cell Genet. 82:32-33(1998).  
 RN [5]  
 RP SEQUENCE OF 1-256 FROM N.A.  
 RC TTSUE=Lung;  
 RX MEDLINE=22386257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wanner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,  
 RA Stepleton M., Soares W.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Tothilyk S., Carninci P., Prange C.,  
 RA Rana S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,  
 RA Vallalao D.K., Muzny D.M., Sodegryn E.J., Lu X., Gibbs R.A.,  
 RA Paley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Botcheffeld Y.S.N., Krzywinski M.I., Skolba M.A.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Mitra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).  
 RN [6]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., Didonato J.A., Lin A.,  
 RT "Coordinate regulation of Ikkapab kinases by mitogen-activated protein  
 RL kinase kinase kinase 1 and NF-kappaB-inducing kinase."  
 RN Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [7]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.,  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 RL inflammation and protection."  
 RN Am. J. Physiol. 278:C451-C462(2000).  
 RN [8]  
 RP IDENTIFICATION IN A COMPLEX WITH CREBBP; NCOA2; NCOA3; IKKA AND IKKB.  
 RX MEDLINE=12968797; PubMed=11971985;  
 RA Wu R.C., Qin J., Hoshimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,  
 RA O'Malley B.W.,  
 RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator  
 RL activity by I kappa B kinase."  
 RN Mol. Cell. Biol. 22:3549-3561(2002).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 CC the dissociation of the inhibitor/NF-kappa-B complex and  
 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3 (by similarity).  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKB-alpha-P65-P50  
 CC complex. Phosphorylated IKB-alpha is further released from the  
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG  
 CC and CREBBP.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal  
 CC muscle, kidney, pancreas, spleen, thymus, prostate, testis and  
 CC peripheral blood.  
 CC -1- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.  
 CC Weakly autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPAB KINASE SUBFAMILY.  
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DR EMBL; AF029684; AAC51860.1; -.
DR EMBL; AF080158; MAD08997.1; -.
DR EMBL; AF031416; AAC64675.1; -.
DR EMBL; BC006231; AAH06231.1; -.
DR HSSP; O63450; 1A06.
DR Genew; HGNC:5960; IKKB.
DR MIM; 603258; -.
DR GO; GO:0005737; C:cytoplasm; NAS.
DR GO; GO:0005524; F:ATP binding activity; NAS.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
DR GO; GO:0016563; F:transcriptional activator activity; NAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
DR InterPro; IPR000718; Prot_Kinase.
DR InterPro; IPR002290; Ser_Thr_Kinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00240; Ubiquitin; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferase; Serine/threonine-protein kinase; ATP-binding;
  Phosphorylation.
KM DOMAIN 15 300 PROTEIN_KINASE.
FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
FT NP_BIND 737 742 NEMO-BINDING.
FT BINDING 21 29 ATP (BY SIMILARITY).
FT ACT_SITE 44 44 ATP (BY SIMILARITY).
FT MOD_RES 145 145 BY SIMILARITY.
FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 177 177 PHOSPHORYLATION.
FT MOD_RES 181 181 PHOSPHORYLATION.
FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO
  EFFECT ON BINDING TO NIK.
FT MUTAGEN 177 177 S->A: DECREASE OF ACTIVITY.
FT MUTAGEN 177 177 S->E: FULL ACTIVATION.
FT MUTAGEN 181 181 S->A: DECREASE OF ACTIVITY.
FT CONFLICT 231 255 H->E: FULL ACTIVATION.
  WSKYRKSEVDIVSEDLNGTKF -> CYWMPGTVVHS
  CNPSTLGRGRMI (IN REF. 5).
FT CONFLICT 425 425 Q -> H (IN REF. 1).
FT SEQUENCE 756 AA; 86563 MW; P9CADP677ABE14E CRC4;

Query Match 90.0%; Score 36; DB 1; Length 756;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSM 5
DB 737 LDMSM 741

RESULT 6
IKKB MOUSE STANDARD; PRT; 757 AA.
AC 088351, QSR16;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (IC 2.7.1.1-)
  (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (I-kappa-B kinase
  DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1B).
GN IKKB OR IKK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
[1]
RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEKK1.
RC STRAIN=C57BL/6; TISSUE=Spleen;
RX MEDLINE=96186238; PubMed=9520401;
RA Nakano H., Shindo W., Sakon S., Nishinaka S., Mihara M., Yagita H.,

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RA Okumura K.;
RT "Differential regulation of Ikkapab kinase alpha and beta by two
RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
RT protein kinase/ERK kinase kinase-1."
RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Qiu W.R.;
RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that
RT constitutively phosphorylates serine residues of IKB."
RL submitted (AUG-1998) to the EMBL/Genbank/DBJ databases.
RN [3]
RP DEVELOPMENTAL STAGE.
RA MEDLINE=99455228; PubMed=10523828;
RX Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
RT pathway activates Ikkapab kinase (IKK-alpha/beta) and IKK-beta is a
RT developmentally regulated protein kinase."
RL Oncogene 18:5514-5524(1999).
RN [4]
RP IKK PHOSPHORYLATION.
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., Didonato J.A., Lin A.;
RT "Coordinate regulation of Ikkapab kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase."
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RN [5]
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RA MEDLINE=20178139; PubMed=10712233;
RX Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
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CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
  the dissociation of the inhibitor/NF-kappa-B complex and
  ultimately the degradation of the inhibitor. Also phosphorylates
  NCOA3.
CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
  also as a homodimer. Directly interacts with IKK-gamma/NEMO.
  Heterodimers form the active complex. The tripartite complex can
  also bind to MEKK1, MAP3K14/NIK, IKAP and IKB-ALPHA-P65-P50
  complex. Phosphorylated IKB-alpha is further released from the
  complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG
  and CREBBP (by similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
CC -1- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout
  the mouse embryo, at E9.5 day its expression begins to be
  localized to the brain, neural ganglia, neural tube, and in liver
  at E12.5 day. At E15.5 day, the expression is further restricted
  to specific tissues of the embryo.
CC -1- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
  Weakly autophosphorylated.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
  IKAPAB KINASE SUBFAMILY.
CC
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  or send an email to license@sib-sib.ch).
CC
DR EMBL; AF026524; AAC23557.1; -.
DR EMBL; AF088910; AAD52095.1; -.
DR HSSP; O63450; 1A06.
DR MGD; MGI:1338071; Ikdkb.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR002290; Ser_Thr_Kinase.
DR InterPro; IPR001245; Tyr_Kinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.

```



DR Prodom: PD000001; Prot kinase: 1.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; FALSE\_NEG.  
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.  
 DR PROSITE: PS00109; PROTEIN KINASE ST; 1.  
 DR TRANSFERASE: Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation.  
 FT DOMAIN 15 300 PROTEIN KINASE.  
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 FT DOMAIN 737 742 NEMO-BINDING.  
 FT BINDING 21 29 ATP (BY SIMILARITY).  
 FT ACT SITE 145 145 ATP (BY SIMILARITY).  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).  
 FT CONFLICT 343 343 N -> D (IN REF. 2).  
 FT CONFLICT 356 356 N -> B (IN REF. 2).  
 FT CONFLICT 390 390 L -> F (IN REF. 2).  
 FT CONFLICT 406 406 P -> Q (IN REF. 2).  
 FT CONFLICT 573 573 K -> R (IN REF. 2).  
 FT CONFLICT 736 757 TLDMSW/LQMEDERCSLEQACD -> VTA (IN REF. 2).  
 SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;  
 Query Match 90.0%; Score 36; DB 1; Length 757;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSW 5  
 Db 737 LDMSW 741  
 RESULT 7  
 IKKB RAT STANDARD; PRT; 757 AA.  
 AC 09078; 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (BC 2.7.1.-)  
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase  
 2) (IKK) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1K2).  
 GN IKKB OR IKK.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang Y., Sun S., Rayld K.;  
 RT "IKK beta in megakaryocyte differentiation."  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP IKK PHOSPHORYLATION.  
 RA MEDLINE=9038238; PubMed=9819420;  
 RA Nemoto S., DiDonato J.A., Lin A.;  
 RT "Coordinate regulation of I-kappaB kinases by mitogen-activated protein  
 kinase kinase kinase 1 and NF-kappaB-inducing kinase."  
 RL Mol. Cell. Biol. 18:7336-7343 (1998).  
 RN [3]  
 RP REVIEW.  
 RA MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 inflammation and protection."  
 RL Am. J. Physiol. 278:C451-C462 (2000).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 the dissociation of the inhibitor/NF-kappa-B complex and  
 ultimately the degradation of the inhibitor. Also phosphorylates  
 NCOA3.  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but

CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-alpha-p65-p50  
 CC complex. Phosphorylated IKK-alpha is further released from the  
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKK $\alpha$ , IKK $\beta$   
 CC and CREBBP (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.  
 CC Weakly autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPAB KINASE SUBFAMILY.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AF115282; AAF21978.1; -.  
 CC HSSP: O63450; 1A06.  
 DR InterPro: IPR000719; Prot kinase.  
 DR InterPro: IPR002290; Ser\_Thr\_kinase.  
 DR InterPro: IPR001245; Tyr\_kinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR PRODOM: PD000001; Prot kinase; 1.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; FALSE\_NEG.  
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.  
 DR PROSITE: PS00109; PROTEIN KINASE ST; 1.  
 KW TRANSFERASE: Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation.  
 FT DOMAIN 15 300 PROTEIN KINASE.  
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 FT DOMAIN 737 742 NEMO-BINDING.  
 FT NP\_BIND 21 29 ATP (BY SIMILARITY).  
 FT BINDING 145 145 ATP (BY SIMILARITY).  
 FT ACT SITE 145 145 BY SIMILARITY.  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 757 AA; 86660 MW; 3AF6A6A7DF919FC CRC64;  
 Query Match 90.0%; Score 36; DB 1; Length 757;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSW 5  
 Db 737 LDMSW 741  
 RESULT 8  
 EPB3 CHICK STANDARD; PRT; 983 AA.  
 ID EPB3\_CHICK  
 AC P29318; 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ephrin type-A receptor 3 precursor (BC 2.7.1.112) (Tyrosine-protein  
 kinase receptor ETK) (CEK4).  
 GN EPB3 OR ETK OR CEK4.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=92031278; PubMed=1657122;  
 RA Sajjadi F.G., Pasquale B.B., Subramani S.;  
 RT "Identification of a new eph-related receptor tyrosine kinase gene

RT from mouse and chicken that is developmentally regulated and encodes  
 at least two forms of the receptor."  
 RL New Biol. 3:769-778(1991).  
 CC -1- FUNCTION: RECEPTOR FOR THE EPHRIN-A FAMILY. BINDS TO  
 CC EPHRIN-A2, -A3, -A4 AND -A5.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING BRAIN AND  
 CC EMBRYONIC TISSUES. IN ADULT, THE GREATEST LEVELS OF EXPRESSION  
 CC OCCURS IN THE BRAIN. IT IS EXPRESSED IN A GRADED MANNER ACROSS THE  
 CC RETINA WITH THE HIGHEST EXPRESSION AT ITS TEMPORAL POLE.  
 CC DETECTABLE IN ALL OTHER ADULT TISSUES EXAMINED, EXCEPT THE LIVER.  
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.  
 CC -1- SIMILARITY: Contains 2 fibronectin type iii domain.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC RECEPTOR SUBFAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M68514, AAA48666.1; .  
 DR PIR: B45583; B45583.  
 DR HSPB: P00523; 2PTK.  
 DR InterPro: IPR006209; EGF\_1like.  
 DR InterPro: IPR001090; Ephrin\_receptor.  
 DR InterPro: IPR003961; FNIII.  
 DR InterPro: IPR003962; FNIII\_subd.  
 DR InterPro: IPR000719; Prot\_Kinase.  
 DR InterPro: IPR001660; SAM.  
 DR InterPro: IPR001245; Tyr\_Kinase.  
 DR InterPro: IPR001426; Kinase\_receptor.  
 DR Pfam: PF01404; EPH\_1bd; 1.  
 DR Pfam: PF00041; FN3; 2.  
 DR Pfam: PF00069; Kinase; 1.  
 DR Pfam: PF00536; SAM; 1.  
 DR PRINTS: PRO0014; FNTYPEIII.  
 DR PRINTS: PRO0109; TYRKINASE.  
 DR ProDom: PD001495; Ephrin\_receptor; 1.  
 DR ProDom: PD000001; Prot\_Kinase; 1.  
 DR SMART: SM00615; EPH\_1bd; 1.  
 DR SMART: SM00060; FN3; 2.  
 DR SMART: SM00454; SAM; 1.  
 DR SMART: SM00219; Tyrc; 1.  
 DR PROSITE: PS01186; EGF\_2; UNKNOWN 1.  
 DR PROSITE: PS01017; PROTEIN KINASE\_ATP; 1.  
 DR PROSITE: PS50011; PROTEIN KINASE\_DOM; 1.  
 DR PROSITE: PS00109; PROTEIN KINASE\_TYR; 1.  
 DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR PROSITE: PS50105; SAM\_DOMAIN; 1.  
 DR TranserBase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 FT SIGNAL 1 19  
 FT CHAIN 20 983  
 FT DOMAIN 20 540  
 FT TRANSMEM 541 564  
 FT DOMAIN 565 583  
 FT DOMAIN 188 321  
 FT DOMAIN 322 431  
 FT DOMAIN 432 529  
 FT DOMAIN 621 882  
 FT DOMAIN 911 975  
 FT SITE 981 983  
 FT NP\_BIND 627 635  
 FT BINDING 653 653  
 FT ACT\_SITE 746 746  
 FT MOD\_RES 596 596

FT MOD\_RES 602 602  
 FT MOD\_RES 779 779  
 FT CARBOHYD 231 231  
 FT CARBOHYD 336 336  
 FT CARBOHYD 390 390  
 FT CARBOHYD 403 403  
 FT CARBOHYD 492 492  
 SQ SEQUENCE 983 AA; 109910 MW; E8895F0BDF7651B CRC64;  
 Query Match 90.0%; Score 36; DA 1; Length 983;  
 Best local similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSW 5  
 Db 342 LDMSW 346  
 RESULT 9  
 ID EPB3 HUMAN STANDARD; PRT; 983 AA.  
 AC P29330; Q9H2V3; Q9H2V4;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ephrin type-A receptor 3 precursor (BC 2.7.1.112) (Tyrosine-protein  
 DE kinase receptor ETK1) (HEK) (HEK4).  
 GN EPB3 OR ETK1 OR ETK OR HEK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=92179233; PubMed=1311845;  
 RA Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.;  
 RT "Molecular cloning of HEK, the gene encoding a receptor tyrosine  
 RT kinase expressed by human lymphoid tumor cell lines."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).  
 RL [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC Tissue=Melanoma;  
 RA Chlari R., Hames G., Stroobant V., Maille B., Texier C., Mach B.,  
 RA Boon T., Coulle P.G.;  
 RT "Identification of a tumor specific shared antigen derived from an  
 RT Eph-receptor and presented to CD4 T cells on HLA class II  
 RT molecules."  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION.  
 RX MEDLINE=92147681; PubMed=1737782;  
 RA Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wicks A.,  
 RA Welch K., Loudovaris M., Rockman S., Bumanns I.;  
 RT "Isolation and characterization of a novel receptor-type protein  
 RT tyrosine kinase (hek) from a human pre-B cell line."  
 RL J. Biol. Chem. 267:3262-3267(1992).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO  
 CC EPHRIN-A2, -A3, -A4 AND -A5. COULD PLAY A ROLE IN LYMPHOID  
 CC FUNCTION.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1);  
 CC SECRETED (ISOFORM 2).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=P29320-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=P29320-2; Sequence=VSP\_002995; VSP\_002996;  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST LEVEL IN PLACENTA.  
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.  
 CC -1- SIMILARITY: Contains 2 fibronectin type iii domain.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN



DR InterPro; IPR006209; BGF\_like.  
 DR InterPro; IPR001090; Ephrin\_receptor.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003962; FnIII\_subd.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001660; SAM.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR InterPro; IPR001426; Ykase\_receptorV.  
 DR Pfam; PF01404; EPH\_1bd; 1.  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00536; SAM; 1.  
 DR PRINTS; PR000104; FNTYPEIII.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD001495; Ephrin\_receptor; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00615; EPH\_1bd; 1.  
 DR SMART; SM00060; FN3; 2.  
 DR SMART; SM00454; SAM; 1.  
 DR SMART; SM00219; Tyrc; 1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS01107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR PROSITE; PS50105; SAM\_DOMAIN\_1.  
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
 KW Alternative splicing.  
 FT SIGNAL 1 20 BY SIMILARITY.  
 FT CHAIN 21 983 EPHRIN TYPE-A RECEPTOR 3.  
 FT DOMAIN 21 540 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 541 564 POTENTIAL.  
 FT DOMAIN 565 983 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 188 321 CYS-RICH.  
 FT DOMAIN 322 431 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 432 529 FIBRONECTIN TYPE-III 2.  
 FT DOMAIN 621 882 PROTEIN KINASE.  
 FT DOMAIN 911 975 SAM.  
 FT SITE 981 983 PDZ-BINDING MOTIF (POTENTIAL).  
 FT NP\_BIND 627 635 ATP (BY SIMILARITY).  
 FT BINDING 653 653 ATP (BY SIMILARITY).  
 FT ACT\_SITE 746 746 BY SIMILARITY.  
 FT MOD\_RES 596 596 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT MOD\_RES 602 602 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT MOD\_RES 779 779 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT CARBOHYD 231 231 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 336 336 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 390 390 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 403 403 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 492 492 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT VARSPLIC 530 983 Missing (in isoform short).  
 FT SEQUENCE 983 AA; 109955 MW; BE44A655D8107A2 CRC64;  
 SQ

Query Match 90.0%; Score 36; DB 1; Length 983;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5  
 DB 342 LDMSW 346

RESULT 11  
 EPHA3\_RAT STANDARD; PRT; 984 AA.  
 AC 008650;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein

DR kinase receptor REK4 (TYRO-4).  
 GN EPHA3 OR REK4 OR TYRO4.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=98120505; PubMed=9458884;  
 RA Li Y.Y., McIernan C.F., Feldman A.M.;  
 RT "IL-1 beta alters the expression of the receptor tyrosine kinase gene  
 r-EphA3 in neonatal rat cardiomyocytes";  
 RL Am. J. Physiol. 274:H331-H341(1998).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO  
 CC EPHRIN-A2, -A3, -A4 AND -A5.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN THE HEART, BRAIN AND LUNG.  
 CC -1- INDUCTION: DOWN-REGULATED BY IL-1-BETA IN NEONATAL CARDIAC  
 CC MYOCYTES.  
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.  
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC RECEPTOR SUBFAMILY.  
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 CC  
 CC EMBL; U69278; AAC06273.1; -.  
 CC HSSP; P00523; 2PTK.  
 DR InterPro; IPR006209; EGF\_1like.  
 DR InterPro; IPR001090; Ephrin\_receptor.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003962; FnIII\_subd.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001660; SAM.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR InterPro; IPR001426; Ykase\_receptorV.  
 DR Pfam; PF01404; EPH\_1bd; 1.  
 DR Pfam; PF00041; fn3; 2.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR PRINTS; PR000104; FNTYPEIII.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD001495; Ephrin\_receptor; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00615; EPH\_1bd; 1.  
 DR SMART; SM00060; FN3; 2.  
 DR SMART; SM00454; SAM; 1.  
 DR SMART; SM00219; Tyrc; 1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS01107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR PROSITE; PS50105; SAM\_DOMAIN\_1.  
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
 KW Alternative splicing.  
 FT SIGNAL 1 20 BY SIMILARITY.  
 FT CHAIN 21 984 EPHRIN TYPE-A RECEPTOR 3.  
 FT DOMAIN 21 541 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 542 565 POTENTIAL.  
 FT DOMAIN 566 984 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 189 322 CYS-RICH.  
 FT DOMAIN 328 431 FIBRONECTIN TYPE-III 1.

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FT DOMAIN 436 528 FIBRONECTIN TYPE-III 2.
FT PROSITE 622 883 PROTEIN KINASE.
FT DOMAIN 912 976 SAM.
FT SITE 984 984 PDI-BINDING MOTIF (POTENTIAL).
FT NP_BIND 628 636 ATP (BY SIMILARITY).
FT BINDING 654 654 ATP (BY SIMILARITY).
FT ACT_SITE 747 747 BY SIMILARITY.
FT MOD_RES 597 597 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 603 603 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 780 780 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 493 493 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 984 AA; 110227 MW; F170C49312F7A0AB CRC64;

Query Match 90.0%; Score 36; DB 1; Length 984;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
DB 343 LDMSW 347

RESULT 12
POLC_BUCAI STANDARD; PRT; 411 AA.
AC P57255;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE POLC bifunctional protein [includes: Polyphosphoglucamate synthase
DE (EC 6.3.2.17) (Folypolyphosphate synthetase) (PPGS);
DE dihydrofolate synthase (EC 6.3.2.12)].
GN POLC OR Bui167
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCB1_TaxId=118099;
[1]
RN RP SEQUENCE FROM N.A.
RX STRAIN=Tokyo 1998;
RX MEDLINE=20445113; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. ABS.";
RL Nature 407:81-86(2000).
CC -1- FUNCTION: CONVERSION OF FOLATES TO POLYGLUTAMATE DERIVATIVES.
CC -1- CATALYTIC ACTIVITY: ATP + (tetrahydrofolyl-[Glu]) (N) + L-glutamate
CC = ADP + phosphate + {tetrahydrofolyl-[Glu]} (N+1).
CC -1- CATALYTIC ACTIVITY: ATP + dihydropterate + L-glutamate = ADP +
CC phosphate + dihydrofolate.
CC -1- PATHWAY: BACTERIA REQUIRE FOLATE FOR THE BIOSYNTHESIS OF GLYCINE,
CC METHIONINE, FORMYL-MET-TRNA, THYMIDYLATES, PURINES, AND
CC PANTOTHENATE.
CC -1- SIMILARITY: Belongs to the folypolyglutamate synthase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF001118; BAB1285.1; -.
CC HSSP; P15925; 1FGS.
CC InterPro; IPR001645; Fpolypgl synthase.
CC InterPro; IPR000713; Mur_ligase.
CC Pfam; PF01225; Mur_ligase; 1.

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DR TIGRPM6; TIGR01499; folC; 1.
DR PROSITE; PS01011; FOLYPOLYGLU SYNT_1; 1.
DR PROSITE; PS01012; FOLYPOLYGLU SYNT_2; FALSE NEG.
KM Multifunctional enzyme; Ligase; One-carbon metabolism; ATP-binding;
KW Folate biosynthesis; Complete proteome.
FT NP_BIND 50 56 ATP (BY SIMILARITY).
SQ SEQUENCE 411 AA; 46970 MW; 5DDC2DC6539935A CRC64;

Query Match 85.0%; Score 34; DB 1; Length 411;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5
DB 219 LDMSW 223

RESULT 13
PGLR_PENGR STANDARD; PRT; 376 AA.
ID PGLR_PENGR
AC 093883;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase).
GN PGG1.
OS Penicillium griseoformeum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocommataceae; mitosporic Trichocommataceae; Penicillium.
OX NCB1_TaxId=84562;
[1]
RN RP SEQUENCE FROM N.A.
RX STRAIN=CCT 6421;
RA Ribon A.B., Coelho J.L.C., Barros E.G., Araujo E.F.;
RT "Cloning and characterization of a gene encoding the
RT endopolygalacturonase of Penicillium griseoformeum";
RT Submitted (Aug-1998) to the EMBL/Genbank/DBD databases.
CC -1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
CC galactosiduronic linkages in pectate and other galacturonans.
CC -1- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
CC (POLYGLACTURONASES).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF085238; AAC83692.1; -.
CC InterPro; IPR000743; GLYCO_hydro_28.
CC InterPro; IPR006626; Pbh1.
DR Pfam; PF00295; Glyco_hydro_28; 1.
DR SMART; SM00710; Pbh1; 5.
DR PROSITE; PS00502; POLYGLACTURONASE; 1.
DR HYDROLASE; Glycosidase; Cell wall, Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 376 POLYGLACTURONASE.
SQ SEQUENCE 376 AA; 38068 MW; 1EDB1C56D56928 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 376;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
DB 350 DMSWA 354

RESULT 14
NRAM_IAMWL STANDARD; PRT; 453 AA.
ID NRAM_IAMWL

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AC P03470;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Wilson-Smith/33).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxId=11487;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82192605; PubMed=7077751;
RA Hilt A.L., Nayak D.P.;
RT "Complete nucleotide sequence of the neuraminidase gene of human
RT Influenza virus A/WEN/33."
RT J. Virol. 41:730-734 (1982).
RL
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitates
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL J02177; AAA43397.1; ALT_SEQ.
DR HSSP; P03472; 20WC.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur. 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
KW Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT DOMAIN 36 74 ANCHOR.
FT TRANSMEM 7 35 HYPERVARIABLE STALK REGION.
FT ACT_SITE 259 259 HEAD OF NEURAMINIDASE.
FT ACT_SITE 261 261 PROBABLE.
FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 453 AA; 49623 MW; 7DC56A4416A47B8 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 453;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSW 5
DB 437 VDMSW 441

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OS Influenza A virus (strain A/Puerto Rico/8/34).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxId=11455;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81148841; PubMed=7010182;
RA Fields S., Winter G., Brownlee G.G.;
RT "Structure of the neuraminidase gene in human influenza virus
RT A/PR/8/34."
RT Nature 290:213-217 (1981).
RL
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitates
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL J02146; AAA43412.1; -.
DR HSSP; P03472; 20WC.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur. 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
KW Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT DOMAIN 36 75 ANCHOR.
FT TRANSMEM 7 35 HYPERVARIABLE STALK REGION.
FT ACT_SITE 260 260 HEAD OF NEURAMINIDASE.
FT ACT_SITE 262 262 PROBABLE.
FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 454 AA; 50143 MW; A0DC4C08A2B53705 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 454;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSW 5
DB 438 VDMSW 442

```

Search completed: February 18, 2004, 14:28:04  
Job time : 4.55263 secs

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds  
(without alignments)  
89.145 Million cell updates/sec

Title: US-09-643-260-5

Perfect score: 40

Sequence: 1 LDMSWA 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPTRMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriopl:\*
- 17: sp\_archae:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	242	12 Q919K8	Q919K8 culex nigri
2	37	92.5	304	16 Q91719	Q91719 pseudomonas
3	37	92.5	433	16 Q8P4A1	Q8P4A1 pseudomonas
4	37	92.5	438	16 Q8P4V8	Q8P4V8 xanthomonas
5	36	90.0	258	5 Q45498	Q45498 caenorhabdi
6	36	90.0	361	16 Q8P955	Q8P955 xanthomonas
7	36	90.0	374	16 Q9H210	Q9H210 pseudomonas
8	36	90.0	409	10 Q9M3F6	Q9M3F6 arabidopsis
9	36	90.0	463	5 Q8MMJ0	Q8MMJ0 apis cerana
10	36	90.0	538	11 Q8C9K6	Q8C9K6 mus musculu
11	36	90.0	581	5 Q8MSH3	Q8MSH3 drosophila
12	36	90.0	597	5 Q9VGP2	Q9VGP2 drosophila
13	36	90.0	740	6 Q95KV1	Q95KV1 bos taurus
14	36	90.0	745	11 Q8CBT3	Q8CBT3 mus musculu
15	36	90.0	756	6 Q95KV0	Q95KV0 bos taurus
16	36	90.0	984	11 Q8C3U1	Q8C3U1 mus musculu

17	36	90.0	984	11 Q8BRB1	Q8BRB1 mus musculu
18	34	85.0	85	16 Q8PBL8	Q8PBL8 escherichia
19	34	85.0	211	9 Q80148	Q80148 bacterioph
20	34	85.0	211	9 Q21903	Q21903 bacterioph
21	34	85.0	237	10 Q8H2P9	Q8H2P9 oryza sativ
22	34	85.0	245	4 Q8N241	Q8N241 homo sapien
23	34	85.0	297	11 Q8BGS0	Q8BGS0 mus musculu
24	34	85.0	309	2 Q9P163	Q9P163 amycolatops
25	34	85.0	323	12 Q9QTR2	Q9QTR2 marek's dis
26	34	85.0	328	2 Q8KPM8	Q8KPM8 saccharopol
27	34	85.0	394	5 Q9U2T2	Q9U2T2 caenorhabdi
28	34	85.0	611	16 Q8DKF5	Q8DKF5 synchococc
29	34	85.0	616	2 Q33749	Q33749 synchococc
30	34	85.0	1139	16 Q8ZC91	Q8ZC91 yerbinda pe
31	34	85.0	1941	16 Q8G751	Q8G751 bifidobacte
32	33	82.5	97	12 Q9Q7I1	Q9Q7I1 svcs2 plect
33	33	82.5	110	16 Q8DY14	Q8DY14 streptococc
34	33	82.5	173	16 Q8E5U2	Q8E5U2 streptococc
35	33	82.5	173	16 Q8E065	Q8E065 streptococc
36	33	82.5	178	10 Q8LH06	Q8LH06 oryza sativ
37	33	82.5	198	16 Q9PA54	Q9PA54 xylella fas
38	33	82.5	232	17 Q8ZSR8	Q8ZSR8 pyrobaculum
39	33	82.5	234	16 Q9X897	Q9X897 streptomyc
40	33	82.5	236	3 Q9E527	Q9E527 neurospora
41	33	82.5	236	3 Q8NUT9	Q8NUT9 biorectria
42	33	82.5	240	3 Q8NUT1	Q8NUT1 biorectria
43	33	82.5	246	16 Q8CWD6	Q8CWD6 escherichia
44	33	82.5	270	4 Q8NCJ2	Q8NCJ2 homo sapien
45	33	82.5	273	10 Q94JW4	Q94JW4 arabidopsis

## ALIGNMENTS

### RESULT 1

Q919K8 PRELIMINARY, PRT, 242 AA.  
AC Q919K8  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE CUN068 hypothetical protein.  
GN CUN068.  
OS Culex nigripalpus baculovirus.  
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.  
OX NCBI\_TaxId=130556;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Florida1997;  
RX MEDLINE=2148685; PubMed=11602755;  
RA Afonso C.L., Tulman B.R., Lu Z., Balinsky C.A., Moser B.A.,  
RA Becnel J.J., Rock D.L., Kutish G.F.;  
RT "Genome Sequence of a Baculovirus Pathogenic for Culex nigripalpus.";  
RT J. Virol. 75:11157-11165(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Florida1997;  
RA Afonso C.L., Tulman B.R., Lu Z., Balinsky C.A., Moser B.A.,  
RA Becnel J.J., Rock D.L., Kutish G.F.;  
RT Submitted (Jun-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL, AF403738; AKK94146.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 242 AA; 27222 MW; 6014967531110E52 CRC64;

Query Match 100.0%; Score 40; DB 12; Length 242;

Best Local Similarity 100.0%; Pred. No. 55;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6  
|||||  
Db 79 LDMSWA 84

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RESULT 2
ID 091719 PRELIMINARY; PRT; 304 AA.
AC 091719;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Probable cytochrome c oxidase assembly factor.
GN PA0113.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10964043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey W.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.R., Coulter S.N., Folger K.R., Kas A., Larbig K., Lam R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004449; AAC03503.1; -.
DR InterPro; IPR006369; CyoE_Ctab.
DR InterPro; IPR000537; UblA.
DR Pfam; PF01040; UblA; 1.
DR TIGRfam; TIGR01473; cyoE_ctab; 1.
DR PROSITE; PS00943; UblA; 1.
KM Complete proteome.
SQ SEQUENCE 304 AA; 33430 MW; DC278071764B671C CRC64;

Query Match 92.5%; Score 37; DB 16; Length 304;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6
DB 259 LDMSWA 264

RESULT 3
ID 08P41 PRELIMINARY; PRT; 433 AA.
AC 08P41;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cationic amino acid transporter.
GN XCC3809.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Parah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardoso J., Chamberg F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katayama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Moreira E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rosa A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Secubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE012036; AAM38706.1; -.
DR InterPro; IPR002293; AA/re1_permease1.
DR InterPro; IPR004841; Permease.
DR Pfam; PF00324; aa_permeases; 1.
KM Complete proteome.
SQ SEQUENCE 433 AA; 45795 MW; 921AC5AC60A545E2 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 433;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6
DB 182 VDMWSA 187

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RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Secubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE012036; AAM38706.1; -.
DR InterPro; IPR002293; AA/re1_permease1.
DR InterPro; IPR004841; Permease.
DR Pfam; PF00324; aa_permeases; 1.
KM Complete proteome.
SQ SEQUENCE 433 AA; 45128 MW; EF217D2A7C516533 CRC64;

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Query Match 92.5%; Score 37; DB 16; Length 433;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6
DB 180 VDMWSA 185

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RESULT 4
ID 08P41 PRELIMINARY; PRT; 438 AA.
AC 08P41;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cationic amino acid transporter.
GN XAC3864.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Parah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardoso J., Chamberg F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katayama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rosa A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Secubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE012036; AAM38706.1; -.
DR InterPro; IPR002293; AA/re1_permease1.
DR InterPro; IPR004841; Permease.
DR Pfam; PF00324; aa_permeases; 1.
KM Complete proteome.
SQ SEQUENCE 438 AA; 45795 MW; 921AC5AC60A545E2 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 438;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6
DB 182 VDMWSA 187

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RESULT 5
O45498      PRELIMINARY;      PRT;      258 AA.
ID O45498;
AC O45498;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE P3982.5 protein.
GN P3982.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peldoderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Dobson R.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z92834; CAB07386.1; -.
DR WormDep; P3982.5; CE16011.
DR InterPro; IPR000980; SH2.
DR Pfam; PF00017; SH2; 1.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00253; SH2; 1.
DR SMART; SM00253; SOCS; 1.
DR PROSITE; PS50021; SH2; 1.
DR PROSITE; PS50225; SOCS; 1.
SQ SEQUENCE 258 AA; 30897 MW; 820D4D73DC5C8060 CRC64;

Query Match      90.0%; Score 36; DB 5; Length 258;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LDMSWA 6
Db 21 LDMSWA 26

RESULT 6
O8P955      PRELIMINARY;      PRT;      361 AA.
ID O8P955;
AC O8P955;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DE 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Exopolysaccharide biosynthesis protein.
GN XCC2011.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Purlan L.R.,
RA Queiroz R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
RA Caramonte G., Canavani F., Cardozo J., Chamberg F., Clapina L.P.,
RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Porri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Mendes J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

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RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Teal S.M., White F.F.,
RA Setubal J.C., Kikajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE012305; AA041300.1; -.
DR InterPro; IPR002656; Acyl_transf_3.
DR Pfam; PF01757; Acyl_transf_3; 1.
KW Complete proteome.
SQ SEQUENCE 361 AA; 39147 MW; 37AB21791BE0393F CRC64;

Query Match      90.0%; Score 36; DB 16; Length 361;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSW 5
Db 117 LDMSW 121

RESULT 7
O9H210      PRELIMINARY;      PRT;      374 AA.
ID O9H210;
AC O9H210;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DE 01-OCT-2001 (TRENBLrel. 18, Last annotation update)
DE Hypothetical protein PA3230.
GN PA3230.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Golter L., Tolentino E., Westbrook-Madman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Rolger K.R., Kas A., Lardig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004746; AAC06618.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 374 AA; 42269 MW; 31EF185C4F683884 CRC64;

Query Match      90.0%; Score 36; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSWA 6
Db 81 DMSWA 85

RESULT 8
O9M3F6      PRELIMINARY;      PRT;      409 AA.
ID O9M3F6;
AC O9M3F6;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Putative replication protein.
GN T14K23_110.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

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OC euroside II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Nyakatura G., Fartmann B., Dauner D., Steer W., Holland R.,  
 RA Weichselgartner M., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.,  
 RA Quetier F., Salanoubat M.,  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL132909; CAB87732.1;  
 DR InterPro; IPR003871; DUF223.  
 DR Pfam; PF02721; DUF223;  
 SQ SEQUENCE 409 AA; 45738 MW; ADDCAEF5597BAEB4 CRC64;  
 Query Match 90.0%; Score 36; DB 10; Length 409;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSW 5  
 DB 190 LDMSW 194

RESULT 9  
 OBMW10 PRELIMINARY; PRT; 463 AA.

AC QBMW10;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Major royal jelly protein MRJP2 precursor.  
 GN MRJP.  
 OS Apis cerana (Indian honeybee).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
 OC Apidae; Apis.  
 OX NCBI\_TaxID=7461;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Nurse heads;  
 RA Sitcitrinreed S., Imjonglirak C.;  
 RT "Molecular Cloning of Major Royal Jelly Protein (MRJP2) cDNA from Apis  
 cerana in Thailand."  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF525777; AAM8282.1;  
 DR InterPro; IPR003534; RoyalJelly.  
 DR Pfam; PF03022; MRJP.1  
 DR PRINTS; PR01366; ROYALJELLY.  
 KW Signal.  
 FT SIGNAL  
 SQ SEQUENCE 463 AA; 52412 MW; D648AE2BAF1EDDE9 CRC64;  
 Query Match 90.0%; Score 36; DB 5; Length 463;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSWA 6  
 DB 110 DMSWA 114

## RESULT 10

OBC9K6 PRELIMINARY; PRT; 538 AA.  
 ID OBC9K6;  
 AC OBC9K6;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Eph receptor A3.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=C57BL/6J; TISSUE=Thymus;  
 RC MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs."  
 RL Nature 420:563-573 (2002).  
 DR EMBL; AK041935; BAC31104.1;  
 SQ SEQUENCE 538 AA; 60659 MW; EEDAB12B0369EA19 CRC64;  
 Query Match 90.0%; Score 36; DB 11; Length 538;  
 Best Local Similarity 100.0%; Pred. No. 5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSW 5  
 DB 343 LDMSW 347

## RESULT 11

OBSMH3 PRELIMINARY; PRT; 581 AA.

AC OBSMH3;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE GH4640p.  
 GN CG6728.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkely;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farrell D., Fries B.,  
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nuroo J., Paclob J., Paragas V., Park S.,  
 RA Patel S., Phounehavong S., Wan K., Yu C., Lewis S.B., Rubin G.M.,  
 RA Ceoliker S.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY118818; AAM50678.1;  
 DR FlyBase; FBgn0037896; CG6728.  
 DR InterPro; IPR000172; SHPox.  
 DR InterPro; IPR000169; SHPox.  
 DR Pfam; PF00732; GMC\_oxred.  
 DR PROSITE; PS00639; THIOX\_PROTEASE\_HIS.1  
 SQ SEQUENCE 581 AA; 63475 MW; A2F13BEC25E496D CRC64;

Query Match 90.0%; Score 36; DB 5; Length 581;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSWA 6  
 DB 159 DMSWA 163

## RESULT 12

O9VGP2 PRELIMINARY; PRT; 597 AA.  
 ID O9VGP2;  
 AC O9VGP2;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE CG6728 protein.

GN CG6728.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 ON NCBI\_TaxId=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731122;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brannon R.C., Rogers Y.-H.C., Blazer V., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abri J.P., Doyle A.C., Axelsen J., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolhakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Maye A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,  
 RA Foslter A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,  
 RA Goddek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,  
 RA Jallali M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Koditz C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laeko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nussekern D.R., Paclob J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003691; AAF54634.1; -;  
 DR FlyBase: FBgn0037896; CG6728.  
 DR InterPro: IPR000172; GMC\_oxred.  
 DR InterPro: IPR000169; SHProt\_acslike.  
 DR Pfam: PF00732; GMC\_oxred; 1.  
 DR PROSITE: PS00624; GMC\_OXRED 2; 1.  
 DR PROSITE: PS00639; THIOL\_PROTEASE\_HIS; 1.  
 SQ SEQUENCE 597 AA; 65274 MW; 8C4C362AF80902A CRC64;

Query Match 90.0%; Score 36; DB 5; Length 597;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
 DB 159 DMSWA 163

RESULT 13  
 ID 095KV1 PRELIMINARY; PRT; 740 AA.  
 AC 095KV1;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Ikb kinase-alpha.  
 GN BIKKALPHA.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 ON NCBI\_TaxId=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Rottenberg S., Dobbelaere D.A.E., Heusler V.T.;  
 RT "Identification and characterisation of the bovine Ikb kinases (IKKs)  
 RT alpha, beta and gamma.";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL: AJ141555; CAC93686.1; -;  
 DR InterPro: IPR000719; Prot\_kinase.  
 DR InterPro: IPR002290; Ser\_thr\_kinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR ProDom: PD000001; Prot\_kinase; 1.  
 DR SMART: SM00220; S\_TKc; 1.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.  
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 740 AA; 84343 MW; 01903BE1F44D176 CRC64;

Query Match 90.0%; Score 36; DB 6; Length 740;  
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5  
 DB 733 LDMSW 737

RESULT 14  
 ID 08CBT3 PRELIMINARY; PRT; 745 AA.  
 AC 08CBT3;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Conserved helix-loop-helix ubiquitous kinase.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sclugonathi; Muridae; Mus.  
 ON NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The PANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 DR EMBL: AK035326; BAC29034.1; -;  
 SQ SEQUENCE 745 AA; 84770 MW; 48C9E01C17A61184 CRC64;

Query Match 90.0%; Score 36; DB 11; Length 745;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5  
 DB 738 LDMSW 742

RESULT 15  
 ID 095KV0 PRELIMINARY; PRT; 756 AA.  
 AC 095KV0;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)  
 DE IKB kinase-beta.  
 GN BIKKBEA.  
 OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Rottenberg S., Dobbelaere D.A.E., Heusler V.T.;  
 RT "Identification and characterisation of the bovine IKB kinases (IKBs)  
 RT alpha, beta and gamma."  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; AJ14556; CAC93687.1; -  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 756 AA; 86647 MW; A072D15614A176E5 CRC64;

Query March 90.0%; Score 36; DB 6; Length 756;  
 Best Local Similarity 100.0%; Pred. NO. 7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSM 5  
 |||||  
 DB 737 LDMSM 741

Search completed: February 18, 2004, 14:35:40  
 Job time : 19.3684 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds  
(without alignments)  
87.531 Million cell updates/sec

Title: US-09-643-260-5

Perfect score: 40

Sequence: 1 LDMWA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database :

1: PIR 76:\*  
2: PIR:\*  
3: PIR:\*  
4: PIR:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	92.5	304	2 F83632	probable cytochrome
2	36	90.0	258	2 T21987	hypothetical prote
3	36	90.0	362	2 S23471	uroporphyrinogen d
4	36	90.0	374	2 B83241	conserved hypothet
5	36	90.0	409	2 T47298	probable replicati
6	36	90.0	745	1 I49101	conserved helix-lo
7	36	90.0	983	2 B45583	receptor tyrosine
8	36	90.0	983	2 A38224	protein-tyrosine k
9	36	90.0	983	2 A45583	receptor tyrosine
10	34	85.0	211	2 T03355	gene e12 protein -
11	34	85.0	411	2 B84949	tetrahydrofolylpol
12	34	85.0	433	2 T31511	hypothetical prote
13	34	85.0	616	2 T14235	NADH dehydrogenas
14	34	85.0	1139	2 A10379	probable potassium
15	33	82.5	198	2 B82531	conserved hypothet
16	33	82.5	234	2 T36162	probable integral
17	33	82.5	275	2 T05822	hypothetical prote
18	33	82.5	316	2 AB2931	hypothetical prote
19	33	82.5	316	2 D98351	dipterite ABC tran
20	33	82.5	322	2 A13395	NADH dehydrogenas
21	33	82.5	324	2 AB3548	vegetable incomp
22	33	82.5	360	2 S60888	ferric exochelin b
23	33	82.5	415	2 AB1844	hypothetical prote
24	33	82.5	421	2 T31787	hypothetical prote
25	33	82.5	436	2 E69371	bile acid-inducibl
26	33	82.5	453	1 NMIV3	exo-alpha-stalidas
27	33	82.5	454	1 NMIV	hypothetical prote
28	33	82.5	464	1 S75362	hypothetical prote
29	33	82.5	492	2 S03098	aerolysin precuro

30	33	82.5	516	2 T10000	cytochrome P450 (C
31	33	82.5	524	2 T09999	cytochrome P450 -
32	33	82.5	524	2 T09944	probable cytochrom
33	33	82.5	539	2 T15256	hypothetical prote
34	33	82.5	610	2 T35222	hypothetical prote
35	33	82.5	656	2 A56975	VI polysaccharide
36	33	82.5	656	2 A56975	VI polysaccharide
37	33	82.5	836	2 D82177	conserved hypothet
38	33	82.5	840	1 A42970	H+-exporting ATPas
39	33	82.5	885	2 C83441	two-component sens
40	33	82.5	1334	2 T50568	probable multi-dom
41	33	82.5	1575	2 T18545	lysobactin synthet
42	33	82.5	1842	2 T43409	probable fatty-act
43	33	82.5	1842	2 T38781	fatty acid synthas
44	33	80.0	53	2 T11353	H+-transporting tw
45	32	80.0	83	2 S24712	Ig alpha chain - h

#### ALIGNMENTS

##### RESULT 1

F83632

probable cytochrome c oxidase assembly factor PA0113 [Imported] - Pseudomonas aeruginosa

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C/Accession: F83632

R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; L

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Larbig, K.; L

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: F83632

A>Status: preliminary

A/Molecule type: DNA

A/Residues: 1-304 <STO>

A/Cross-references: GB:AE004449; GB:AE004091; NID:G9945928; PIDN:AA03503.1; GSPDB:GN0

A/Experimental source: strain PA01

C/Genetics:

A/Gene: PA0113

C/Superfamily: heme O synthase

Query Match 92.5%; Score 37; DB 2; Length 304;

Best Local Similarity 83.3%; Pred. No. 50;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMWA 6  
Db 259 LDMWA 264

##### RESULT 2

T21987

hypothetical protein F39B2.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C/Accession: T21987

R/Dobson, R.

submitted to the EMBL Data Library, March 1997

A/Reference number: Z19498

A/Accession: T21987

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-258 <ML>

A/Cross-references: EMBL:Z92834; PIDN:CA807386.1; GSPDB:GN00019; CESP:F39B2.5

A/Experimental source: clone F39B2

C/Genetics:

A/Gene: CESP:F39B2.5

A/Map position: 1

A/Introns: 16/2; 58/1; 97/3

Query Match 90.0%; Score 36; DB 2; Length 258;

Best Local Similarity 83.3%; Pred. No. 61;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSWA 6  
|||  
21 LDWKMA 26

# RESULT 3

urophosphorylase decarboxylase (EC 4.1.1.37) - yeast (*Saccharomyces cerevisiae*)  
N/Alternate names: protein YD9609.03; protein YDR047w  
C/Species: *Saccharomyces cerevisiae*

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 22-Jun-1999  
C/Accession: S23471; S33965; S54033; S20190; S27348; S3312  
R/Garay, J.R.; Labbe-Bois, R.; Chelstowska, A.; Rytke, J.; Harrison, L.; Kushner, J.; Le  
Bur, J. Biochem. 205, 1011-1016, 1992  
A/Title: Urophosphorylase decarboxylase in *Saccharomyces cerevisiae*. HEM12 gene sequence  
A/Reference number: S23471; MUID:92249304; PMID:1576986  
A/Accession: S23471

A/Molecule type: DNA  
A/Residues: 1-362 <GAR>  
A/Cross-references: EMBL:X63721; NID:G3766; PIDN:CAA45253.1; PID:G3767  
R/Difflumer, C.; Laroque, R.; Keng, T.  
Yeast 9, 613-623, 1993  
A/Title: Molecular analysis of HEM6 (HEM12) in *Saccharomyces cerevisiae*, the gene for ur  
A/Reference number: S33965; MUID:93348774; PMID:8346678  
A/Accession: S33965

A/Molecule type: DNA  
A/Residues: 1-362 <DIF>  
A/Cross-references: EMBL:Z19089; NID:G4775; PIDN:CAA79514.1; PID:G4776  
R/Hunt, S.; Bowman, S.; Hartle, D.  
Submitted to the EMBL Data Library, May 1995  
A/Reference number: S54031

A/Accession: S54033  
A/Molecule type: DNA  
A/Residues: 1-362 <HUN>  
A/Cross-references: EMBL:Z49209; NID:G798897; PIDN:CAA89078.1; PID:G798900; MIPS:YDR047w  
C/Genetics:  
A/Gene: HEM12; HEM6; POP3  
A/Cross-references: MIPS:YDR047w; SGD:S0002454  
A/Map position: 4R  
C/Superfamily: urophosphorylase decarboxylase  
C/Keywords: carbon-carbon lyase; carboxy-lyase; porphyrin biosynthesis

Query Match 90.0%; Score 36; DB 2; Length 362;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5  
|||  
279 LDMSW 283

# RESULT 4

B83241 conserved hypothetical protein PA3230 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
C/Species: *Pseudomonas aeruginosa*

C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C/Accession: B83241  
R/Skovor, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Ladbis, K.; Lim,  
L.O.; S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho  
A/Reference number: A82950; MUID:20437337; PMID:10984043  
A/Accession: B83241  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-374 <STO>  
A/Cross-references: GB:AE004746; GB:AE004091; NID:G9949350; PIDN:AA06618.1; GSPDB:GN001  
C/Genetics:

A/Gene: PA3230

Query Match 90.0%; Score 36; DB 2; Length 374;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6  
|||  
81 DMSWA 85

# RESULT 5

probable replication protein - *Arabidopsis thaliana*  
N/Alternate names: protein T14K23.110  
C/Species: *Arabidopsis thaliana* (mouse-ear cress)  
C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C/Accession: T47298  
R/Nyakatura, G.; Fattmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.  
Mayer, K.F.X.  
Submitted to the Protein Sequence Database, April 2000  
A/Reference number: Z24458  
A/Accession: T47298  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-409 <NYA>  
A/Cross-references: EMBL:AL132909  
A/Experimental source: cultivar Columbia; BAC clone T14K23  
C/Genetics:  
A/Map position: 3  
A/Insertions: 47/3; 95/3; 131/2; 175/3; 240/2; 281/3; 304/1; 336/3  
A/Note: T14K23.110

Query Match 90.0%; Score 36; DB 2; Length 409;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5  
|||  
190 LDMSW 194

# RESULT 6

149101 conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.-) CHUK - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C/Accession: I49101  
R/Mock, B.A.; Connolly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.  
Genomics 27, 348-351, 1995  
A/Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosom  
A/Reference number: I49101; MUID:96044444; PMID:7558004  
A/Accession: I49101

A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-745 <RBS>  
A/Cross-references: EMBL:U12473; NID:G1079492; PIDN:AAC52589.1; PID:G1079493  
C/Genetics:  
A/Gene: CHUK  
C/Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homo.  
C/Keywords: ATP; phosphotransferase  
F/13-283/Domain: protein kinase homology <KIN>

Query Match 90.0%; Score 36; DB 1; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5  
|||  
738 LDMSW 742

# RESULT 7

B45583  
 receptor tyrosine kinase Cck4 - chicken  
 C.Species: Gallus gallus (chicken)  
 C.Date: 22-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 18-Jun-1999  
 C.Accession: B45583  
 R.Sajjadi, F.G.; Paeguale, E.B.; Subramani, S.  
 New Biol. 3, 769-778, 1991  
 A>Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse and rat  
 A.Reference number: A45583; MUID:92031278; PMID:1657122  
 A.Accession: B45583  
 A.Status: preliminary  
 A.Molecule type: mRNA  
 A.Residues: 1-983 <SNJ>  
 A.Cross-references: GB:M68514; NID:9454809; PIDN:AAA48666.1; PID:9211447  
 A.Note: sequence extracted from NCBI backbone (NCBIN:62405; NCBI:62411)  
 C.Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
 C.Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein  
 F:619-885/Domain: protein kinase homology <KIN>  
 F:627-635/Region: protein kinase ATP-binding motif

Query Match  
 Best Local Similarity 90.0%; Score 36; DB 2; Length 983;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5  
 |||||  
 Db 342 LDMSW 346

RESULT 8  
 A88224  
 protein-tyrosine kinase (EC 2.7.1.112) hek precursor - human  
 C.Species: Homo sapiens (man)  
 C.Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 18-Jun-1999  
 C.Accession: A38224; B38224  
 R.Wicks, L.P.; Wilkison, D.; Salvaris, E.; Boyd, A.W.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 1611-1615, 1992  
 A>Title: Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expressed in HEK293 cells  
 A.Reference number: A38224; MUID:92179233; PMID:1311845  
 A.Accession: A38224  
 A.Molecule type: mRNA  
 A.Residues: 1-983 <WIC>  
 A.Cross-references: GB:M83941; NID:9183931; PIDN:AAA56633.1; PID:9183932  
 A.Experimental source: pre-B-cell leukemia cell line LK63  
 A.Note: sequence extracted from NCBI backbone (NCBI:86627)  
 A.Accession: B38224  
 A.Molecule type: protein  
 A.Residues: 21-39/810-860 <WIC>  
 C.Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
 C.Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase;  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-983/Product: protein-tyrosine kinase hek #status experimental <WAT>  
 F:542-565/Domain: transmembrane #status predicted <TM>  
 F:619-885/Domain: protein kinase homology <KIN>  
 F:627-635/Region: protein kinase ATP-binding motif  
 F:233,337,391,404,493/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match  
 Best Local Similarity 90.0%; Score 36; DB 2; Length 983;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5  
 |||||  
 Db 343 LDMSW 347

RESULT 9  
 A45583  
 receptor tyrosine kinase Nek4 - mouse  
 C.Species: Mus musculus (house mouse)  
 C.Date: 22-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 18-Jun-1999  
 C.Accession: A45583  
 R.Sajjadi, F.G.; Paeguale, E.B.; Subramani, S.

New Biol. 3, 769-778, 1991  
 A>Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse  
 A.Reference number: A45583; MUID:92031278; PMID:1657122  
 A.Accession: A45583  
 A.Status: preliminary  
 A.Molecule type: mRNA  
 A.Residues: 1-983 <SNJ>  
 A.Cross-references: GB:M68513; NID:9199119; PIDN:AAA39521.1; PID:9199120  
 A.Note: sequence extracted from NCBI backbone (NCBIN:62398; NCBI:62401)  
 C.Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
 C.Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein  
 F:619-885/Domain: protein kinase homology <KIN>  
 F:627-635/Region: protein kinase ATP-binding motif

Query Match  
 Best Local Similarity 90.0%; Score 36; DB 2; Length 983;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 5  
 |||||  
 Db 342 LDMSW 346

RESULT 10  
 T03355  
 gene e12 protein - Lactococcus phage b1170  
 C.Species: Lactococcus phage b1170  
 C.Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 04-Mar-2000  
 C.Accession: T03355  
 R.Critz-Le Coq, A.M.; Cesselin, B.; Commissaire, J.; Anba, J.; Kyriakidis, S.; Chopin, J.  
 Submitted to the EMBL Data Library, June 1997  
 A.Description: Sequence and organization of the lactococcal isometric b1170 phage gene  
 A.Reference number: Z14903  
 A.Accession: T03355  
 A.Status: preliminary; translated from GB/EMBL/DBJ  
 A.Molecule type: DNA  
 A.Residues: 1-211 <CRU>  
 A.Cross-references: EMBL:AF009630; NID:93282260; PIDN:AACT7226.1; PID:93282307  
 C.Genetics:  
 A.Gene: e12  
 C.Superfamily: Lactococcus phage b1170 gene e12 protein

Query Match  
 Best Local Similarity 85.0%; Score 34; DB 2; Length 211;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSW 6  
 |||||  
 Db 29 LDMSW 34

RESULT 11  
 B84949  
 tetrahydrofolylpolyglutamate synthase (EC 6.3.2.17) [imported] - Buchnera sp. (strain ?  
 C.Species: Buchnera sp.  
 C.Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
 C.Accession: B84949  
 R.Shigenobu, S.; Matsumbe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.  
 Nature 407, 81-86, 2000  
 A>Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.  
 A.Reference number: B84930; MUID:20445173; PMID:10993077  
 A.Accession: B84949  
 A.Status: preliminary  
 A.Molecule type: DNA  
 A.Residues: 1-411 <STO>  
 A.Cross-references: GB:AP000398; GSPDB:GN00144  
 A.Experimental source: strain ABS  
 C.Genetics:  
 A.Gene: folC; BUI67  
 C.Superfamily: folylpolyglutamate synthase  
 C.Keywords: ligase

Query Match  
 Best Local Similarity 85.0%; Score 34; DB 2; Length 411;

Best Local Similarity 80.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSW 5  
DB 219 IDMSW 223

## RESULT 12

T13511  
hypothetical protein Y116A8C.9 - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*  
C/Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 04-Mar-2000

C/Accession: T13511  
R/McMurray, A.

submitted to the EMBL Data Library, October 1999  
A/Reference number: Z21041

A/Accession: T13511

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-433 <WIL>

A/Cross-references: EMBL:AL17204; PIDN:CA855145.1; CESP:Y116A8C.9

A/Experimental source: clone Y116A8C

C/Genetics:

A/Genes: CESP:Y116A8C.9

A/Introns: 16/2; 42/2; 75/2; 107/3; 173/3; 230/3; 262/3; 318/3; 373/1; 398/1

C/Superfamily: *Caenorhabditis elegans* hypothetical protein Y116A8C.9

Query Match  
Best Local Similarity 85.0%; Score 34; DB 2; Length 433;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSW 6  
DB 174 VDMTWA 179

## RESULT 13

T14235  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - *Synechococcus* sp. (strain PCC 70

C/Species: *Synechococcus* sp.

A/Variety: strain PCC 7002

C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 03-Jun-2002

C/Accession: T14235

R/Kluhhammer, B.; Sultemeyer, D.; Badger, M.R.; Price, G.D.

submitted to the EMBL Data Library, April 1997

A/Description: Involvement of ndh3, ndh3 and ORF427 genes in high affinity CO2 uptake

A/Reference number: Z17936

A/Accession: T14235

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-616 <KLU>

A/Cross-references: EMBL:U97516; NID:G2232044; PIDN:AA862184.1

A/Experimental source: strain PCC 7002

C/Genetics:

A/Note: ndh3

C/Superfamily: NADH dehydrogenase (ubiquinone) chain 5

C/Keywords: membrane-associated complex; NAD; oxidoreductase

Query Match  
Best Local Similarity 85.0%; Score 34; DB 2; Length 616;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 LDMSW 6  
DB 115 MDMSWA 120

## RESULT 14

A10379  
probable potassium efflux system YPO3129 [imported] - *Yersinia pestis* (strain CO92)

C/Species: *Yersinia pestis*  
C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001

C/Accession: A10379  
R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tubb, R.W.; Holden, M.T.G.; Prentice, M.J.  
demo-Tarrag, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.  
11. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett.  
Nature 413, 523-527, 2001

A/Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A/Reference number: AB0001; MID:21470413; PMID:11586360

A/Accession: A10379

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1139 <KUR>

A/Cross-references: GB:AL590842; PIDN:CA92364.1; PID:G15981067; GSPDB:GN0175

C/Genetics:

A/Genes: YPO3129

Query Match  
Best Local Similarity 85.0%; Score 34; DB 2; Length 1139;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSW 5  
DB 480 MDMSW 484

## RESULT 15

B82531  
conserved hypothetical protein XF2666 [imported] - *Xylella fastidiosa* (strain 9a5c)

C/Species: *Xylella fastidiosa*

C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 17-Nov-2000

C/Accession: B82531

R/Anonymous. The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequ

Nature 406, 151-157, 2000

A/Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A/Reference number: A82515; MID:20365717; PMID:10910347

A/Note: for a complete list of authors see reference number A59328 below

A/Accession: B82531

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-198 <SLM>

A/Cross-references: GB:AE004072; GB:AE003849; NID:9107884; PIDN:AA85463.1; GSPDB:GN01

A/Experimental source: strain 9a5c

R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrero, D.M.; Carrer,

de-Neco, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.V.S.

submitted to GenBank, June 2000

A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fro

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laiz

Chado, M.A.; Medeira, A.M.B.N.; Medeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins,

A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmiter, D

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

M.; Toubko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A/Reference number: A59328

A/Contents: annotation

C/Genetics:

A/Genes: XF2666

C/Superfamily: conserved hypothetical protein MD1677

Query Match  
Best Local Similarity 82.5%; Score 33; DB 2; Length 198;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 DMSWA 6  
DB 135 DMMSWA 139

Search completed: February 18, 2004, 14:38:38  
Job time : 8.5921 secs



GenCore version 5.1.6  
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OM proteain - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds  
(without alignments)  
75.239 Million cell updates/sec

Title: US-09-643-260-5  
Perfect score: 40  
Sequence: 1 LDMSWA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	10	US-09-847-946A-5
2	40	100.0	6	11	US-09-847-946A-5
3	40	100.0	6	11	US-09-847-946A-10
4	40	100.0	6	11	US-09-847-946A-62
5	40	100.0	7	11	US-09-847-946A-66
6	40	100.0	8	11	US-09-847-946A-59
7	40	100.0	8	11	US-09-847-946A-67
8	40	100.0	9	11	US-09-847-946A-58
9	40	100.0	9	11	US-09-847-946A-61
10	40	100.0	9	11	US-09-847-946A-64
11	40	100.0	9	11	US-09-847-946A-65
12	40	100.0	10	11	US-09-847-946A-57
13	40	100.0	10	11	US-09-847-946A-60
14	40	100.0	10	11	US-09-847-946A-63
15	36	90.0	6	10	US-09-847-946B-2

16	36	90.0	6	11	US-09-847-946A-2	Sequence 2, Appli
17	36	90.0	6	11	US-09-847-946A-33	Sequence 33, Appli
18	36	90.0	6	11	US-09-847-946A-41	Sequence 41, Appli
19	36	90.0	6	11	US-09-847-946A-73	Sequence 73, Appli
20	36	90.0	7	11	US-09-847-946A-37	Sequence 37, Appli
21	36	90.0	7	11	US-09-847-946A-77	Sequence 77, Appli
22	36	90.0	8	11	US-09-847-946A-30	Sequence 30, Appli
23	36	90.0	8	11	US-09-847-946A-38	Sequence 38, Appli
24	36	90.0	8	11	US-09-847-946A-70	Sequence 70, Appli
25	36	90.0	8	11	US-09-847-946A-78	Sequence 78, Appli
26	36	90.0	9	11	US-09-847-946A-29	Sequence 29, Appli
27	36	90.0	9	11	US-09-847-946A-32	Sequence 32, Appli
28	36	90.0	9	11	US-09-847-946A-35	Sequence 35, Appli
29	36	90.0	9	11	US-09-847-946A-36	Sequence 36, Appli
30	36	90.0	9	11	US-09-847-946A-69	Sequence 69, Appli
31	36	90.0	9	11	US-09-847-946A-72	Sequence 72, Appli
32	36	90.0	9	11	US-09-847-946A-75	Sequence 75, Appli
33	36	90.0	9	11	US-09-847-946A-76	Sequence 76, Appli
34	36	90.0	10	11	US-09-847-946A-31	Sequence 31, Appli
35	36	90.0	10	11	US-09-847-946A-34	Sequence 34, Appli
36	36	90.0	10	11	US-09-847-946A-71	Sequence 71, Appli
37	36	90.0	10	11	US-09-847-946A-74	Sequence 74, Appli
38	36	90.0	11	11	US-09-847-946A-28	Sequence 28, Appli
39	36	90.0	11	11	US-09-847-946A-68	Sequence 68, Appli
40	36	90.0	11	11	US-09-847-946A-132	Sequence 132, App
41	36	90.0	11	11	US-09-847-946A-140	Sequence 140, App
42	36	90.0	12	11	US-09-847-946A-43	Sequence 43, Appli
43	36	90.0	13	11	US-09-847-946A-143	Sequence 143, App
44	36	90.0	13	11	US-09-847-946A-144	Sequence 144, App
45	36	90.0	13	11	US-09-847-946A-145	Sequence 145, App

## ALIGNMENTS

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RESULT 1
US-09-847-946B-5
; Sequence 5, Application US/09847946B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIORITY FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
US-09-847-946B-5

Query Match      100.0%; Score 40; DB 10; Length 6;
Beet Local Similarity 100.0%; Pred. NO. 7e+05;
Matches      6; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 LDMSWA 6
Db      1 LDMSWA 6

RESULT 2
US-09-847-946A-5
; Sequence 5, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

```

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; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-5

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Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LDMSWA 6
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Db       1 LDMSWA 6

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RESULT 3
US-09-847-946A-40
; Sequence 40, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-40

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Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LDMSWA 6
        |||||
Db       1 LDMSWA 6

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RESULT 4
US-09-847-946A-62
; Sequence 62, Application US/09847946A
; Publication No. US20030054999A1

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; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-62

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Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LDMSWA 6
        |||||
Db       1 LDMSWA 6

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```

RESULT 5
US-09-847-946A-66
; Sequence 66, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-66

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Query Match          100.0%; Score 40; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
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QY      1 LDMSWA 6
        |||||
Db       1 LDMSWA 6

```

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RESULT 6

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US-09-847-946A-59  
; Sequence 59, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Pindels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-59

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Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6  
Db 3 LDMSWA 8

RESULT 7  
US-09-847-946A-67  
; Sequence 67, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Pindels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
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; SEQ ID NO 67  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-67

Query Match 100.0%; Score 40; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6  
Db 1 LDMSWA 6

RESULT 8  
US-09-847-946A-58  
; Sequence 58, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Pindels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 58  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-58

Query Match 100.0%; Score 40; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6  
Db 1 LDMSWA 6

RESULT 9  
US-09-847-946A-61  
; Sequence 61, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Pindels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 61  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-61

Query Match 100.0%; Score 40; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6  
Db 1 LDMSWA 6

## RESULT 10

US-09-847-946A-64  
Sequence 64, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
PRIORITY FILING DATE: 2001-05-02  
PRIORITY FILING DATE: 2000-05-02  
PRIORITY FILING DATE: 2000-08-22  
PRIORITY FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 64  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-64

Query Match 100.0%; Score 40; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6  
Db 3 LDMSWA 8

## RESULT 11

US-09-847-946A-65  
Sequence 65, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
PRIORITY FILING DATE: 2001-05-02  
PRIORITY FILING DATE: 2000-05-02  
PRIORITY FILING DATE: 2000-08-22  
PRIORITY FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 65  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-65

Query Match 100.0%; Score 40; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6  
Db 2 LDMSWA 7

## RESULT 12

US-09-847-946A-57  
Sequence 57, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
PRIORITY FILING DATE: 2001-05-02  
PRIORITY FILING DATE: 2000-05-02  
PRIORITY FILING DATE: 2000-08-22  
PRIORITY FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 57  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-57

Query Match 100.0%; Score 40; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6  
Db 2 LDMSWA 7

## RESULT 13

US-09-847-946A-60  
Sequence 60, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
PRIORITY FILING DATE: 2001-05-02  
PRIORITY FILING DATE: 2000-05-02  
PRIORITY FILING DATE: 2000-08-22  
PRIORITY FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 60  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-60

US-09-847-946A-60

Query Match 100.0%; Score 40; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMWSA 6  
DB 2 LDMWSA 7

## RESULT 14

US-09-847-946A-63  
; Sequence 63, Application US/09847946A  
; Publication No. US2003054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Pindels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 63  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-63

Query Match 100.0%; Score 40; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMWSA 6  
DB 3 LDMWSA 8

## RESULT 15

US-09-847-940B-2  
; Sequence 2, Application US/09847940B  
; Patent No. US20020156000A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J.  
; APPLICANT: Ghosh, Sankar  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-117CP  
; CURRENT APPLICATION NUMBER: US/09/847,940B  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants  
US-09-847-940B-2

Query Match 90.0%; Score 36; DB 10; Length 6;

Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 1 LDMWS 5  
DB 1 LDMWS 5

Search completed: February 18, 2004, 15:41:55  
Job time : 16.7529 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds  
(without alignments)  
89.145 Million cell updates/sec

Title: US-09-643-260-4  
Perfect score: 40  
Sequence: 1 ADMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

SPTRMBL.23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriophage:\*
- 17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	205	16	Q9ACRS
2	40	100.0	227	4	Q8IXK8
3	40	100.0	355	11	Q8BIT9
4	40	100.0	452	4	Q96AB7
5	40	100.0	477	11	Q9CTU6
6	40	100.0	484	4	Q9BTU6
7	37	92.5	154	11	Q8BBD2
8	37	92.5	1083	13	Q9OMQ8
9	37	92.5	1083	13	Q8AXU2
10	37	92.5	1100	13	Q9OMQ9
11	37	92.5	1329	16	Q9CD30
12	36	90.0	48	16	Q8VXB2
13	36	90.0	236	3	Q8NVY9
14	36	90.0	261	2	Q9AQG7
15	36	90.0	273	16	Q8NS79
16	36	90.0	274	16	Q8G659

17	36	90.0	310	2	Q9XB87	Q9XB87 zymomonas m
18	36	90.0	310	16	Q8FRF1	Q8FRF1 corynebacte
19	36	90.0	358	10	Q50002	Q50002 prunus arme
20	36	90.0	703	10	Q9FIS0	Q9FIS0 arabidopsis
21	36	90.0	703	10	Q8GYG3	Q8GYG3 arabidopsis
22	36	90.0	740	6	Q9SKV1	Q9SKV1 bos taurus
23	36	90.0	745	11	Q8CBT3	Q8CBT3 mus musculu
24	36	90.0	747	16	Q69735	Q69735 mycobacteri
25	36	90.0	756	6	Q9SKV0	Q9SKV0 bos taurus
26	36	90.0	803	17	Q97UH8	Q97UH8 sulfolobus
27	36	90.0	889	16	Q9AAZ6	Q9AAZ6 caulobacter
28	36	90.0	996	2	Q9A0H0	Q9A0H0 caldicellul
29	36	90.0	1005	10	Q9XGZ2	Q9XGZ2 arabidopsis
30	36	90.0	1139	16	Q8EC91	Q8EC91 yersinia pe
31	36	90.0	1345	16	Q9L060	Q9L060 streptomyce
32	36	90.0	1426	2	Q9X3P6	Q9X3P6 caldicellul
33	36	90.0	1751	2	Q9A0G4	Q9A0G4 caldicellul
34	36	90.0	1770	2	Q9X3P5	Q9X3P5 caldicellul
35	36	90.0	5435	2	Q9L4X2	Q9L4X2 streptomyce
36	35	87.5	49	6	Q8SPU6	Q8SPU6 equus caball
37	35	87.5	161	6	Q8MJT3	Q8MJT3 oryctolagus
38	35	87.5	161	11	Q9Z1P9	Q9Z1P9 rattus norv
39	35	87.5	200	16	Q8NSJ3	Q8NSJ3 corynebacte
40	35	87.5	241	16	Q8PR42	Q8PR42 corynebacte
41	35	87.5	323	6	Q9TT79	Q9TT79 ovib aries
42	35	87.5	562	16	Q9BAG0	Q9BAG0 rhizobium 1
43	35	87.5	565	2	Q9KJ20	Q9KJ20 actinopolys
44	35	87.5	596	5	Q8SSN6	Q8SSN6 dictyosell
45	35	87.5	616	17	Q27025	Q27025 methanobact

## ALIGNMENTS

RESULT 1

Q9ACRS PRELIMINARY; PRT; 205 AA.

AC Q9ACRS; 01-JUN-2001 (TRMBLrel. 17, Created)

DT 01-JUN-2001 (TRMBLrel. 17, Last sequence update)

DT 01-OCT-2002 (TRMBLrel. 22, Last annotation update)

DE Hypothetical protein SCP1.253.

GN SCP1.253.

OS Streptomyces coelicolor.

OG Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycinae; Streptomycetaceae; Streptomyces.

NCBI\_TaxID=1902;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);

RX MEDLINE=21996410; PubMed=12000953;

RA Bentley S.D., Chaker K.F., Cerdano-Tarraga A.-M., Challis G.L.,

RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,

RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,

RA Rabinovitch E., Rajandream M.A., Rutherford K., Rutter S.,

RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,

RA Hopwood D.A.,

RT "Complete genome sequence of the model actinomycete Streptomyces

RT coelicolor A3(2).";

RL Nature 417:141-147(2002).

DR EMBL; AL590464; CAC36779.1; "

KW Hypothetical protein; Plasmid; Complete proteome.

SQ SEQUENCE 205 AA; 23051 MW; 6602396CF933F2D9 CRC64;

Query Match 100.0%; Score 40; DB 16; Length 205;

Best Local Similarity 100.0%; Pred. No. 75;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          10 ADMSWL 15

RESULT 2
Q81XK8      PRELIMINARY; PRT; 227 AA.
AC Q81XK8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Similar to hypothetical protein BC017335.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Struhsberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RW EMBL; BC040173; AA040173.1; -.
KW Hypothetical protein.
SQ SEQUENCE 227 AA; 25487 MW; F1A71EA57062A05 CRC64;

Query Match          100.0%; Score 40; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
Db          113 ADMSWL 118

RESULT 3
Q8BIT9      PRELIMINARY; PRT; 355 AA.
AC Q8BIT9;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Mitochondrial ribosomal protein L41 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002)
DR EMBL; AK087998; BAC40084.1; -.
SQ SEQUENCE 355 AA; 40183 MW; FE98546127402D58 CRC64;

Query Match          100.0%; Score 40; DB 11; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
Db          215 ADMSWL 220

RESULT 4
Q96AB7      PRELIMINARY; PRT; 452 AA.
ID Q96AB7;
AC Q96AB7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

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DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein FLJ90634.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Struhsberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Iwogal T., Oca T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuhara Y., Ono T., Okano K., Yoshikawa Y., Aoyama S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Minomiyama K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RW EMBL; BC017335; AA017335.1; -.
DR EMBL; AK075115; BAC11411.1; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 452 AA; 50575 MW; B79D25EE38096733 CRC64;

Query Match          100.0%; Score 40; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6
Db          338 ADMSWL 343

RESULT 5
Q9CYU6      PRELIMINARY; PRT; 477 AA.
ID Q9CYU6;
AC Q9CYU6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE 2810443J12R1K protein (Mitochondrial ribosomal protein L41
DE homolog).
GN 2810443J12R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=1217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Komno H., Aichi J., Fukuda S.,
RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamanae I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kanakawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesl C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schmitt L.M., Steinhilber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Baran G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Maehama J., Mazzarelli J., Monbarte P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

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RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilmig L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).

RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Mesonephros;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium.  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK013297; BAB28775.1; -  
 DR EMBL; AK078448; BAC37279.1; -  
 DR MGD; MGI:1914478; 2810443J12R1k.  
 DR InterPro; IPR001680; WD40.  
 DR Pfam; PF00400; WD40; 3.  
 DR SMART; SM00320; WD40; 4.  
 DR PROSITE; PS00678; WD\_REPEATS\_1; 2.  
 DR PROSITE; PS50082; WD\_REPEATS\_2; 1.  
 DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
 KM Repeat; WD repeat.  
 SQ SEQUENCE 477 AA; 53201 MW; 2655573524A4BA9C CRC64;

Query Match 100.0%; Score 40; DB 11; Length 477;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6  
 DB 337 ADMSWL 342

RESULT 6  
 Q9BTV6 PRELIMINARY; PRT; 484 AA.  
 ID Q9BTV6;  
 AC Q9BTV6;  
 DT 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Tissue=Brain;  
 RA Strausberg R.;  
 RL Submitted (PEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC003123; AAH03123.1; -  
 DR InterPro; IPR001680; WD40.  
 DR Pfam; PF00400; WD40; 2.  
 DR SMART; SM00320; WD40; 3.  
 DR PROSITE; PS00678; WD\_REPEATS\_1; 2.  
 DR PROSITE; PS50082; WD\_REPEATS\_2; 1.  
 DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
 KM Hypothetical protein; Repeat; WD repeat.  
 FT NON\_TER  
 SQ SEQUENCE 484 AA; 54088 MW; 1A2CA3237CB7358E CRC64;

Query Match 100.0%; Score 40; DB 4; Length 484;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6  
 DB 370 ADMSWL 375

RESULT 7

Q9BGD2 PRELIMINARY; PRT; 154 AA.  
 ID Q9BGD2;  
 AC Q9BGD2;  
 DT 01-MAR-2003 (TREMblrel. 23, Created)  
 DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium.  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK043157; BAC31480.1; -  
 DR EMBL; AK049078; BAC33535.1; -  
 KM Hypothetical protein.  
 FT NON\_TER  
 SQ SEQUENCE 154 AA; 16524 MW; A526724D4074D88 CRC64;

Query Match 92.5%; Score 37; DB 11; Length 154;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6  
 DB 9 ADMSWL 14

RESULT 8  
 Q9OWQ8 PRELIMINARY; PRT; 1083 AA.  
 ID Q9OWQ8;  
 AC Q9OWQ8;  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Inducible nitric oxide synthase (EC 1.14.13.39).  
 GN INOS.  
 OS Oncomyrchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Teleostei;  
 OC Procaractopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Tissue=gonad;  
 RA Wang T., Ward M., Grabowski P.S., Secombes C.J.;  
 RT "Molecular cloning, gene organization and expression of rainbow trout  
 RT (Oncorhynchus mykiss) inducible nitric oxide synthase (inos) gene."  
 RL J. Biochem. 358:747-755(2001).  
 DR EMBL; AJ300555; CAC83069.1; -  
 DR InterPro; IPR003097; FAD binding.  
 DR InterPro; IPR001094; Flavodoxin like.  
 DR InterPro; IPR001226; Flavodoxin.  
 DR InterPro; IPR001709; FPN\_cyt\_redcse.  
 DR InterPro; IPR004030; NO\_synthase.  
 DR InterPro; IPR001433; Oxred\_FAD/NAD(P).  
 DR Pfam; PF00667; FAD binding\_1; 1.  
 DR Pfam; PF00258; Flavodoxin\_1.  
 DR Pfam; PF00175; NAD binding\_1; 1.  
 DR Pfam; PF02898; NO\_synthase; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 DR PROSITE; PS60001; NOS; 1.  
 KM Oxidoreductase.  
 SQ SEQUENCE 1083 AA; 123060 MW; 53EADFD2FA5A8B5D CRC64;



Query Match 92.5%; Score 37; DB 13; Length 1083;  
 Best Local Similarity 83.3%; Pred. No. 1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWL 6  
 Db 402 ADMAML 407

## RESULT 9

Q8AXU2 PRELIMINARY; PRT; 1083 AA.

AC Q8AXU2; 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Inducible nitric oxide synthase (EC 1.14.13.39).  
 GN INOS.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Proteocephala; Cyprinodontiformes; Salmonidae; Oncorhynchus.  
 NX NCBI\_TaxID=8022;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA Wang T., Bole N., Secombes C.J.;  
 RT "Two promoters of inducible nitric oxide synthase gene exist in  
 rainbow trout evidenced by studies with RTs-11 and RTG-2 cell lines."  
 RL Submitted (INOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ295230; CAC82807.1; -.  
 KM Oxidoreductase.  
 SQ SEQUENCE 1083 AA; 123033 MW; B0F95C3F033AF249 CRC64;

Query Match 92.5%; Score 37; DB 13; Length 1083;  
 Best Local Similarity 83.3%; Pred. No. 1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWL 6  
 Db 402 ADMAML 407

## RESULT 10

Q90M09 PRELIMINARY; PRT; 1100 AA.

AC Q90M09; 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Inducible nitric oxide synthase (EC 1.14.13.39).  
 GN INOS.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Proteocephala; Cyprinodontiformes; Salmonidae; Oncorhynchus.  
 NX NCBI\_TaxID=8022;  
 RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;  
 RA Wang T., Ward M., Grabowski P.S., Secombes C.J.;  
 RT "Molecular cloning, gene organization and expression of rainbow trout  
 (Oncorhynchus mykiss) inducible nitric oxide synthase (INOS) gene."  
 RL J. Biochem. 358:747-755(2001).  
 DR EMBL; AJ295231; CAC82808.1; -.  
 DR InterPro; IPR003097; PAD binding.  
 DR InterPro; IPR001094; Flavodoxin like.  
 DR InterPro; IPR001226; Flavodoxin.  
 DR InterPro; IPR001709; FPN\_cyt\_redctase.  
 DR InterPro; IPR004030; NO\_synthase.  
 DR Pfam; PF00667; PAD binding (P).  
 DR Pfam; PF00258; Flavodoxin; 1.  
 DR Pfam; PF00175; NAD\_binding\_1; 1.

DR Pfam; PF02898; NO\_synthase; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PROSITE; PS60001; NOS; 1.  
 KM Oxidoreductase.

SQ SEQUENCE 1100 AA; 125079 MW; E4763388C97D608F CRC64;

Query Match 92.5%; Score 37; DB 13; Length 1100;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWL 6  
 Db 419 ADMAML 424

## RESULT 11

Q9CD30 PRELIMINARY; PRT; 1329 AA.

AC Q9CD30; 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical protein ML2535.  
 GN ML2535.  
 OS Mycobacterium leprae.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 NX NCBI\_TaxID=1769;  
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=TN;  
 RX MEDLINE=21128732; PubMed=11234002;  
 RA Cole S.T., Eigemeier K., Parkhill J., James K.D., Thomson N.R.,  
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,  
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,  
 RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,  
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,  
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,  
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,  
 RA Barrell B.G.;  
 RT "Massive gene decay in the leprosy bacillus."  
 RL Nature 409:1007-1011(2001).  
 DR EMBL; AL583926; CAC32066.1; -.  
 DR Lepitoma; ML2535;  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR InterPro; IPR002543; FtsK\_SpoIIIE.  
 DR Pfam; PF01580; FtsK\_SpoIIIE; 2.  
 DR SMART; SM00382; AAA; 3.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 1329 AA; 146129 MW; F8A85758D60E7D8 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 1329;  
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWL 6  
 Db 260 SDMSWL 265

## RESULT 12

Q8VXB2 PRELIMINARY; PRT; 48 AA.

AC Q8VXB2; 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical protein MT0946.  
 GN MT0946.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J.F., Deboy R., Dodson R., Gilm M.L., Halc D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Unayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains";  
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF006980; AAK45193.1; -  
 DR TIGR; MT0946; -  
 KM Hypothetical protein.  
 SQ SEQUENCE 48 AA; 5265 MW; C0BFA9D6AA2EF8DF CRC64;

Query Match 90.0%; Score 36; DB 16; Length 48;  
 Best Local Similarity 83.3%; Pred. No. 69;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6  
 DB 13 ADMSWL 18

## RESULT 13

Q8NJT9 PRELIMINARY; PRT; 236 AA.

ID Q8NJT9  
 AC Q8NJT9;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Endoglucanase.  
 GN CEL12C.  
 OS Bionectria ochroleuca.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreales; Bionectriaceae; Bionectria.  
 OX NCBI\_TaxID=29856;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=22067395; PubMed=12073090;  
 RA Gedegebur F., Fowler T., Phillips J., van der Kley P.,  
 RA van Solingen P., Dankmeyer L., Power S.D.;  
 RT "Cloning and relational analysis of 15 novel fungal endoglucanases  
 RT from family 12 glycosyl hydrolase";  
 RL Curr. Genet. 41:89-98(2002).  
 DR EMBL; AF435065; AAM77708.1; -  
 DR InterPro; IPR002594; Glyco\_hydro.12.  
 DR Pfam; PF01670; Glyco\_hydro.12; 1.  
 DR ProDom; PD004316; Glyco\_hydro.12; 1.  
 SQ SEQUENCE 236 AA; 26024 MW; C3DBA7E33F0C41D8 CRC64;

Query Match 90.0%; Score 36; DB 3; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 5  
 DB 63 ADMSWL 67

## RESULT 14

Q9AOG7 PRELIMINARY; PRT; 261 AA.

ID Q9AOG7  
 AC Q9AOG7;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Glycosyl hydrolase 6 (Fragment).  
 OS Caldicielluloseiuptor sp. Tok7B.1.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;

OC Caldicielluloseiuptor.  
 OX NCBI\_TaxID=80339;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Tok7B.1;  
 RX MEDLINE=20171169; PubMed=10706665;  
 RA Gibbs W.D., Reeves R.A., Farrington G.K., Anderson P., Williams D.P.,  
 RA Bergquist P.L.;  
 RT "Multidomain and multifunctional glycosyl hydrolases from the extreme  
 RT thermophile Caldicielluloseiuptor isolate Tok7B.1";  
 RL Curr. Microbiol. 40:333-340(2000).  
 DR EMBL; AF078040; AAK06391.1; -  
 DR HSSP; Q06851; INBC.  
 DR InterPro; IPR001956; CBD\_3.  
 DR Pfam; PF00942; CBM\_3; 1.  
 DR ProDom; PD001947; CBD\_3; 1.  
 KM Hydrolase.  
 FT NON\_TER 1 1  
 FT NON\_TER 261 261  
 SQ SEQUENCE 261 AA; 28759 MW; 4771744A26AE04 CRC64;

Query Match 90.0%; Score 36; DB 2; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6  
 DB 237 DMSWL 241

## RESULT 15

Q8NS79 PRELIMINARY; PRT; 273 AA.

ID Q8NS79  
 AC Q8NS79;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Monophosphatase family.  
 GN CG10800.  
 OS Corynebacterium glutamicum (Brevibacterium flavum).  
 OC Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
 OX NCBI\_TaxID=1718;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;  
 RA Nakagawa S.;  
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032";  
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF005276; BAB98193.1; -  
 DR InterPro; IPR000760; inositol\_P.  
 DR Pfam; PF00459; inositol\_P; 1.  
 KM Complete proteome.  
 SQ SEQUENCE 273 AA; 29072 MW; C132E2C67E0BBA4D CRC64;

Query Match 90.0%; Score 36; DB 16; Length 273;  
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWL 6  
 DB 225 ADMSWL 230

Search completed: February 18, 2004, 14:35:38  
 Job time : 18.3684 secs

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds  
(without alignments)  
79.423 Million cell updates/sec

Title: US-09-643-260-4  
Perfect score: 40  
Sequence: 1 ADMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	90.0	470	1 NOS2_ONCMY	Q92091 oncorhynch
2	36	90.0	470	1 NRAM_IADBU	Q07570 influenza a
3	36	90.0	470	1 NRAM_IADCH	Q07571 influenza a
4	36	90.0	470	1 NRAM_IADH2	Q07572 influenza a
5	36	90.0	470	1 NRAM_IADH2	Q07573 influenza a
6	36	90.0	470	1 NRAM_IADH3	Q07599 influenza a
7	36	90.0	470	1 NRAM_IAGFN	Q07574 influenza a
8	36	90.0	470	1 NRAM_IADGD	Q07577 influenza a
9	36	90.0	470	1 NRAM_IADH1	Q07578 influenza a
10	36	90.0	470	1 NRAM_IADAB	Q07583 influenza a
11	36	90.0	470	1 NRAM_IADTL	Q07585 influenza a
12	36	90.0	745	1 IKKA_HUMAN	O15111 h inhibitor
13	36	90.0	745	1 IKKA_MOUSE	Q06880 m inhibitor
14	36	90.0	756	1 IKKB_HUMAN	O14920 homo sapien
15	36	90.0	757	1 IKKB_MOUSE	O08351 mus musculu
16	36	90.0	757	1 IKKB_RAT	Q09478 ratu
17	36	90.0	1039	1 GUNB_CALSA	Q09478 ratu
18	36	90.0	1275	1 RFBP_MYXXA	P10474 c endogluc
19	35	87.5	99	1 NOS3_SHEEP	Q05864 myxococcu
20	35	87.5	914	1 GUX2_CLOSR	P73209 ovis arles
21	35	87.5	1201	1 NOS3_HUMAN	P50900 clostridum
22	35	87.5	1202	1 NOS3_MOUSE	P73313 mus musculu
23	35	87.5	1204	1 NOS3_BOVIN	P23474 homo sapien
24	35	87.5	1204	1 NOS3_PIG	P23473 bos tauru
25	34	85.0	220	1 Y132_METVA	Q07596 sus scrofa
26	34	85.0	282	1 3MG2_ECOLI	Q04395 escherichia
27	34	85.0	410	1 Y801_DEIRA	O92468 delnoccoc
28	34	85.0	529	1 GUNA_MYCLE	P48810 mycobacteri
29	34	85.0	578	1 YC20_METUA	Q04617 methanococ
30	34	85.0	578	1 YC12_XLEPN	Q04618 klebsiella
31	34	85.0	591	1 NOS2_CANFA	O62699 canis fami
32	34	85.0	1144	1 NOS2_MOUSE	P23477 mus musculu
33	34	85.0	1147	1 NOS2_RAT	Q06518 ratu

34	34	85.0	1147	1 NOS2_HUMAN	O60591 homo sapien
35	34	85.0	1149	1 NOS2_CAVPO	O54705 cavia porce
36	34	85.0	1153	1 NOS2_HUMAN	P35228 homo sapien
37	34	85.0	1331	1 MANB_CALSA	P22533 caldocellum
38	34	85.0	1742	1 GUNA_CALSA	P22533 caldocellum
39	33	82.5	232	1 CIB3_SHEEP	P80943 ovis arles
40	33	82.5	333	1 CIB2_SHEEP	Q29422 ovis arles
41	33	82.5	336	1 NOS0_BACSU	O34453 bacillus su
42	33	82.5	339	1 YJGB_ECOLI	P27250 escherichia
43	33	82.5	376	1 PGLR_PENGR	O93883 penicillium
44	33	82.5	421	1 PNK1_SCHPO	O13911 schizosacch
45	33	82.5	470	1 NRAM_IADIT	Q07584 influenza a

## ALIGNMENTS

RESULT 1  
ID NOS2\_ONCMY STANDARD; PRT; 470 AA.  
AC Q92091;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)  
DE (Inducible NOS) (NOS) (Fragment).  
GN NOS2.  
OS Oncochrychus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncochrychus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Grabowski P.S., Laling K.J., Hardie L., Macgilligan F., Ralston S.,  
RA Secombe C.J.;  
RT "Detection of mRNA for a nitric oxide synthase in macrophages and  
RT gill of rainbow trout challenged with an attenuated bacterial  
RT pathogen."  
RL (in) Moncada S., Stamler J.J., Higgs E.A. (eds.);  
RL 4th International meeting on the biology of nitric oxide, Amelia  
RL Island, Florida, Sep. 1995, pp.10:48-48, Portland Press,  
RL Brookfield (1996).  
CC -!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO  
CC MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.  
CC -!- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +  
CC nitric oxide + N NADP(+)  
CC -!- COFACTOR: HEME. BINDS ONE MOLE EACH OF PAD AND FMN. ALSO REQUIRES  
CC TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
CC THE ENZYME (BY SIMILARITY).  
CC -!- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN (BY  
CC SIMILARITY).  
CC -!- SUBUNIT: Homodimer (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE NOS FAMILY.  
CC -!- SIMILARITY: BELONGS TO THE Flavo-doxin-like domain.  
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DR EMBL: X97013; CAA65736.1; -.  
DR HSPR: P29477; NOS.  
DR InterPro: IPR003037; PAD binding.  
DR InterPro: IPR001094; Flavo-doxin-like.  
DR InterPro: IPR001226; Flavo-doxin.  
DR InterPro: IPR004030; NO synthase.  
DR Pfam: PF00667; PAD binding 1; 1.  
DR Pfam: PF00258; Flavo-doxin; 1.

DR Pfam; PF02898; NO\_gynthase; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PROSITE; PS50902; FLAVODOXIN LIKE; 1.  
 DR PROSITE; PS60001; NOS; PARTIAL.  
 KW Oxidoreductase; NADP; PAD; FMN; Calmodulin-binding; Heme.  
 FT NON\_TER 1  
 FT DOMAIN 139 159 CALMODULIN-BINDING (POTENTIAL).  
 FT DOMAIN 169 307 FLAVODOXIN-LIKE.  
 FT NP\_BIND 253 284 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
 FT NP\_BIND 398 409 PAD (ADP PART) (BY SIMILARITY).  
 FT NON\_TER 470 470  
 SQ SEQUENCE 470 AA; 53329 MW; 40B6717BE500B64D CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;  
 Best Local Similarity 83.3%; Pred. No. 82;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSW 6  
 Db 89 ADMWDL 94

RESULT 2  
 NRAM\_IADBU STANDARD; PRT; 470 AA.  
 ID NRAM\_IADBU  
 AC 007570;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuraminidase (EC 3.2.1.18).  
 GN NA.  
 OS Influenza A virus (strain A/Duck/Burjatta/552/88).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza A viruses; Influenzavirus A.  
 OX NCBI\_TaxID=38957;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RA MEDLINE=93212520; PubMed=8460490;  
 RA Saito T., Kawoka Y., Webster R.G.;  
 RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A  
 virus";  
 RL Virology 193:868-876(1993).  
 CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side  
 chains of the host cell surface proteins and from the viral  
 envelope. Such a reaction prevents self-aggregation and facilitate  
 the mobility of the virus to and from the site of infection.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,  
 alpha-(2->8)-glycosidic linkages of terminal sialic residues in  
 oligosaccharides, glycoproteins, glycolipids, colominic acid and  
 synthetic substrates.  
 CC -1- SUBUNIT: Homotrimer.  
 CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED  
 SPIKE ON THE SURFACE OF THE VIRION.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.  
 CC -----  
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 CC -----  
 DR EMBL; L06572; AAA43365.1; -;  
 DR HSSP; P06820; 2BAT.  
 DR InterPro; IPR001860; Glyco\_hydro\_34.  
 DR Pfam; PF00064; neur; 1.  
 DR ProDom; PD000431; Glyco\_hydro\_34; 1.  
 KW Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.  
 FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).  
 FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.  
 FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.  
 FT ACT\_SITE 273 273 BY SIMILARITY.

FT ACT\_SITE 275 275 BY SIMILARITY.  
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 470 AA; 51989 MW; DIA6F07460F6F8AD CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 82;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
 Db 453 ADMSW 457

RESULT 3  
 NRAM\_IADCH STANDARD; PRT; 470 AA.  
 ID NRAM\_IADCH  
 AC 007571;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuraminidase (EC 3.2.1.18).  
 GN NA.  
 OS Influenza A virus (strain A/Duck/Chabarovsk/1610/72).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza A viruses; Influenzavirus A.  
 OX NCBI\_TaxID=38957;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA MEDLINE=93212520; PubMed=8460490;  
 RA Saito T., Kawoka Y., Webster R.G.;  
 RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A  
 virus";  
 RL Virology 193:868-876(1993).  
 CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side  
 chains of the host cell surface proteins and from the viral  
 envelope. Such a reaction prevents self-aggregation and facilitate  
 the mobility of the virus to and from the site of infection.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,  
 alpha-(2->8)-glycosidic linkages of terminal sialic residues in  
 oligosaccharides, glycoproteins, glycolipids, colominic acid and  
 synthetic substrates.  
 CC -1- SUBUNIT: Homotrimer.  
 CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED  
 SPIKE ON THE SURFACE OF THE VIRION.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.  
 CC -----  
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 CC -----  
 DR EMBL; L06573; AAA43367.1; -;  
 DR HSSP; P06820; 2BAT.  
 DR InterPro; IPR001860; Glyco\_hydro\_34.  
 DR Pfam; PF00064; neur; 1.  
 DR ProDom; PD000431; Glyco\_hydro\_34; 1.  
 KW Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.  
 FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).  
 FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.  
 FT ACT\_SITE 273 273 BY SIMILARITY.  
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL)  
 SQ SEQUENCE 470 AA; 52070 MW; 169AB89FEB8006DC CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 82;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADM5W 5  
 DB 453 ADM5W 457

RESULT 4  
 ID NRAM\_IADH2 STANDARD; PRT; 470 AA.  
 AC 007572;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuraminidase (EC 3.2.1.18).  
 GN NA.  
 OS Influenza A virus (strain A/Duck/Hokkaido/8/80).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza A viruses; Influenzavirus A.  
 OX NCBI\_TaxID=11358;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93212520; PubMed=8460490;  
 RA Saito T., Kawoka Y., Webster R.G.;  
 RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A  
 RT virus".  
 RL Virology 193:868-876(1993).  
 CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side  
 CC chains of the host cell surface proteins and from the viral  
 CC envelope. Such a reaction prevents self-aggregation and facilitates  
 CC the mobility of the virus to and from the site of infection.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,  
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in  
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and  
 CC synthetic substrates.  
 CC -1- SUBUNIT: Homotrimer.  
 CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED  
 CC SPIKE ON THE SURFACE OF THE VIRION.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.  
 CC  
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 CC  
 CC -----  
 CC EMBL: L06574; AAA43372.1; -.  
 CC HSRP; P06820; 2BRT.  
 CC InterPro: IPR001860; Glyco\_hydro\_34.  
 CC Pfam: PF00064; neu; 1.  
 CC ProDom: PD000431; Glyco\_hydro\_34; 1.  
 CC HydroLase; Glycosidase; Glycoprotein; Transmembrane.  
 CC TRANSMEM 7 38 ANCHOR (BY SIMILARITY).  
 CC DOMAIN 39 88 HYPERVARIABLE STALK REGION.  
 CC ACT SITE 273 273 HEAD OF NEURAMINIDASE.  
 CC ACT SITE 275 275 BY SIMILARITY.  
 CC CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 470 AA; 52015 MW; E1C1DBE2C650B93C CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 82;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADM5W 5  
 DB 453 ADM5W 457

RESULT 5  
 ID NRAM\_IADH2 STANDARD; PRT; 470 AA.  
 AC 007573;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuraminidase (EC 3.2.1.18).  
 GN NA.  
 OS Influenza A virus (strain A/Duck/Memphis/92/874).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza A viruses; Influenzavirus A.  
 OX NCBI\_TaxID=11367;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93212520; PubMed=8460490;  
 RA Saito T., Kawoka Y., Webster R.G.;  
 RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A  
 RT virus".  
 RL Virology 193:868-876(1993).  
 CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side  
 CC chains of the host cell surface proteins and from the viral  
 CC envelope. Such a reaction prevents self-aggregation and facilitates  
 CC the mobility of the virus to and from the site of infection.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,  
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in  
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and  
 CC synthetic substrates.  
 CC -1- SUBUNIT: Homotrimer.  
 CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED  
 CC SPIKE ON THE SURFACE OF THE VIRION.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.  
 CC  
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 CC  
 CC -----  
 CC EMBL: L06575; AAA43404.1; -.  
 CC HSRP; P06820; 2BRT.  
 CC InterPro: IPR001860; Glyco\_hydro\_34.  
 CC Pfam: PF00064; neu; 1.  
 CC ProDom: PD000431; Glyco\_hydro\_34; 1.  
 CC HydroLase; Glycosidase; Glycoprotein; Transmembrane.  
 CC TRANSMEM 7 38 ANCHOR (BY SIMILARITY).  
 CC DOMAIN 39 88 HYPERVARIABLE STALK REGION.  
 CC ACT SITE 273 273 HEAD OF NEURAMINIDASE.  
 CC ACT SITE 275 275 BY SIMILARITY.  
 CC CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 470 AA; 52146 MW; 30F5F9F3E364C1F49 CRC64;

QY 1 ADMSW 5  
Db 453 ADMSW 457

RESULT 6  
ID NRAM\_IADU3 STANDARD; PRT; 470 AA.  
AC 007579;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuraminidase (EC 3.2.1.18).  
GN NA.  
OS Influenza A virus (strain A/Duck/Ukraine/1/53).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza A viruses; Influenzavirus A.  
OX NCBI\_TaxId=11374;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93212520; PubMed=8460490;  
RA Saito T., Kawakita Y., Webster R.G.;  
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A  
RT viruses.";  
RL Virology 193:868-876(1993).  
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side  
CC chains of the host cell surface proteins and from the viral  
CC envelope. Such a reaction prevents self-aggregation and facilitate  
CC the mobility of the virus to and from the site of infection.  
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,  
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in  
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and  
CC synthetic substrates.  
CC -1- SUBUNIT: Homotrimer.  
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED  
CC SPIKE ON THE SURFACE OF THE VIRION.  
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.  
CC  
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CC  
CC EMBL; L06576; AAA16234.1; -  
DR HSSP; P06820; 28AT.  
DR InterPro; IPR001860; Glyco\_hydro\_34.  
DR Pfam; PF00064; neur; 1.  
DR ProDom; PD000431; Glyco\_hydro\_34; 1.  
KW Hydroxylase; Glycoprotein; Transmembrane.  
FT DOMAIN 7 37 ANCHOR (BY SIMILARITY).  
FT CARBOHYD 38 88 HYPERVARIABLE STALK REGION.  
FT ACT\_SITE 273 273 HEAD OF NEURAMINIDASE.  
FT DOMAIN 89 470 PROBABLE.  
FT ACT\_SITE 273 273  
FT CARBOHYD 46 46  
FT CARBOHYD 54 54 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 84 84 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 144 144 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 398 398 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 470 AA; 51960 MW; B46D54A03AC84CCE CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
Db 453 ADMSW 457

RESULT 7  
ID NRAM\_IAGFN STANDARD; PRT; 470 AA.  
AC 007574;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuraminidase (EC 3.2.1.18).  
GN NA.  
OS Influenza A virus (strain A/Guinea fowl/New York/4-3587/84).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza A viruses; Influenzavirus A.  
OX NCBI\_TaxId=18963;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93212520; PubMed=8460490;  
RA Saito T., Kawakita Y., Webster R.G.;  
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A  
RT viruses.";  
RL Virology 193:868-876(1993).  
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side  
CC chains of the host cell surface proteins and from the viral  
CC envelope. Such a reaction prevents self-aggregation and facilitate  
CC the mobility of the virus to and from the site of infection.  
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,  
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in  
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and  
CC synthetic substrates.  
CC -1- SUBUNIT: Homotrimer.  
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED  
CC SPIKE ON THE SURFACE OF THE VIRION.  
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.  
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CC  
CC EMBL; L06584; AAA43428.1; -  
DR HSSP; P06820; 28AT.  
DR InterPro; IPR001860; Glyco\_hydro\_34.  
DR Pfam; PF00064; neur; 1.  
DR ProDom; PD000431; Glyco\_hydro\_34; 1.  
KW Hydroxylase; Glycoprotein; Transmembrane.  
FT DOMAIN 7 38 ANCHOR (BY SIMILARITY).  
FT CARBOHYD 39 88 HYPERVARIABLE STALK REGION.  
FT ACT\_SITE 273 273 HEAD OF NEURAMINIDASE.  
FT DOMAIN 89 470  
FT ACT\_SITE 273 273  
FT CARBOHYD 46 46  
FT CARBOHYD 54 54 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 84 84 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 144 144 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 293 293 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 398 398 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 470 AA; 52348 MW; D3BD2AC0159FB66 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DN Neuraminidase (EC 3.2.1.18).
OS Influenza A virus (strain A/Herring gull/DE/677/88).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=39544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaka Y., Webster R.G.;
RT "Phylogenetic analysis of the NA neuraminidase gene of Influenza A
RT viruses.";
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC
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CC
DR EMBL: L06585; AAA3368.1; -
DR HSSP: P06820; 2BAT.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur; 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
KM Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 275 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52265 MW; 28AF0B75EB0539B7 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 9
NRAM_IAMJI STANDARD; PRT; 470 AA.
AC 007578;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).

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GN NA.
OS Influenza A virus (strain A/Equine/J111n/1/89).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11401;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaka Y., Webster R.G.;
RT "Phylogenetic analysis of the NA neuraminidase gene of Influenza A
RT viruses.";
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC
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CC
DR EMBL: L06579; AAA3374.1; -
DR HSSP: P06820; 2BAT.
DR InterPro: IPR001860; Glyco_hydro_34.
DR Pfam: PF00064; neur; 1.
DR ProDom: PD000431; Glyco_hydro_34; 1.
KM Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 275 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52234 MW; CE50B21050A37668 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 10
NRAM_IAMAE STANDARD; PRT; 470 AA.
AC 007583;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DN Neuraminidase (EC 3.2.1.18).
OS Influenza A virus (strain A/Mallard/Edmonton/220/90).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.

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OX NCBI_TaxID=38965;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawakita Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
virus."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC
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CC -----
DR EMBL; L06586; AAA43369.1; -
DR HSRP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
DR HydroLase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT HEAD OF NEURAMINIDASE.
FT ACT_SITE 89 470 BY SIMILARITY.
FT ACT_SITE 273 273 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52070 MW; 557630C3E1F2765 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 11
NRAM_IATKL STANDARD; PRT; 470 AA.
ID NRAM_IATKL
AC Q07585;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Turkey/Minnesota/501/78).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38984;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
```

```
RA Saito T., Kawakita Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
virus."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06588; AAA43410.1; -
DR HSRP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
DR HydroLase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 273 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52352 MW; D8573742ABF1868 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 12
IKKA_HUMAN STANDARD; PRT; 745 AA.
ID IKKA_HUMAN
AC O15111; Q14666; Q13132; Q92467.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
DE (I-kappa-B kinase alpha) (IKBA) (IKK-alpha) (IKK-A) (I-kappa-B kinase)
DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitin
DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).
GN CHUK OR IKKA.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RC TISSUE=T-cell;
RX MEDLINE=97386461; PubMed=9244310;
```





FT MUTAGEN 176 176 ACTIVITY.  
 FT MUTAGEN 179 179 S->E: FULL ACTIVATION.  
 FT MUTAGEN 180 180 T->A: NO CHANGE IN PHOSPHORYLATION.  
 FT CONFLICT 543 543 S->A: NO CHANGE IN PHOSPHORYLATION.  
 FT CONFLICT 604 604 E->G (IN REF. 2).  
 FT CONFLICT 604 604 L->R (IN REF. 5).  
 FT CONFLICT 679 680 TS->AY (IN REF. 5).  
 FT CONFLICT 684 684 P->A (IN REF. 3 AND 5).  
 FT CONFLICT 686 687 TS->DL (IN REF. 5).  
 SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 745;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 739 DMSWL 743

Qy 2 DMSWL 6  
 |||||

RESULT 13  
 ID IKKA MOUSE STANDARD; PRT; 745 AA.  
 AC Q60680; Q9D2X3; 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Inhibitor of nuclear factor kappa-B kinase subunit (EC 2.7.1.-)  
 DE (I kappa-B kinase alpha) (IKK-alpha) (IKK-A) (Ikkappa kinase  
 DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous  
 DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKB1KA).  
 GN CHUK OR IKKA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID:10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=BALB/c;  
 RX MEDLINE=9604444; PubMed=7558004;  
 RA Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.;  
 RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human  
 RT chromosome 10 and mouse chromosome 19.";  
 RL Genomics 27:348-351(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=BALB/c;  
 RX MEDLINE=96258427; PubMed=8777433;  
 RA Connolly M.A., Marcu K.B.;  
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper  
 RT families of interacting proteins, contains a serine-threonine kinase  
 RT catalytic domain.";  
 RL Cell. Mol. Biol. Res. 41:537-549(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RC STRAIN=C57BL/6J; TISSUE=Colon;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Iehi Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kanakawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schiraldi L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai J., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,  
 RA Blake J., Botfield D., Boujunga N., Carmignoli P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Guignicich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohbanki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [4]  
 RP ALTERNATIVE SPLICING.  
 RX MEDLINE=20198447; PubMed=10733566;  
 RA McKenzie F.R., Connolly M.A., Balzarano D., Mueller J.R.,  
 RA Gelezianus R., Marcu K.B.;  
 RT "Functional isoforms of Ikkappa kinase alpha (IKKalpha) lacking  
 RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and  
 RT IKKbeta have different activation requirements.";  
 RL Mol. Cell. Biol. 20:2635-2649(2000).  
 RN [5]  
 RP PHOSPHORYLATION BY MAP3K14/NIK.  
 RX MEDLINE=98188238; PubMed=9520401;  
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,  
 RA Okumura K.;  
 RT "Differential regulation of Ikkappa kinase alpha and beta by two  
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated  
 RT protein kinase/ERK kinase kinase-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).  
 RN [6]  
 RP IKK-IRK-B BINDING.  
 RX MEDLINE=99212141; PubMed=10195894;  
 RA Delhase M., Hayakawa M., Chen Y., Karin M.;  
 RT "Positive and negative regulation of Ikkappa kinase activity through  
 RT IKKbeta subunit phosphorylation.";  
 RL Science 284:309-313(1999).  
 RN [7]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., DiDonato J.A., Lin A.;  
 RT "Coordinate regulation of Ikkappa kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [8]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 RT inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 CC the dissociation of the inhibitor/NF-kappa-B complex and  
 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3.  
 CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated  
 CC when dephosphorylated.  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but  
 CC also as an homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MAP3K14/NIK, MEK1, IKAP and IKK-alpha-P65-P50  
 CC complex. A weak interaction with TRAF2 cannot be excluded. Part of  
 CC a complex composed of NCOA2, NCOA3, IKK2, IKK3 and CREBBP (by  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=3;  
 CC Name=1:  
 CC IsoId=Q60680-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Delta LH;  
 CC IsoId=Q60680-2; Sequence=VSP\_004866; VSP\_004867;  
 CC Name=3; Synonyms=Delta H;  
 CC IsoId=Q60680-3; Sequence=VSP\_004868; VSP\_004869;  
 CC TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and  
 CC 3 are expressed predominantly in brain and T-lymphocytes.  
 CC -1- DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by  
 CC E11, E15 and E17 days. In the limb development, its expression  
 CC predominates in the limb buds at E12.5 day.  
 CC -1- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by  
 CC MEK1, and dephosphorylated by PP2A. Autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.



RA O'Malley B.W.:  
 RT "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator  
 activity by I kappa B kinase.";  
 RL Mol. Cell. Biol. 22:3549-3561(2002).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 the dissociation of the inhibitor/NF-kappa-B complex and  
 ultimately the degradation of the inhibitor. Also phosphorylates  
 NCOA3 (By similarity).  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-alpha-p65-p50  
 complex. Phosphorylated IKK-alpha is further released from the  
 complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB  
 and CREBBP.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal  
 muscle, kidney, pancreas, spleen, thymus, prostate, testis and  
 peripheral blood.  
 CC -1- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.  
 CC Weakly autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPBAP KINASE SUBFAMILY.  
 CC -----  
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 or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 CC EMBL: AF028684; AAC51860.1; -  
 CC EMBL: AF080158; AAD08997.1; -  
 CC EMBL: AF031416; AAC64675.1; -  
 CC EMBL: BC006231; AAH06231.1; -  
 CC HSSP: O63450; 1A06.  
 CC GeneW: HGNC:5960; IKKB.  
 CC MIM: 603258; -  
 CC DR GO: GO:0005737; C:cytoplasm; NAS.  
 CC DR GO: GO:0005524; F:ATP binding activity; NAS.  
 CC DR GO: GO:0004674; F:protein serine/threonine kinase activity; NAS.  
 CC DR GO: GO:0016563; F:transcriptional activator activity; NAS.  
 CC DR GO: GO:0004686; P:protein amino acid phosphorylation; NAS.  
 CC DR InterPro: IPR000719; Prot\_kinase.  
 CC DR InterPro: IPR002290; Ser\_Thr\_kinase.  
 CC DR Pfam: PF00069; kinase; 1.  
 CC DR Pfam: PF00240; ubiquitin; 1.  
 CC DR ProDom: PD000001; Prot\_kinase; 1.  
 CC DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 CC DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 CC DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC KM Transferrase: Serine/threonine-protein kinase; ATP-binding;  
 KM Phosphorylation.  
 CC FT DOMAIN 15 300 PROTEIN KINASE.  
 CC FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 CC FT DOMAIN 737 742 MEMO-BINDING.  
 CC FT NP\_BIND 21 29 ATP (BY SIMILARITY).  
 CC FT BINDING 44 44 ATP (BY SIMILARITY).  
 CC FT ACT\_SITE 145 145 BY SIMILARITY.  
 CC FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 CC FT MOD\_RES 177 177 PHOSPHORYLATION.  
 CC FT MOD\_RES 181 181 PHOSPHORYLATION.  
 CC FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO  
 EFFECT ON BINDING TO NIK.  
 CC FT MUTAGEN 177 177 S->A: DECREASE OF ACTIVITY.  
 CC FT MUTAGEN 177 177 S->E: FULL ACTIVATION.  
 CC FT MUTAGEN 181 181 S->A: DECREASE OF ACTIVITY.  
 CC FT MUTAGEN 181 181 S->E: FULL ACTIVATION.  
 CC FT CONFLICT 231 255 HSKR0KSEVIVSEDLNFTVF -> CYRMMPGTVAHS  
 CC FT CONFLICT 425 425 Q -> H (IN REF. 1).  
 CC FT SEQUENCE 756 AA; 86563 MW; F9CADP671AE9E14E CRC64;

Query Match 90.0%; Score 36; DB 1; Length 756;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DMSWL 6  
 DB 738 DMSWL 742  
 RESULT 15  
 ID IKKB MOUSE STANDARD; PRT; 757 AA.  
 AC 088351; Q9RLJ6;  
 DT 16-OCT-2001 (Ref. 40, Created)  
 DT 16-OCT-2001 (Ref. 40, Last sequence update)  
 DT 28-FEB-2003 (Ref. 41, Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (NC 2.7.1.-)  
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase  
 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).  
 GN IKKB OR IKKB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. AND PHOSPHORYLATION BY MEKK1.  
 RC STRAIN=C57BL/6; TISSUE=Spleen;  
 RX MEDLINE=98188238; PubMed=9520401;  
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,  
 Okumura K.;  
 RT "Differential regulation of Ikkapab kinase alpha and beta by two  
 upstream kinases, NF-kappaB-inducing kinase and mitogen-activated  
 protein kinase/ERK kinase kinase-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;  
 RT "Murine IKK kinase-B, a developmentally regulated protein kinase that  
 constitutively phosphorylates serine residues of Ikb.";  
 RL Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP DEVELOPMENTAL STAGE.  
 RX MEDLINE=99455228; PubMed=10523628;  
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;  
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling  
 pathway activates Ikkapab kinases (IKK-alpha/beta) and IKK-beta is a  
 developmentally regulated protein kinase.";  
 RL Oncogene 18:3514-3524(1999).  
 RN [4]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., Didonato J.A., Lin A.;  
 RT "Coordinate regulation of Ikkapab kinases by mitogen-activated protein  
 kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [5]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 the dissociation of the inhibitor/NF-kappa-B complex and  
 ultimately the degradation of the inhibitor. Also phosphorylates  
 NCOA3.  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-alpha-p65-p50  
 complex. Phosphorylated IKK-alpha is further released from the  
 complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB

```

CC and CREBBP (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
CC -1- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout
CC the mouse embryo, at E9.5 day its expression begins to be
CC localized to the brain, neural ganglia, neural tube, and in liver
CC at E12.5 day. At E15.5 day, the expression is further restricted
CC to specific tissues of the embryo.
CC -1- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.
CC Weakly autophosphorylated.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPPAB KINASE SUBFAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF026524; AAC23557.1; -.
CC EMBL: AF088910; AAD52095.1; -.
CC HSP: O63450; 1A06.
CC MGD: MGI:1338071; Ikbb.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_kinase.
CC DR Pfam: PF00069; Pkinase; 1.
CC DR PRINTS: PR00109; TYRKINASE.
CC DR ProDom: PD000001; Prot_kinase; 1.
CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC KW transferase; Serine/threonine-protein kinase; ATP-binding;
CC Phosphorylation.
CC FT DOMAIN 15 300 PROTEIN KINASE.
CC FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
CC FT DOMAIN 737 742 NEMO-BINDING.
CC FT NP_BIND 21 29 ATP (BY SIMILARITY).
CC FT BINDING 44 44 ATP (BY SIMILARITY).
CC FT ACT_SITE 145 145 BY SIMILARITY.
CC FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
CC FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
CC FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
CC FT CONFLICT 56 56 N -> D (IN REF. 2).
CC FT CONFLICT 343 343 N -> E (IN REF. 2).
CC FT CONFLICT 356 356 K -> B (IN REF. 2).
CC FT CONFLICT 390 390 L -> F (IN REF. 2).
CC FT CONFLICT 406 406 P -> Q (IN REF. 2).
CC FT CONFLICT 573 573 K -> R (IN REF. 2).
CC FT CONFLICT 736 757 TLDMSWLQWDEERCSLEQACD -> VTA (IN REF.
CC FT CONFLICT 2).
CC SQ SEQUENCE 757 AA; 86690 MW; PED962F095449CSE CRC64;

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Query Match          90.0%; Score 36; DB 1; Length 757;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 2 DMSWL 6
DB 738 DMSWL 742

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Search completed: February 18, 2004, 14:28:03  
Job time : 3.55263 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds  
(without alignments)  
87.531 Million cell updates/sec

Title: US-09-643-260-4

Perfect score: 40

Sequence: 1 ADMSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	132	2	mel-13a protein -
2	37	92.5	1329	2	conserved hypothet
3	36	90.0	122	2	Ig V-D-J region (M
4	36	90.0	745	1	conserved helix-10
5	36	90.0	747	2	hypothetical prote
6	36	90.0	803	2	hypothetical prote
7	36	90.0	889	2	Tomb-dependent rec
8	36	90.0	915	2	cellulase (EC 3.2.
9	36	90.0	1039	2	cellulase (EC 3.2.
10	36	90.0	1139	2	probable potassium
11	36	90.0	1275	2	O-antigen biosynth
12	35	87.5	616	2	type I restriction
13	35	87.5	1202	2	nitric-oxide synth
14	35	87.5	1203	1	nitric-oxide synth
15	35	87.5	1205	1	nitric-oxide synth
16	35	87.5	1409	2	alkaline phosphata
17	35	87.5	1879	2	extracellular nucl
18	34	85.0	214	2	hypothetical prote
19	34	85.0	220	2	restriction modifi
20	34	85.0	248	2	3-oxoacyl-l-acyl-ca
21	34	85.0	276	2	hypothetical prote
22	34	85.0	282	1	DGEEMA
23	34	85.0	282	2	DNA-3-methyladenin
24	34	85.0	282	2	3-methyl-adenine D
25	34	85.0	283	2	probable glycocy
26	34	85.0	287	2	hypothetical prote
27	34	85.0	289	2	DNA-3-methyladenin
28	34	85.0	304	1	probable ribB prot
29	34	85.0	368	2	Aa3-600 quinol oxi

30	34	85.0	368	2	Aa3-600 quinol oxi
31	34	85.0	410	2	lycopene cyclase -
32	34	85.0	529	2	probable GMP synth
33	34	85.0	548	2	hypothetical prote
34	34	85.0	578	2	restriction modifi
35	34	85.0	590	2	GMP synthase (gluc
36	34	85.0	623	2	type I restriction
37	34	85.0	1144	1	nitric-oxide synth
38	34	85.0	1147	1	nitric-oxide synth
39	34	85.0	1147	1	nitric-oxide synth
40	34	85.0	1147	1	nitric-oxide synth
41	34	85.0	1147	1	nitric-oxide synth
42	34	85.0	1147	2	nitric-oxide synth
43	34	85.0	1147	2	nitric-oxide synth
44	34	85.0	1147	2	nitric-oxide synth
45	34	85.0	1147	2	nitric-oxide synth

#### ALIGNMENTS

##### RESULT 1

mel-13a protein - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 26-Aug-1999  
C/Accession: S65785  
R/Tetnu, O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.  
Biochem. Biophys. Acta 1305, 109-112, 1996  
A/Title: Cloning and characterization of two transcripts generated from the mel-13 gen  
A/Reference number: S65785; MUID:96180310; PMID:8597592  
A/Accession: S65785  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-132 <TER>  
A/Cross-references: EMBL:U35309  
C/Genetics:  
A/Gene: mel-13  
C/Superfamily: mouse mel-13a protein  
C/Keywords: alternative splicing

Query Match 92.5%; Score 37; DB 2; Length 132;  
Best Local Similarity 83.3%; Pred. No. 28;  
Matches 5; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 ADMSWL 6  
:|||||  
Db 57 SDMSWL 62

RESULT 2  
D87226  
conserved hypothetical protein ML2535 [imported] - Mycobacterium leprae

C/Species: Mycobacterium leprae  
C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001  
C/Accession: D87226  
R/Cole, S.T.; Sigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; I  
R.; Davies, R.M.; Devlin, K.; Dutchy, S.; Fellwell, T.; Fraser, A.; Hamlin, N.; Holroy  
eam, M.A.; Rutherford, K.M.  
Nature 409, 1007-1011, 2001  
A/Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; I  
A/Title: Massive gene decay in the leprosy bacillus.  
A/Reference number: A86909; MUID:21128732; PMID:11234002  
A/Accession: D87226  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1329 <SNO>  
A/Cross-references: GB:AL450380; NID:q13093796; PIDN:CAC32066.1; GSPDB:GN00147  
C/Genetics:  
A/Gene: ML2535

Query Match 92.5%; Score 37; DB 2; Length 1329;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADMSWL 6  
 :|||||  
 Db 260 DMSWL 265

## RESULT 3

569909  
 Ig V-D-J region (MS) - human  
 C/Species: Homo sapiens (man)  
 C/Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
 C/Accession: S69909  
 R/Saotia, S.; Hamblin, T.; Oester, D.G.; Stevenson, F.K.  
 Leukemia 8, 1285-1289, 1994  
 A/Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi  
 A/Reference number: S69909; MUID:9433515; PMID:8057663  
 A/Accession: S69909  
 A/Status: preliminary; nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-122 <SA>  
 A/Cross-references: EMBL:Z33399; NID:G871348; PIDN:CAA83850.1; PID:G871349  
 A/Note: the sequence of residues 112-122 and the corresponding nucleic acid sequence are  
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 F:15-97/Domain: Immunoglobulin homology <IM>

Query Match 90.0%; Score 36; DB 2; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6  
 :|||||  
 Db 33 DMSWL 37

## RESULT 4

149101  
 conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.-) CHUK - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C/Accession: I49101  
 R/Mock, B.A.; Connolly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.  
 Genomics 27, 348-351, 1995  
 A/Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome  
 A/Reference number: I49101; MUID:96044444; PMID:7558004  
 A/Accession: I49101  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-745 <RES>  
 A/Cross-references: EMBL:U12473; NID:G1079492; PIDN:AAC52589.1; PID:G1079493  
 C/Genetics:  
 A/Gene: CHUK  
 C/Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homolo  
 C/Keywords: ATP, phosphotransferase  
 F:13-283/Domain: protein kinase homology <KIN>

Query Match 90.0%; Score 36; DB 1; Length 745;  
 Best Local Similarity 100.0%; Pred. No. 2,3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6  
 :|||||  
 Db 739 DMSWL 743

## RESULT 5

D70802  
 hypothetical protein Rv3870 - Mycobacterium tuberculosis (strain H37RV)  
 C/Species: Mycobacterium tuberculosis  
 C/Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
 C/Accession: D70802  
 R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
 ; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
 Nature 393, 537-544, 1998  
 A/Authors: Squares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrett, B.G.  
 A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom  
 A/Reference number: A70500; MUID:9825987; PMID:9634230  
 A/Accession: D70802  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-747 <COL>  
 A/Cross-references: GB:AL022120; GB:AL123456; NID:G3261558; PIDN:CAA17962.1; PID:G2960  
 A/Experimental source: strain H37RV  
 C/Genetics:  
 A/Gene: Rv3870

Query Match 90.0%; Score 36; DB 2; Length 747;  
 Best Local Similarity 100.0%; Pred. No. 2,3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6  
 :|||||  
 Db 267 DMSWL 271

## RESULT 6

F90485  
 hypothetical protein SSO3039 [imported] - Sulfolobus solfataricus  
 C/Species: Sulfolobus solfataricus  
 C/Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
 C/Accession: F90485  
 R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Anayez, M.J.; Cha  
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,  
 arett, R.A.; Ragan, M.A.; Sersen, C.W.; Van der Oost, J.  
 submitted to Genbank, April 2001  
 A/Description: Sulfolobus solfataricus complete genome.  
 A/Reference number: A93139  
 A/Accession: F90485  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-803 <KUR>  
 A/Cross-references: GB:AB006641; NID:G13816440; PIDN:AAK43141.1; GSPDB:GN00155  
 C/Genetics:  
 A/Gene: SSO3039

Query Match 90.0%; Score 36; DB 2; Length 803;  
 Best Local Similarity 100.0%; Pred. No. 2,4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6  
 :|||||  
 Db 540 DMSWL 544

## RESULT 7

E87304  
 TonB-dependent receptor [imported] - Caulobacter crescentus  
 C/Species: Caulobacter crescentus  
 C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001  
 C/Accession: E87304  
 R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.  
 B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kol  
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.  
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A/Title: Complete Genome Sequence of Caulobacter crescentus.  
 A/Reference number: A87249; MUID:21173698; PMID:11259647  
 A/Accession: E87304  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-889 <STO>  
 A/Cross-references: GB:AB005673; NID:G13421615; PIDN:AAK22433.1; GSPDB:GN00148  
 C/Genetics:  
 A/Gene: CC0446

Query Match 90.0%; Score 36; DB 2; Length 889;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
|||||

Db 618 ADMSW 622

## RESULT 8

A43802  
cellulase (EC 3.2.1.4) / cellulose 1,4-beta-cellulobiosidase (EC 3.2.1.91) - Caldocellum  
N/Alternate names: endo-1,4-beta-glucanase  
C/Species: Caldocellum saccharolyticum  
C/Date: 30-Jan-1993 #sequence\_revision 30-Sep-1993 #text\_change 10-Jul-1998  
C/Accession: A43802  
R/Saul, D.J.; Williams, L.C.; Grayling, R.A.; Chamley, L.W.; Love, D.R.; Bergquist, P.L.  
Appl. Environ. Microbiol. 56, 3117-3124, 1990  
A/Title: celB, a gene coding for a bifunctional cellulase from the extreme thermophile  
A/Reference number: A43802; MUID:91136262; PMID:2126700  
A/Accession: A43802  
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A/Molecule type: DNA  
A/Residues: 1-915 <SAU>  
A/Cross-references: EMBL:X13602  
C/Function:  
A/Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as ce  
A/Pathway: cellulose degradation  
C/Superfamily: Streptomyces endo-1,4-beta-xyylanase A homology  
C/Keywords: glycosidase; hydrolase; polysaccharide degradation  
F/20-320/Domain: Streptomyces endo-1,4-beta-xyylanase A homology <SXY>

Query Match 90.0%; Score 36; DB 2; Length 915;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6  
|||||

Db 469 DMSWL 473

## RESULT 9

S02711  
cellulase (EC 3.2.1.4) precursor - Caldocellum saccharolyticum  
N/Alternate names: endo-1,4-beta-glucanase  
N/Contains: cellulase (EC 3.2.1.4); cellulose 1,4-beta-cellulobiosidase (EC 3.2.1.91)  
C/Species: Caldocellum saccharolyticum  
C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 08-Oct-1999  
C/Accession: S02711  
R/Saul, D.J.; Williams, L.C.; Love, D.R.; Chamley, L.W.; Bergquist, P.L.  
Nucleic Acids Res. 17, 439, 1989  
A/Title: Nucleotide sequence of a gene from Caldocellum saccharolyticum encoding for exc  
A/Reference number: S02711; MUID:8908398; PMID:2789517  
A/Accession: S02711  
A/Molecule type: DNA  
A/Residues: 1-1039 <SAU>  
A/Cross-references: EMBL:X13602; NID:g40645; PIDN:CAA1936.1; PID:g40646  
C/Genetics:  
A/Gene: celB  
C/Function:  
A/Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as ce  
A/Pathway: cellulose degradation  
C/Superfamily: Streptomyces endo-1,4-beta-xyylanase A homology  
C/Keywords: glycosidase; hydrolase; polysaccharide degradation  
F/1-28/Domain: signal sequence #status predicted <SIG>  
F/9-1039/Product: cellulase #status predicted <MAT>  
F/72-373/Domain: Streptomyces endo-1,4-beta-xyylanase A homology <SXY>

Query Match 90.0%; Score 36; DB 2; Length 1039;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6  
|||||

Db 540 DMSWL 544

## RESULT 10

A10379  
probable potassium efflux system YPO3129 [imported] - Yersinia pestis (strain CO92)  
C/Species: Yersinia pestis  
C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C/Accession: A10379  
R/Parhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.J.  
deno-Parragh, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.  
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell  
Nature 413, 523-527, 2001  
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A/Reference number: AB0001; MUID:21470413; PMID:11586360  
A/Accession: A10379  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1139 <KIR>  
A/Cross-references: GB:AU590842; PIDN:CAC92364.1; PID:g15981067; GSPDB:GN00175  
C/Genetics:  
A/Gene: YPO3129

Query Match 90.0%; Score 36; DB 2; Length 1139;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6  
|||||

Db 481 DMSWL 485

## RESULT 11

T18556  
O-antigen biosynthesis protein homolog rfbC - Myxococcus xanthus  
C/Species: Myxococcus xanthus  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C/Accession: T18556  
R/Guo, D.; Bowden, M.G.; Pershad, R.; Kaplan, H.B.  
J. Bacteriol. 178, 1631-1639, 1996  
A/Title: The Myxococcus xanthus rfbABC operon encodes an ATP-binding cassette transport  
A/Reference number: Z18970; MUID:96198166; PMID:8626291  
A/Accession: T18556  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1275 <GGO>  
A/Cross-references: EMBL:U36795; NID:g1235659; PID:g1235662; PIDN:AB05019.1  
C/Genetics:  
A/Note: rfbC

Query Match 90.0%; Score 36; DB 2; Length 1275;  
Best Local Similarity 83.3%; Pred. No. 3.9e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWL 6  
|||||

Db 348 ADMSWL 353

## RESULT 12

C69226  
type I restriction modification enzyme, subunit M - Methanobacterium thermoautotrophic  
C/Species: Methanobacterium thermoautotrophicum  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 29-Sep-1999  
C/Accession: C69226  
R/Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
i Oiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Mierzbowski, J.; Gibson, R.; Jiwani, N.  
Kl.S.; Church, G.M.; Daniels, C.J.; Mo, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func  
A/Reference number: A69000; MUID:98037514; PMID:9371463  
A/Accession: C69226  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown



A.Molecule type: DNA  
 A.Residues: 1-616 <MTH>  
 A.Cross-references: GB:AE000868; GB:AE000666; NID:g2622025; PIDN:AA85440.1; PID:g2622004  
 A.Experimental source: strain Delta H  
 C.Genetics:  
 A.Gene: MTH942  
 A.Start codon: GTG  
 C.Superfamily: type I site-specific deoxyribonuclease chain hcdm

Query Match 87.5%; Score 35; DB 2; Length 616;  
 Beef Local Similarity 66.7%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6  
 |||:  
 DB 425 ADMAWI 430

RESULT 13  
 S71424  
 nitrlic-oxide synthase (EC 1.14.13.39), endothelial - mouse  
 C.Species: Mus musculus (house mouse)  
 C.Date: 09-Dec-1997 #sequence\_revision 09-Dec-1997 #text\_change 04-Mar-2000  
 C.Accession: S71424  
 R.Gnmapenditthen, K.; Chen, Z.; Kau, C.L.; Gorczyński, R.M.; Marsden, P.A.  
 Biochim. Biophys. Acta 1308, 103-106, 1996  
 A>Title: Cloning and characterization of murine endothelial constitutive nitrlic oxide sy  
 A.Reference number: S71424; MUID:96350460; PMID:8764825  
 A.Accession: S71424  
 A.Molecule type: mRNA  
 A.Residues: 1-1202 <GNA>  
 A.Cross-references: EMBL:U53142; NID:g1518955; PIDN:AA52766.1; PID:g1518956  
 A.Experimental source: fetal cardiac  
 C.Genetics:  
 A.Gene: NOS  
 C.Superfamily: nitrlic-oxide synthase; flavodoxin binding; NADPH-ferrhemoprotein reduct  
 C.Keywords: blocked amino end; calmodulin binding; chromoprotein; FAD; flavoprotein; FMN  
 F.490-503/Region: calmodulin binding #status predicted  
 F.519-1158/Domain: NADPH-ferrhemoprotein reductase homology <FEH>  
 F.521-702/Domain: Flavodoxin homology <FLX>  
 F.647-679/Region: FMN binding #status predicted  
 F.790-803/Region: FAD-pyrophosphate binding #status predicted  
 F.934-945/Region: FAD-isoloxazine binding #status predicted  
 F.1009-1027/Region: NADP-ribose binding #status predicted  
 F.1107-1123/Region: NADP-adenine binding #status predicted  
 F.2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F.3/Modified site: aspartic acid (Asn) #status predicted  
 F.183/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 87.5%; Score 35; DB 2; Length 1202;  
 Beef Local Similarity 66.7%; Pred. No. 5.2e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6  
 |||:  
 DB 442 ADMAWI 447

RESULT 14  
 A47501  
 nitrlic-oxide synthase (EC 1.14.13.39), endothelial - human  
 C.Species: Homo sapiens (man)  
 C.Date: 02-Jun-1995 #sequence\_revision 21-Jul-1995 #text\_change 03-Mar-2000  
 C.Accession: A47501; S24052; X58948; A49813; A42867; S45691; I37361  
 R.Marsden, P.A.; Heng, H.H.Q.; Scherer, S.W.; Stewart, R.J.; Hall, A.V.; Shi, X.M.; Tard  
 U. Biol. Chem. 268, 17478-17486, 1993  
 A>Title: Structure and chromosomal localization of the human constitutive endothelial ni  
 A.Reference number: A47501; MUID:93352539; PMID:7688726  
 A.Accession: A47501  
 A.Molecule type: DNA  
 A.Residues: 1-1203 <MAR>  
 A.Cross-references: GB:L10709; NID:g348235; PIDN:AAA36365.1; PID:g348237; GB:L10693; NID  
 0698; NID:g348224; GB:L10699; NID:g348225; GB:L10700; NID:g348226; GB:L10701; NID:g34822

[illegible]

F:186/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 87.5%; Score 35; DB 1; Length 1203;

Best Local Similarity 66.7%; Pred. No. 5.2e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6

DB 443 ADMAMI 448

# RESULT 15

A38943

nitric-oxide synthase (EC 1.14.13.39), endothelial - bovine

N.Alternate names: ECNOS; nitric-oxide synthase type III

C.Species: Bos primigenius taurus (cattle)

C.Date: 02-Jun-1995 #sequence\_revision 02-Jun-1995 #text\_change 03-Mar-2000

C.Accession: A38943; A46033; I45945; A42841; I45946; A38944

R.Lamas, S.; Marsden, P.A.; Li, G.K.; Tempst, P.; Michel, T.

submitted to GenBank, July 1992

A.Reference number: A38943

A.Accession: A38943

A.Molecule type: mRNA

A.Residues: 1-1205 <LAM1>

A.Cross-References: GB:M89952; NID:G162976; PIDN:AAA30494.1; PID:G162977

A.Experimental source: aortic endothelial cells

R.Lamas, S.; Marsden, P.A.; Li, G.K.; Tempst, P.; Michel, T.

Proc. Natl. Acad. Sci. U.S.A. 89, 6348-6352, 1992

A>Title: Endothelial nitric oxide synthase: molecular cloning and characterization of a

A.Reference number: A46033; MUID:9233525; PMID:1378626

A.Accession: A46033

A>Status: nucleic acid sequence not shown

A.Molecule type: mRNA

A.Residues: 1-860; 'T', 862-1205 <LAM2>

A.Cross-References: GB:M89952; NID:G162976

A.Experimental source: endothelial

A>Note: sequence extracted from NCBI backbone (NCBIP:108720)

R.Nishida, K.; Harrison, D.G.; Navas, J.P.; Fisher, A.A.; Dockery, S.P.; Nerem, R.M.; Al

J. Clin. Invest. 90, 2092-2096, 1992

A>Title: Molecular Cloning and Characterization of the constitutive bovine aortic Endoth

A.Reference number: I45945; MUID:9305452; PMID:1385480

A.Accession: I45945

A>Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-1205 <NIS>

A.Cross-References: GB:M99057; NID:G163421; PIDN:AAA30667.1; PID:G163422

R.Seeger, W.C.; Harrison, J.K.; Barber, C.M.; Zeng, D.; Durieux, M.B.; D'Angelo, D.D.; Ly

J. Biol. Chem. 267, 15274-15276, 1992

A>Title: Molecular cloning and expression of a cDNA encoding endothelial cell nitric oxi

A.Reference number: A42841; MUID:92348367; PMID:1379225

A.Accession: A42841

A>Status: nucleic acid sequence not shown

A.Molecule type: mRNA

A.Residues: 1-51; 'N', 53-99; 'R', 101-147; 'M', 149-164; 'I', 166-317; 'GA', 320; 'HTGVVRGP', 329-3

'K', 517-692; 'G', 694-740; 'A', 742-753; 'N', 755-799; 'N', 801-803; 'SA', 806-856; 'V', 858-906; 'LV

A.Experimental source: aortic endothelial cells

A>Note: sequence extracted from NCBI backbone (NCBIP:109564); contains a number of typog

A.Accession: I45946

A>Status: nucleic acid sequence not shown

A.Molecule type: mRNA

A.Residues: 1-99; 'R', 101-164; 'I', 166-317; 'GA', 320; 'HTGVVRGP', 329-454; 'Y', 456-458; 'P', 460

A.Cross-References: GB:M95674; NID:G163426; PIDN:AAA30669.1; PID:G163427

A.Experimental source: aortic endothelial cells

A>Note: submitted to GenBank, August 1992

A>Note: GenBank entry BOVNO5, release 103.0, has a typographical error in the reference

C.Function:

A.Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH

C.Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct

C.Keywords: blocked amino end; calmodulin binding; chromoprotein; FAD; flavoprotein; FMN

F:493-512/Region: calmodulin binding #status predicted

F:522-1161/Domain: NADPH-ferrihemoprotein reductase homology <PEH>

F:524-705/Domain: flavodoxin homology <FLX>

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:3/Modified site: aspartic acid (Asn) #status predicted

F:186/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 87.5%; Score 35; DB 1; Length 1205;

Best Local Similarity 66.7%; Pred. No. 5.2e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6

DB 445 ADMAMI 450

Search completed: February 18, 2004, 14:38:36  
Job time : 7.5921 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds  
(without alignments)  
75.239 Million cell updates/sec

Title: US-09-643-260-4

Perfect score: 40

Sequence: 1 ADMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	10	US-09-847-940B-4
2	40	100.0	6	11	US-09-847-946A-4
3	40	100.0	6	11	US-09-847-946A-39
4	40	100.0	6	11	US-09-847-946A-51
5	40	100.0	7	11	US-09-847-946A-55
6	40	100.0	7	11	US-09-847-946A-48
7	40	100.0	8	11	US-09-847-946A-47
8	40	100.0	9	11	US-09-847-946A-50
9	40	100.0	9	11	US-09-847-946A-53
10	40	100.0	10	11	US-09-847-946A-54
11	40	100.0	10	11	US-09-847-946A-49
12	40	100.0	10	11	US-09-847-946A-52
13	40	100.0	11	11	US-09-847-946A-46
14	40	100.0	11	11	US-10-171-311-234
15	40	100.0	501	15	Sequence 234, App

16	38	95.0	312	12	US-10-306-762-23	Sequence 23, App1
17	38	95.0	605	15	US-10-156-761-9070	Sequence 9070, App
18	36	90.0	6	10	US-09-847-940B-2	Sequence 2, App11
19	36	90.0	6	11	US-09-847-946A-2	Sequence 2, App11
20	36	90.0	6	11	US-09-847-946A-33	Sequence 33, App1
21	36	90.0	6	11	US-09-847-946A-41	Sequence 41, App1
22	36	90.0	6	11	US-09-847-946A-73	Sequence 73, App1
23	36	90.0	7	11	US-09-847-946A-37	Sequence 37, App1
24	36	90.0	7	11	US-09-847-946A-77	Sequence 77, App1
25	36	90.0	8	11	US-09-847-946A-30	Sequence 30, App1
26	36	90.0	8	11	US-09-847-946A-38	Sequence 38, App1
27	36	90.0	8	11	US-09-847-946A-70	Sequence 70, App1
28	36	90.0	8	11	US-09-847-946A-78	Sequence 78, App1
29	36	90.0	9	11	US-09-847-946A-29	Sequence 29, App1
30	36	90.0	9	11	US-09-847-946A-32	Sequence 32, App1
31	36	90.0	9	11	US-09-847-946A-35	Sequence 35, App1
32	36	90.0	9	11	US-09-847-946A-36	Sequence 36, App1
33	36	90.0	9	11	US-09-847-946A-69	Sequence 69, App1
34	36	90.0	9	11	US-09-847-946A-72	Sequence 72, App1
35	36	90.0	9	11	US-09-847-946A-75	Sequence 75, App1
36	36	90.0	9	11	US-09-847-946A-76	Sequence 76, App1
37	36	90.0	10	11	US-09-847-946A-31	Sequence 31, App1
38	36	90.0	10	11	US-09-847-946A-34	Sequence 34, App1
39	36	90.0	10	11	US-09-847-946A-71	Sequence 71, App1
40	36	90.0	10	11	US-09-847-946A-74	Sequence 74, App1
41	36	90.0	11	11	US-09-847-946A-28	Sequence 28, App1
42	36	90.0	11	11	US-09-847-946A-68	Sequence 68, App1
43	36	90.0	11	11	US-09-847-946A-132	Sequence 132, App
44	36	90.0	11	11	US-09-847-946A-140	Sequence 140, App
45	36	90.0	13	11	US-09-847-946A-143	Sequence 143, App

## ALIGNMENTS

```
RESULT 1
US-09-847-940B-4
; Sequence 4, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
US-09-847-940B-4

Query Match      100.0%; Score 40; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADMSWL 6
        |||||
DB       1 ADMSWL 6

RESULT 2
US-09-847-946A-4
; Sequence 4, Application US/09847946A
; Publication No. US20030054959A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
```

```

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-4
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Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 ADMSWL 6
        |||||
Db      1 ADMSWL 6
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RESULT 3
US-09-847-946A-39
; Sequence 39, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-39
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Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 ADMSWL 6
        |||||
Db      1 ADMSWL 6
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RESULT 4
US-09-847-946A-51
; Sequence 51, Application US/09847946A
; Publication No. US20030054999A1
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; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-51
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Query Match          100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 ADMSWL 6
        |||||
Db      1 ADMSWL 6
```

```

RESULT 5
US-09-847-946A-55
; Sequence 55, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-55
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Query Match          100.0%; Score 40; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 ADMSWL 6
        |||||
Db      1 ADMSWL 6
```

```

RESULT 6
```

US-09-847-946A-48  
; Sequence 48, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Firdels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 48  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-48  
Query Match 100.0%; Score 40; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWL 6  
Db 3 ADMSWL 8

RESULT 7  
US-09-847-946A-56  
; Sequence 56, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Firdels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 56  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-56  
Query Match 100.0%; Score 40; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWL 6  
Db 1 ADMSWL 6

RESULT 8  
US-09-847-946A-47  
; Sequence 47, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Firdels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 47  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-47  
Query Match 100.0%; Score 40; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWL 6  
Db 1 ADMSWL 6

RESULT 9  
US-09-847-946A-50  
; Sequence 50, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Firdels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 50  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-50  
Query Match 100.0%; Score 40; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 ADMSWL 6

## RESULT 10

US-09-847-946A-53  
Sequence 53, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Pindels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 53  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: MEMO binding  
US-09-847-946A-53

Query Match 100.0%; Score 40; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 3 ADMSWL 8

## RESULT 11

US-09-847-946A-54  
Sequence 54, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Pindels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 54  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: MEMO binding  
US-09-847-946A-54

Query Match 100.0%; Score 40; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 ADMSWL 7

## RESULT 12

US-09-847-946A-49  
Sequence 49, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Pindels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 49  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: MEMO binding  
US-09-847-946A-49

Query Match 100.0%; Score 40; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 ADMSWL 7

## RESULT 13

US-09-847-946A-52  
Sequence 52, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Pindels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 52  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: MEMO binding  
US-09-847-946A-52

US-09-847-946A-52

Query Match 100.0%; Score 40; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6  
|||  
Db 3 ADMSWL 8

RESULT 14

US-09-847-946A-46  
; Sequence 46, Application US/09847946A  
; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar

; APPLICANT: Findeis, Mark A

; APPLICANT: Phillips, Kathryn

; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PFI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 46

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

; OTHER INFORMATION: sequence

US-09-847-946A-46

Query Match 100.0%; Score 40; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 17;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6  
|||  
Db 3 ADMSWL 8

RESULT 15

US-10-171-311-234

; Sequence 234, Application US/10171311

; Publication No. US20030087270A1

; GENERAL INFORMATION:

; APPLICANT: Schlegel, Robert

; APPLICANT: Chen, Yan

; APPLICANT: Zhao, Xumei

; APPLICANT: Monahan, John

; APPLICANT: Kamackar, Shubhangt

; APPLICANT: Glatt, Karen

; APPLICANT: Gammavathu, Manjula

; APPLICANT: Hoerish, Sebastian

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY

; TITLE OF INVENTION: OF CERVICAL CANCER

; FILE REFERENCE: MRI-035

; CURRENT APPLICATION NUMBER: US/10/171,311

; CURRENT FILING DATE: 2002-06-12

; PRIOR APPLICATION NUMBER: US 60/298,159

; PRIOR FILING DATE: 2001-06-13

; PRIOR APPLICATION NUMBER: US 60/298,155

; PRIOR FILING DATE: 2001-06-13

; PRIOR APPLICATION NUMBER: US 60/335,936

; PRIOR FILING DATE: 2001-11-14

; NUMBER OF SEQ ID NOS: 238

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 234

; LENGTH: 501

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-171-311-234

Query Match 100.0%; Score 40; DB 15; Length 501;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWL 6  
|||  
Db 387 ADMSWL 392

Search completed: February 18, 2004, 15:41:55  
Job time : 16.7529 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds  
(without alignments)  
35.929 Million cell updates/sec

Title: US-09-643-260-4

Perfect score: 40

Sequence: 1 ADMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA:\*

1: /cgn2\_6/prodata/1/aa/5A.COMB.pep.\*

2: /cgn2\_6/prodata/1/aa/5B.COMB.pep.\*

3: /cgn2\_6/prodata/1/aa/6A.COMB.pep.\*

4: /cgn2\_6/prodata/1/aa/6B.COMB.pep.\*

5: /cgn2\_6/prodata/1/aa/6C.COMB.pep.\*

6: /cgn2\_6/prodata/1/aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	90.0	142	4 US-09-252-991A-31533	Sequence 31533, A
2	36	90.0	174	4 US-09-325-932A-163	Sequence 163, App
3	36	90.0	225	4 US-09-325-932A-162	Sequence 162, App
4	36	90.0	378	4 US-09-325-932A-158	Sequence 158, App
5	36	90.0	616	2 US-09-135-574A-47	Sequence 47, Appl
6	36	90.0	745	2 US-08-887-518-3	Sequence 3, Appl1
7	36	90.0	745	2 US-09-023-321-3	Sequence 3, Appl1
8	36	90.0	745	2 US-08-890-853-4	Sequence 4, Appl1
9	36	90.0	745	2 US-09-032-475-3	Sequence 3, Appl1
10	36	90.0	745	2 US-09-099-125A-4	Sequence 4, Appl1
11	36	90.0	745	2 US-09-032-476-4	Sequence 4, Appl1
12	36	90.0	745	3 US-08-890-854-4	Sequence 4, Appl1
13	36	90.0	745	3 US-09-023-324-4	Sequence 4, Appl1
14	36	90.0	745	3 US-09-168-629-2	Sequence 10, Appl1
15	36	90.0	745	3 US-08-910-820-10	Sequence 10, Appl1
16	36	90.0	745	3 US-08-810-131A-2	Sequence 4, Appl1
17	36	90.0	745	4 US-09-103-986-4	Sequence 10, Appl1
18	36	90.0	745	4 US-09-844-908-10	Sequence 3, Appl1
19	36	90.0	745	4 US-09-868-758-3	Sequence 4, Appl1
20	36	90.0	756	2 US-08-887-518-4	Sequence 4, Appl1
21	36	90.0	756	2 US-09-023-321-4	Sequence 4, Appl1
22	36	90.0	756	2 US-08-890-853-2	Sequence 4, Appl1
23	36	90.0	756	2 US-09-032-475-4	Sequence 2, Appl1
24	36	90.0	756	2 US-09-099-125A-2	Sequence 2, Appl1
25	36	90.0	756	2 US-09-032-476-2	Sequence 2, Appl1
26	36	90.0	756	3 US-09-032-476-2	Sequence 2, Appl1
27	36	90.0	756	3 US-09-032-476-2	Sequence 2, Appl1

28	36	90.0	756	3 US-08-890-854-2	Sequence 2, Appl1
29	36	90.0	756	3 US-09-023-324-2	Sequence 2, Appl1
30	36	90.0	756	3 US-09-168-629-15	Sequence 15, Appl1
31	36	90.0	756	4 US-08-910-820-9	Sequence 9, Appl1
32	36	90.0	756	4 US-09-109-986-2	Sequence 2, Appl1
33	36	90.0	756	4 US-09-844-908-9	Sequence 9, Appl1
34	36	90.0	756	4 US-09-868-758-4	Sequence 4, Appl1
35	36	90.0	997	4 US-09-417-197-123	Sequence 123, App
36	36	90.0	1426	3 US-09-417-197-121	Sequence 121, App
37	36	90.0	1751	3 US-09-136-574A-43	Sequence 43, Appl
38	36	90.0	1751	3 US-09-136-574A-44	Sequence 44, Appl
39	35	87.5	1205	1 US-07-908-245-2	Sequence 2, Appl1
40	35	87.5	1205	2 US-08-319-866-10	Sequence 10, Appl
41	35	87.5	1205	3 US-08-123-708-6	Sequence 6, Appl1
42	35	87.5	1205	3 US-09-133-624-6	Sequence 6, Appl1
43	34	85.0	170	4 US-09-199-637A-339	Sequence 339, App
44	34	85.0	518	4 US-09-065-383-27	Sequence 27, Appl
45	34	85.0	537	4 US-09-655-270A-11	Sequence 11, Appl

#### ALIGNMENTS

RESULT 1  
US-09-252-991A-31533  
; Sequence 31533, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 31533  
; LENGTH: 142  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-31533  
Query Match 90.0%; Score 36; DB 4; Length 142;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ADMSW 5  
DB 94 ADMSW 98  
RESULT 2  
US-09-325-932A-163  
; Sequence 163, Application US/09325932A  
; Patent No. 6451604  
; GENERAL INFORMATION:  
; APPLICANT: Flamm, Barry  
; APPLICANT: Lasham, Annette  
; TITLE OF INVENTION: Compositions affecting programmed cell  
; TITLE OF INVENTION: death and their use in the modification of forestry plant devel  
; FILE REFERENCE: 1022  
; CURRENT APPLICATION NUMBER: US/09/325,932A  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 206  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 163  
; LENGTH: 174  
; TYPE: PRT  
; ORGANISM: Eucalyptus grandis  
US-09-325-932A-163



Query Match 90.0%; Score 36; DB 4; Length 174;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
| | | | |  
Db 109 ADMSW 113

RESULT 3  
US-09-325-932A-162

Sequence 162, Application US/09325932A

Patent No. 6451604

GENERAL INFORMATION:

APPLICANT: Flinn, Barry

APPLICANT: Lasham, Annette

TITLE OF INVENTION: Compositions affecting programmed cell

TITLE OF INVENTION: death and their use in the modification of forestry plant develop

FILE REFERENCE: 1022

CURRENT APPLICATION NUMBER: US/09/325,932A

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 206

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 162

LENGTH: 225

TYPE: PRT

ORGANISM: Eucalyptus grandis

US-09-325-932A-162

QY 1 ADMSW 5  
| | | | |  
Db 100 ADMSW 104

RESULT 4  
US-09-325-932A-158

Sequence 158, Application US/09325932A

Patent No. 6451604

GENERAL INFORMATION:

APPLICANT: Flinn, Barry

APPLICANT: Lasham, Annette

TITLE OF INVENTION: Compositions affecting programmed cell

TITLE OF INVENTION: death and their use in the modification of forestry plant develop

FILE REFERENCE: 1022

CURRENT APPLICATION NUMBER: US/09/325,932A

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 206

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 158

LENGTH: 378

TYPE: PRT

ORGANISM: Eucalyptus grandis

US-09-325-932A-158

QY 1 ADMSW 5  
| | | | |  
Db 128 ADMSW 132

RESULT 5  
US-09-136-574A-47

Sequence 47, Application US/09136574A

Patent No. 6294366

GENERAL INFORMATION:

APPLICANT: Farrington, Graham K.

Anderson, Paige

Gibbs, Moreland

Bergquist, Peter

Daniels, Roy

Morgan, Hugh W.

Williams, Diane P.

TITLE OF INVENTION: Compositions and Methods for

treating Cellulose Containing Fabrics Using Truncated

Cellulase Enzyme Compositions

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Center, P.O. Box 457

CITY: Spring House

STATE: PA

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/136,574A

FILING DATE: 19-Aug-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/932,571

FILING DATE: September 19, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: 1997US001/CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9200

TELEFAX: 215-540-5818

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 616 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-09-136-574A-47

QY 2 DMSWL 6  
| | | | |  
Db 123 DMSWL 127

RESULT 6  
US-08-887-518-3

Sequence 3, Application US/08887518

Patent No. 5843721

GENERAL INFORMATION:

APPLICANT: Roche, Mlke

APPLICANT: Ml, lln

TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-887-518-3

Query Match 90.0%; Score 36; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWL 6  
|||||  
Db 739 DMSWL 743

RESULT 7  
US-09-023-321-3  
Sequence 3, Application US/09023321  
Patent No. 5844073  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,321  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-321-3

Query Match 90.0%; Score 36; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWL 6  
|||||  
Db 739 DMSWL 743

RESULT 8  
US-08-890-853-4  
Sequence 4, Application US/08890853  
Patent No. 5851812  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
TITLE OF INVENTION: IKK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-853-4

Query Match 90.0%; Score 36; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWL 6  
|||||  
Db 739 DMSWL 743

RESULT 9  
US-09-023-475-3  
Sequence 3, Application US/090232475  
Patent No. 5854003  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032.475  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/887,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-032-475-3

Query Match 90.0%; Score 36; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6  
| | | | |  
DB 739 DMSWL 743

RESULT 10  
US-09-099-125A-4  
Sequence 4, Application US/09099125A  
Patent No. 5916760  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099.125A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890.853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-099-125A-4

Query Match 90.0%; Score 36; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6  
| | | | |  
DB 739 DMSWL 743

RESULT 11  
US-09-099-124A-4  
Sequence 4, Application US/09099124A  
Patent No. 5939302  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099.124A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890.853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-099-124A-4

Query Match 90.0%; Score 36; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6  
| | | | |

DB 739 DMSWL 743

```
RESULT 12
US-09-032-476-4
; Sequence 4, Application US/09032476
; Patent No. 6235492
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; APPLICANT: Cao, Zhaoan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK-1 Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,476
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-09-032-476-4
Query Match 90.0%; Score 36; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
DB 739 DMSWL 743

RESULT 13
US-08-890-854-4
; Sequence 4, Application US/08890854
; Patent No. 6235512
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; APPLICANT: Cao, Zhaoan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK-1 Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
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ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,854
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-890-854-4
Query Match 90.0%; Score 36; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6
DB 739 DMSWL 743

RESULT 14
US-09-023-324-4
; Sequence 4, Application US/09023324
; Patent No. 6235513
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; APPLICANT: Cao, Zhaoan
; APPLICANT: R gnier, Catherine
; TITLE OF INVENTION: IKK-1 Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,324
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4341
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
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LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-324-4

Query Match 90.0%; Score 36; DB 3; Length 745;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6  
DB 739 DMSWL 743

RESULT 15  
US-09-168-629-2  
Sequence 2, Application US/09168629  
Patent No. 6242253  
GENERAL INFORMATION:  
APPLICANT: Karin, Michael  
APPLICANT: Didonato, Joseph A.  
APPLICANT: Rothwarf, David M.  
APPLICANT: Hayakawa, Makio  
APPLICANT: Zandi, Ibrahim  
TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same  
FILE REFERENCE: P-UD 3295  
CURRENT APPLICATION NUMBER: US/09/168,629  
CURRENT FILING DATE: 1998-10-08  
EARLIER APPLICATION NUMBER: 60/061,470  
EARLIER FILING DATE: 1997-10-09  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 745  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-168-629-2

Query Match 90.0%; Score 36; DB 3; Length 745;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6  
DB 739 DMSWL 743

Search completed: February 18, 2004, 14:41:46  
Job time : 8.06579 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39 ; Search time 3.55263 Seconds  
(without alignments)  
79.423 Million cell updates/sec

Title: US-09-643-260-3

Perfect score: 26

Sequence: 1 LDASAL 6

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	214	1 RADC_RHOCA	P12255 rhodocacther
2	26	100.0	259	1 ECX2_ARCFU	O29756 archaeoglob
3	26	100.0	550	1 SYR_MYCTU	Q10609 mycobacteri
4	26	100.0	638	1 SCAD_HUMAN	P51172 homo sapien
5	26	100.0	638	1 SCAD_PANTH	O46547 pan troglod
6	26	100.0	745	1 METE_COORU	O48733 corynebacte
7	26	100.0	855	1 GARP_SCHPO	Q10280 schizosacch
8	26	100.0	858	1 SYL_VIRCH	Q93766 vibrio chol
9	26	100.0	1006	1 MT10_SCHPO	O09878 schizosacch
10	26	100.0	1313	1 ACE_FAT	P47820 rattus norv
11	24	92.3	197	1 YET4_METUA	O58869 methanococc
12	24	92.3	298	1 CDK2_HUMAN	P24941 homo sapien
13	24	92.3	298	1 CDK2_HUMAN	O63698 rattus norv
14	24	92.3	346	1 CDK2_MOUSE	P27377 mus musculu
15	24	92.3	358	1 ALF_ECOLI	P11604 eschecherich
16	24	92.3	386	1 ALR_ANNAP	Q6YU96 anabaena sp
17	24	92.3	393	1 DCM_HORCH	Q42829 hordeum chl
18	24	92.3	404	1 ODO2_ECOLI	P07016 eschecherich
19	24	92.3	446	1 DTA2_RALSO	O82866 ralteonla b
20	24	92.3	505	1 HUTN_SALTY	O82866 ralteonla b
21	24	92.3	506	1 HUTN_SALTY	O82866 ralteonla b
22	24	92.3	518	1 FLAA_AQUAE	O67803 aquifex aeo
23	24	92.3	933	1 SLAP_CAMEF	P25847 campylobact
24	24	92.3	964	1 MSH2_YEAST	P25847 campylobact
25	24	92.3	970	1 SBGA_YEAST	O92765 chlamydia p
26	24	92.3	3255	1 POLG_LMYVO	P31999 1 genome po
27	24	92.3	3255	1 POLG_LMYVO	P31999 1 genome po
28	23	88.5	145	1 MA28_DERPA	P39674 dermatophag
29	23	88.5	161	1 PHAB_STNPF	P06113 synecchococ
30	23	88.5	193	1 ACD1_XANAC	P58902 xanthomonas
31	23	88.5	201	1 CTPL_HUMAN	Q16619 homo sapien
32	23	88.5	242	1 PEPGL_PEPBU	O9679 pseudomonas
33	23	88.5	247	1 PEPGL_MYCTU	O06814 mycobacteri

34	23	88.5	249	1 CYSX_SYNY3	P27294 synecchocyt
35	23	88.5	249	1 STXA_HUMAN	O60499 homo sapien
36	23	88.5	295	1 KERS_METMA	O82863 methanobarc
37	23	88.5	351	1 PTA_FICFR	O92639 rickettsia
38	23	88.5	355	1 LEU3_SPIPL	O00412 spilitula p
39	23	88.5	366	1 REO2_XENLA	O9636 xenopus lae
40	23	88.5	372	1 MTGX_SALTY	P58524 salmoneilla
41	23	88.5	372	1 MTGX_SALTY	P58524 salmoneilla
42	23	88.5	380	1 SCHL_STRHA	O05361 streptomyc
43	23	88.5	388	1 REO1_XENLA	O9638 xenopus lae
44	23	88.5	400	1 DCM_MAIZE	O24575 zea mays (m
45	23	88.5	411	1 BHB2_MOUSE	O35185 mus musculu

## ALIGNMENTS

```

RESULT 1
ID RADC_RHOCA STANDARD; PRT; 214 AA.
AC P12255;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA repair protein radc homolog.
GN RADC.
OS Rhododactylus capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhododactylales;
OC Rhododactylaceae; Rhododactylus.
OX NCBI_TaxId=1061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33303 / B10;
RX MEDLINE=20118379; PubMed=10652786;
RA Katsiou E., Mickel C.M., Garcia A.F., Tadros M.H.;
RT "Molecular analysis and identification of the radc gene from the
RT phototrophic bacterium Rhododactylus capsulatus B10."
RL Microbiol. Res. 154:233-239 (1999).
CC -!- FUNCTION: INVOLVED IN DNA REPAIR (BY SIMILARITY).
CC -!- INDUCTION: Induced about five-fold after UV-irradiation.
CC -!- SIMILARITY: Belongs to the radc family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; U74017; AAB18255.1; -.
DR HAMAP; MF_00018; -.
DR InterPro; IPR001405; RadC.
DR Pfam; PF04002; RadC; 1.
DR ProDom; PD007415; RadC; 1.
DR TIGRFAMs; TIGR00608; radc; 1.
DR PROSITE; PS01302; RADC; 1.
KW DNA repair.
SO SEQUENCE 214 AA; 23792 MW; D008997B20C6743D CRC64;

Query Match 100.0%; Score 26; DB 1; Length 214;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 LDASAL 6
Db 154 LDASAL 159

RESULT 2
ECX2_ARCFU STANDARD; PRT; 259 AA.
ID ECX2_ARCFU
AC O29756;

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DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Probable exosome complex exonuclease 2 (EC 3.1.13.-).  
 GN AF0494.  
 OS Archaeoglobus fulgidus.  
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;  
 OC Archaeoglobaceae; Archaeoglobus.  
 ON NCBI\_TaxID=2234;  
 RX STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
 MEDLINE=98049343; PubMed=9399475;  
 RA Kleink H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
 RA Richardson D.L., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
 RA Kirschner E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,  
 RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,  
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
 RA Venter J.C.;  
 RT "The complete genome sequence of the hyperthermophilic, sulphate-  
 RT reducing archaeon Archaeoglobus fulgidus.";  
 RL Nature 390:364-370(1997).  
 CC -1- FUNCTION: Probably involved in the 3'-5' degradation of a variety  
 CC of RNA species (Potential).  
 CC -1- SUBUNIT: Component of the archaeal exosome multienzyme  
 CC ribonuclease complex (Potential).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE RNASE PH FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; AE001070; AAB90743.1; -.  
 CC DR EMBL; AE001070; AAB90743.1; -.  
 CC DR PIR; P69311; F69311.  
 CC DR TIGR; AF0494; -.  
 CC DR HAMAP; MF\_00623; -; 1.  
 CC DR InterPro; IPR001247; 3\_Exonuclease.  
 CC DR Pfam; PF01138; RNase\_PH; 1.  
 CC DR Pfam; PF03725; RNase\_PH\_C; 1.  
 CC KW Exosome; Hydrolase; Nuclease; Exonuclease; Complete proteome.  
 CC SEQUENCE 259 AA; 26646 MW; E8289D46F9DDCCB3 CRC64;  
 SO  
 QY Query Match 100.0%; Score 26; DB 1; Length 259;  
 Db Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDASAL 6  
 Db 149 LDASAL 154  
 RESULT 3  
 ID SYR MYCTU STANDARD; PRT; 550 AA.  
 AC 010609;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ARGS).  
 OS ARGES OR RV1292 OR MT1331 OR MTCY373.12.  
 GN Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.

OK NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37Rv;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Broese R., Partridge L., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eigemeier K., Gas S., Barry C.B. III, Tekle A.,  
 RA Davies R., Devlin K., Brown D., Chillingworth T., Connor R.,  
 RA Badcock K., Bauman D., Brown D., Chillingworth T., Connor R.,  
 RA Hornsby T., Jagsels K., Krogan A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skellern S., Squares S., Squares R.,  
 RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Pleischmann R.D., Allard D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Uitterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishop W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains.";  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +  
 CC di-phosphate + L-arginyl-tRNA(Arg).  
 CC -1- SUBUNIT: Monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to class-I aminoadyl-tRNA synthetase family.  
 CC -----  
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 CC or send an email to [license@isb-eb.ch](mailto:license@isb-eb.ch)).  
 CC -----  
 CC EMBL; Z73419; CA9757.1; -.  
 CC DR EMBL; Z73419; CA9757.1; -.  
 CC DR PIR; H70772; H70772.  
 CC DR TIGR; MT1331; -.  
 CC DR HAMAP; MF\_00123; -; 1.  
 CC DR InterPro; IPR001278; Arg\_tRNA-synt\_1c.  
 CC DR InterPro; IPR005148; N.  
 CC DR InterPro; IPR001412; tRNA-synt\_1.  
 CC DR Pfam; PF03485; N-Arg; 1.  
 CC DR Pfam; PF00750; tRNA-synt\_1d; 1.  
 CC DR PRINTS; PRO1038; TRNASYNTHARG.  
 CC DR TIGRfam; TIGR00456; args; 1.  
 CC DR PROSITE; PS00178; AA\_tRNA\_LIGASE\_I; 1.  
 CC KW Aminoadyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
 CC Complete proteome.  
 CC SEQUENCE 550 AA; 59709 MW; 4F11239A6238124D CRC64;  
 SO  
 QY Query Match 100.0%; Score 26; DB 1; Length 550;  
 Db Best Local Similarity 100.0%; Pred. No. 45;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDASAL 6  
 Db 23 LDASAL 28  
 RESULT 4  
 ID SCAD HUMAN STANDARD; PRT; 638 AA.  
 AC PS1172;

```

DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amino acid-sensitive sodium channel delta-subunit (Epithelial Na+
channel) delta subunit (Delta ENaC) (Nonvoltage-gated sodium channel
1 delta subunit) (SCNED) (Delta NaCh).
GN SCNN1D OR DNACH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96070858; PubMed=7499195;
RA Waldmann R., Champigny G., Bassilana F., Volley N., Lazdunski M.;
RT "Molecular cloning and functional expression of a novel amiloride-
sensitive Na+ channel.";
RL J. Biol. Chem. 270:27411-27414(1995).
CC -1- FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL.
INHIBITED BY THE DIURETIC AMILORIDE. MEDIATES THE ELECTRODIFFUSION
OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
CC ALSO PLAYS A ROLE IN TASTE PERCEPTION.
CC -1- SUBUNIT: HETEROTRIMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNEL
FAMILY.
CC -----
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CC -----
DR EMBL: U38254; AAC50283.1; -
DR PIR: I39196; I39196.
DR GenBank: HGNC:10601; SCNN1D.
DR MIM: 601328; -
DR GO: GO:0015280; F:amiloride-sensitive sodium channel activity; TAS.
DR GO: GO:0006814; P:sodium ion transport; TAS.
DR InterPro: IPR004724; Enac.
DR InterPro: IPR001873; Na-channel_Asc.
DR Pfam: PF00858; Asc. 1.
DR TIGRfam: TIGR00859; Enac. 1.
DR PROSITE: PS01206; Asc. 1.
KW Ionic channel; Transmembrane; Ion transport; Glycoprotein.
FT DOMAIN 1 86
FT TRANSMEM 87 107
FT DOMAIN 108 530
FT TRANSMEM 531 551
FT DOMAIN 552 638
FT CARBOHYD 166 166
FT CARBOHYD 211 211
FT CARBOHYD 384 384
SQ SEQUENCE 638 AA; 70274 MW; 7CD5181F8497F5C6 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 638;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amino acid-sensitive sodium channel delta-subunit (Epithelial Na+
channel) delta subunit (Delta ENaC) (Nonvoltage-gated sodium channel
1 delta subunit) (SCNED) (Delta NaCh).
GN SCNN1D OR DNACH.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX Tissue-Testis;
RA Al-Khaili O.K., Eaton D.C.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ database.
CC -1- FUNCTION: SODIUM PERMEABLE NON-VOLTAGE-SENSITIVE ION CHANNEL.
INHIBITED BY THE DIURETIC AMILORIDE. MEDIATES THE ELECTRODIFFUSION
OF THE LUMINAL SODIUM (AND WATER, WHICH FOLLOWS OSMOTICALLY)
THROUGH THE APICAL MEMBRANE OF EPITHELIAL CELLS. CONTROLS THE
REABSORPTION OF SODIUM IN KIDNEY, COLON, LUNG AND SWEAT GLANDS.
CC ALSO PLAYS A ROLE IN TASTE PERCEPTION (By similarity).
CC -1- SUBUNIT: HETEROTRIMER OF TWO ALPHA, ONE BETA AND ONE GAMMA
SUBUNIT. A DELTA SUBUNIT CAN REPLACE THE ALPHA SUBUNIT (By
similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNEL
FAMILY.
CC -----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF08165; AAB92659.1; -
DR InterPro: IPR004724; Enac.
DR InterPro: IPR001873; Na-channel_Asc.
DR Pfam: PF00858; Asc. 1.
DR PRINTS: PRO1078; AMINACHANNEL.
DR TIGRfam: TIGR00859; Enac. 1.
DR PROSITE: PS01206; Asc. 1.
KW Ionic channel; Transmembrane; Ion transport; Glycoprotein.
FT TRANSMEM 87 107
FT DOMAIN 108 530
FT TRANSMEM 531 551
FT DOMAIN 552 638
FT CARBOHYD 166 166
FT CARBOHYD 211 211
FT CARBOHYD 384 384
SQ SEQUENCE 638 AA; 70187 MW; 321B9597D6A78D38 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 638;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LDASAL 6
DB 551 LDASAL 556
RESULT 5
SCAD PANTR STANDARD; PRT; 638 AA.
AC 046547;

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QY 1 LDASAL 6
DB 551 LDASAL 556
RESULT 6
MTE CORGL
ID MTE CORGL STANDARD; PRT; 745 AA.
AC 08NRB3;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 5-methyltetrahydropteroyltylglytamic acid--homocysteine methyltransferase
(EC 2.1.1.14) (methionine synthase, vitamin-B12 independent isozyme)

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DE (Cobalamin-independent methionine synthase).
GN METE OR CG1139.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Catalyzes the transfer of a methyl group from 5-
CC methylethiohydrofolate to homocysteine resulting in methionine
CC formation (By similarity).
CC -1- CATALYTIC ACTIVITY: 5-methyltetrahydrofolate-L-glutamate + L-
CC homocysteine = tetrahydrofolate-L-glutamate + L-methionine.
CC -1- COFACTOR: Zinc; binds one ion per subunit (By similarity).
CC -1- PATHWAY: Terminal step in the de novo biosynthesis of methionine.
CC -1- SIMILARITY: Belongs to the vitamin-B12 independent methionine
CC synthase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB005277; BAB9632.1; -.
DR HAMAP; MF_00172; -.
DR InterPro; IPR002629; Methionine_synth.
DR InterPro; IPR006276; Met_synth_B12ind.
DR Pfam; PF01717; Methionine_synth; 1.
DR ProDom; PD004692; Methionine_synth; 2.
DR TIGRfam; TIGR01371; met_synth_B12ind; 1.
DR Transfaser; Methyltransferase; Methionine biosynthesis; Zinc; Repeat;
KW Complete proteome.
FT METAL 628 628 ZINC (BY SIMILARITY).
FT METAL 630 630 ZINC (BY SIMILARITY).
FT METAL 713 713 ZINC (BY SIMILARITY).
FT METAL 713 713 ZINC (BY SIMILARITY).
SQ SEQUENCE 745 AA; 81312 MW; 856E05DE7398BDF CRC64;

Query Match 100.0%; Score 26; DB 1; Length 745;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LDASAL 6
Db 140 LDASAL 145

RESULT 7
GAP1_SCHPO STANDARD; PRT; 855 AA.
ID GAP1_SCHPO Q10280; Q94482; Q9USK9;
AC Q10280; Q94482; Q9USK9;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transcription factor gap1 (Gaf1).
DE GAP1 OR SPEC1902.01 OR SPEC417.01C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9712;
RA MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

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RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hildalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsle K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., Mclean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Ocell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbittowitch B.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymmez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Meller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Mosel D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,
RA Beyer P., Zimmermann W., Wedler H., Wambut R., Purcell B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forebury S.L.,
RA Saprakovski G.V., Uesery D., Barrall B.G., Nurse P.,
RA "The genome sequence of Schizosaccharomyces pombe."
RA Nature 415:871-880(2002).
RN [2]
RP SEQUENCE OF 566-855 FROM N.A.
RX MEDLINE=98382525; PubMed=9714831;
RA Hoe K.-L., Yoon H.-S., Chung K.-S., Park S.-K., Kim D.-U., Jang Y.-J.,
RA Yoo O.-J., Yoo H.-S.;
RT "Molecular cloning of gaf1, a Schizosaccharomyces pombe GATA factor,
RT which can function as a transcriptional activator."
RL Gene 215:319-328(1998).
CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: Contains 1 GATA-type zinc finger.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AL035076; CA22647.1; -.
DR EMBL; AL049521; CAB40003.1; -.
DR EMBL; L31601; AAC35593.1; -.
DR PIR; T41336; T41336.
DR HSP; P17429; 4GAT.
DR TRANSFAC; T02831; -.
DR Genedb_Spomb; SPEC1902.01; -.
DR InterPro; IPR000679; Znf_GATA.
DR Pfam; PF00320; GATA; 1.
DR PRINTS; PR00619; GATAZNFINGER.
DR SMART; SM00401; ZNF_GATA; 1.
DR PROSITE; PS00344; GATA_ZNF_FINGER_1; 1.
DR PROSITE; PS50114; GATA_ZNF_FINGER_2; 1.
KW Transcription regulation; Activator; DNA-binding; Zinc-finger;
KW Nuclear protein.
FT ZN FING 635 659 GATA-TYPE.
SQ SEQUENCE 855 AA; 91776 MW; 3D932F83D2DE6774 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 855;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LDASAL 6
Db 211 LDASAL 216

RESULT 8
SYL_VIBCH

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ID  SVL_VIBCH  STANDARD;  PRT;  858  AA.
AC  Q9KTE6;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA Ligase) (Leurs).
GN  LEUS OR VCO956.
OS  Vibrio cholerae.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
CC  Vibrionaceae; Vibrrio.
OX  NCBI_TaxID=666;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=El Tor N16961 / Serotype O1;
RX  MEDLINE=20406833; PubMed=10953301;
RA  Haidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA  Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Uniyam L.A.,
RA  Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA  Esmolaeva M.D., Vamathevan J., Bass S., Qin H., Digdal I., Sellers P.,
RA  McDonald L., Ueberback T., Fleischmann R.D., Niernan W.C., White O.,
RA  Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA  Fraser C.M.;
RT  "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT  cholerae.";
RL  Nature 406:477-483(2000).
CC  -1- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
CC  diphosphate + L-leucyl-tRNA(Leu).
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  EMBL; AE004177; AAP9418.1; ALT_INIT.
DR  TIGR; VCO956; -.
DR  HAMAP; MF_00049; -.
DR  InterPro; IPR002302; Leu-tRNA synthetase.
DR  InterPro; IPR002300; tRNA-synt 1a.
DR  InterPro; IPR001412; tRNA-synt 1.
DR  Pfam; PF00133; tRNA-synt 1; 1.
DR  PRINTS; PRO0096; TRANSYTHLEU.
DR  TIGRfam; TIGR00396; Leus_Dact; 1.
DR  PROSITE; PS00178; AA_tRNA_Ligase_1; 1.
KW  Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW  Complete proteome.
FT  SITE 42 52 "HIGH" REGION.
FT  SITE 618 622 "KMSKS" REGION.
FT  BINDING 621 621 ATP (BY SIMILARITY).
SQ  SEQUENCE 858 AA; 96621 MW; AAD59A2E1CF192 CRC64;
Query Match 100.0%; Score 26; DB 1; Length 858;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GN  SPCC584.01C.
OS  Schizosaccharomyces pombe (fission yeast).
OC  Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
CC  Schizosaccharomycetaceae; Schizosaccharomycetaceae;
OX  NCBI_TaxID=4896;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=972;
RX  MEDLINE=21848401; PubMed=11859360;
RA  Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA  Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA  Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA  Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
RA  Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA  Holtroyd S., Hornsbey T., Howarth S., Huckle S.J., Hunt S., Jagsels K.,
RA  James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA  Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA  Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA  Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA  Skelton J., Simmonds M., Squares R., Stevens K.,
RA  Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA  Woodward J., Wolchert G., Aert R., Robben J., Grynolprez B.,
RA  Weltyens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA  Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA  Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA  Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA  Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motter S.,
RA  Gilbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA  Lucase M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
RA  Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA  Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA  Cerutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
RA  Siparovsky G.V., Useery D., Barrell B.G., Nurse P.;
RT  "The genome sequence of Schizosaccharomyces pombe.";
RL  Nature 415:871-880(2002).
CC  -1- FUNCTION: THIS ENZYME CATALYZES THE 6-ELECTRON REDUCTION OF
CC  SULFITE TO SULFIDE. THIS IS ONE OF SEVERAL ACTIVITIES REQUIRED
CC  FOR THE BIOSYNTHESIS OF L-CYSTEINE FROM SULFATE (BY SIMILARITY).
CC  -1- CATALYTIC ACTIVITY: H(2)S + 3 NADP(+) + 3 H(2)O = sulfite + 3
CC  NADPH.
CC  -1- COFACTOR: THIS SUBUNIT IS A FLAVOPROTEIN THAT BINDS ONE FMN AND
CC  ONE FAD PER CHAIN (BY SIMILARITY).
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CC  or send an email to license@isb-sib.ch).
CC  EMBL; AL032824; CAA21818.2; -.
DR  PIR; T41439; T41439.
DR  HSP; P00386; IAMD.
DR  GeneDB; Spombe; SPCC584.01C; -.
DR  InterPro; IPR003097; FAD binding.
DR  InterPro; IPR001709; FMN_cyc_redctase.
DR  InterPro; IPR001433; Oxred FAD/NAD(P).
DR  Pfam; PF00667; FAD binding_1; 1.
DR  Pfam; PF00175; NAD binding_1; 1.
DR  PRINTS; PRO0371; FMNR.
KW  Oxidoreductase; Flavoprotein; NADP; FAD; FMN; Electron transport;
KW  Cysteine biosynthesis.
FT  NP_BIND 658 669 FAD (ADP PART) (BY SIMILARITY).
FT  NP_BIND 788 798 FAD (FLAVIN PART) (BY SIMILARITY).
SQ  SEQUENCE 1006 AA; 111352 MW; 2EA2086D6561D33 CRC64;
Query Match 100.0%; Score 26; DB 1; Length 1006;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      554 LDASAL 559

RESULT 10
ACE_RAT STANDARD; PRT; 1313 AA.
ID ACE_RAT
AC P47820;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)
DE (ACE) (dipeptidyl carboxypeptidase I) (kininase II).
GN ACE OR DCP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=94121658; PubMed=8292044;
RA Koike G., Krieger J.E., Jacob H.J., Mukoyama M., Pratt R.E.,
RA Dzuu V.J.;
RT "Angiotensin converting enzyme and genetic hypertension: cloning of
RT rat cDNAs and characterization of the enzyme."
RT Biochem. Biophys. Res. Commun. 198;380-386 (1994).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=Lewis/N; TISSUE=Lung;
RA Jafarian-Tehrani M., Liswak S., Barrientos R.M., Michaud A.,
RA Corvol P., Sternberg E.M.;
RT "Characterization of a missense mutation in the angiotensin
RT I-converting enzyme cDNA in exudate inflammation resistant F344/N
RT rats."
RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF
CC THE TERMINAL HIS-LEU. THIS RESULTS IN AN INCREASE OF THE
CC VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.
CC -1- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,
CC oligopeptide-I-Xaa-Xbb, when Xaa is not Pro, and Xbb is neither
CC Asp nor Glu. Converts angiotensin I to angiotensin II.
CC -1- COFACTOR: Binds 2 zinc ions (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Name=Somatic;
CC IsoId=P47820-1; Sequence=Displayed;
CC Name=Testis-specific;
CC IsoId=P47820-2; Sequence=Not described;
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
CC -----
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CC or send an email to license@1sb-sib.ch).
CC -----
DR EMBL: U03708; AAA82110.1; -
DR EMBL: U03734; AAA82111.1; -
DR EMBL: AF201332; AAG35597.1; -
DR PIR: JC2038; JC2038.
DR MEROPS: M02.001; -
DR MEROPS: M02.004; -
DR InterPro: IPR001548; Peptidase_M2.
DR InterPro: IPR006025; Zn_MPeptidase.
DR Pfam: PF01401; Peptidase_M2; 2.
DR PRINTS: PR00791; PEPDIP7ASEA.
DR ProDom: PD004184; Peptidase_M2; 2.
DR PROSITE: PS00142; ZINC_PROTEASE; 2.
KW Hydroxylase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;

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KW Glycoprotein; Transmembrane; Repeat; Signal; Alternative splicing.
FT SIGNAL 1 35
FT CHAIN 36 1313
FT FT
FT DOMAIN 36 1265
FT TRANSMEM 1266 1282
FT DOMAIN 1283 1313
FT REPEAT 233 589
FT REPEAT 831 1187
FT METAL 396 396
FT ACT SITE 397 397
FT METAL 400 400
FT METAL 994 994
FT ACT SITE 995 995
FT METAL 998 998
FT CARBOHYD 44 44
FT CARBOHYD 60 60
FT CARBOHYD 80 80
FT CARBOHYD 117 117
FT CARBOHYD 152 152
FT CARBOHYD 166 166
FT CARBOHYD 324 324
FT CARBOHYD 515 515
FT CARBOHYD 683 683
FT CARBOHYD 701 701
FT CARBOHYD 720 720
FT CARBOHYD 766 766
FT CARBOHYD 948 948
FT CARBOHYD 1197 1197
FT VARIANT 207 207
SQ SEQUENCE 1313 AA; 150907 MW; 8CB5D0015F129591 CRC64;

Query Match
Best Local Similarity 100.0%; Score 26; DB 1; Length 1313;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
DB 600 LDASAL 605

RESULT 11
YER4_METUA STANDARD; PRT; 197 AA.
ID YER4_METUA
AC Q58869;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein MJ1474.
GN MJ1474.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-P., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fummann J.L., Nguyen D.,
RA Utechtack T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Huret M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Moese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RT Science 273:1058-1073 (1996).
CC -1- SIMILARITY: BELONGS TO THE UPF0129 FAMILY.
CC -----
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DR EMBL: U67588; AAB99480.1; -  
 DR PIR: A64484; A64484.  
 DR TIGR: M31474; -  
 DR HAMAP: MF\_00265; - 1.  
 DR InterPro: IPR002851; DUF133.  
 DR InterPro: IPR002716; PIN.  
 DR InterPro: IPR006596; PIN.  
 DR Pfam: PF01850; PIN: 1.  
 DR ProDom: PD013236; DUF133; 1.  
 DR SMART: SM00670; PIN: 1.  
 KW Hypothetical protein; Complete proteome.  
 FT DOMAIN 181 197 LYS-RICH.  
 SQ SEQUENCE 197 AA; 22781 MW; 70075B8626934F58 CRC64;

Query Match 92.3%; Score 24; DB 1; Length 197;  
 Best Local Similarity 83.3%; Pred. No. 51;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
 DB 36 LDASAL 41

RESULT 12  
 CDK2\_HUMAN  
 ID CDK2\_HUMAN STANDARD; PRT; 298 AA.  
 AC P24911;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 15-AUG-1992 (Rel. 23, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Cell division protein kinase 2 (EC 2.7.1.-) (p33 protein kinase).  
 GN CDK2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxId=9606;  
 OX [1]  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=91330891; PubMed=1714386;  
 RA Elledge S.U., Spottswood M.R.;  
 RT "A new human p34 protein kinase, CDK2, identified by complementation  
 RT of a cdc28 mutation in *Saccharomyces cerevisiae*, is a homolog of  
 RT Xenopus Egl.;"  
 RL EMBO J. 10:2653-2659(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=91367262; PubMed=1653904;  
 RA Teal L.H., Harlow E., Meyerson M.;  
 RT "Isolation of the human cdk2 gene that encodes the cyclin A- and  
 RT adenovirus E1A-associated p33 kinase.;"  
 RL Nature 353:174-177(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=92020980; PubMed=1717994;  
 RA Nishitani-Tsuji J., Nomoto S., Yasuda H., Reed S.I., Matsunoto K.;  
 RT "Cloning of a human cDNA encoding a CDK2-related kinase by  
 RT complementation of a budding yeast cdc28 mutation.;"  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9006-9010(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,  
 RA Miyamoto K.B., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,  
 RA Schenkowitz W.S., Sherr C.D., Wittrik L.A., Nickerson D.A.;  
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta; RL

RX MEDLINE=22388257; PubMed=12477932;  
 RA Klausner R.L., Feigold E.A., Grouse L.H., Derge J.G.,  
 RA Krausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
 RA Altshuler S.F., Zeeberg B., Bucoff K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.U., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,  
 RA Schermer A., Schein J.E., Jones S.J.W., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.;"  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]  
 RP PHOSPHORYLATION SITES.  
 RX MEDLINE=93010995; PubMed=1396589;  
 RA Gu Y., Rosenblatt J., O'Morgan D.O.;  
 RT "Cell cycle regulation of CDK2 activity by phosphorylation of Thr160  
 RT and Tyr15.;"  
 RL EMBO J. 11:3995-4005(1992).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).  
 RX MEDLINE=93288132; PubMed=8510751;  
 RA de Bondt H.L., Rosenblatt J., Jancarik J., Jones H.D.,  
 RA Morgan D.O., Kim S.-H.;  
 RT "Crystal structure of cyclin-dependent kinase 2.;"  
 RL Nature 363:595-602(1993).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF COMPLEX WITH CYCLIN A.  
 RX MEDLINE=95356811; PubMed=7630387;  
 RA Jeffrey P.D., Russo A.A., Polyak K., Gibbs E., Hurwitz J.,  
 RA Massague J., Pavletich N.P.;  
 RT "Mechanism of CDK activation revealed by the structure of a  
 RT cyclinA-CDK2 complex.;"  
 RL Nature 376:313-320(1995).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.33 ANGSTROMS) OF COMPLEX WITH L868276.  
 RX MEDLINE=96181476; PubMed=8610110;  
 RA de Azavedo W.F., Jr., Muleer-Dieckmann H.-J., Schulze-Gahmen U.,  
 RA Worland P.J., Sauvillie E., Kim S.-H.;  
 RT "Structural basis for specificity and potency of a flavonoid  
 RT inhibitor of human CDK2, a cell cycle kinase.;"  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:2735-2740(1996).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF COMPLEX WITH CG2A AND KIP1.  
 RX MEDLINE=96300318; PubMed=8684460;  
 RA Russo A.A., Jeffrey P.D., Patena A.K., Massague J., Pavletich N.P.;  
 RT "Crystal structure of the p27kip1 cyclin-dependent-kinase inhibitor  
 RT bound to the cyclin A-CDK2 complex.;"  
 RL Nature 382:325-331(1996).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH CG2A.  
 RX MEDLINE=96311326; PubMed=8756328;  
 RA Russo A.A., Jeffrey P.D., Pavletich N.P.;  
 RT "Structural basis of cyclin-dependent kinase activation by  
 RT phosphorylation.;"  
 RL Nat. Struct. Biol. 3:696-700(1996).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=97075215; PubMed=917641;  
 RA Schulze-Gahmen U., de Bondt H.L., Kim S.-H.;  
 RT "High-resolution crystal structures of human cyclin-dependent kinase  
 RT 2 with and without ATP: bound waters and natural ligand as guides for  
 RT inhibitor design.;"  
 RL J. Med. Chem. 39:4540-4546(1996).

RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=97475219; PubMed=9334743;  
 RA Lawrie A.M., Noble M.E.M., Tunnah P., Brown N.R., Johnson L.N.,  
 RA Endicott J.A.,  
 RT "Protein kinase inhibition by staurosporine revealed in details of  
 RT the molecular interaction with CDK2.";  
 RL Nat. Struct. Biol. 4:796-801(1997).  
 RP [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH GSK1.  
 RX MEDLINE=96182647; PubMed=8601310;  
 RA Bourne Y., Watson M.H., Hickey M.J., Holmes W., Rocque W., Reed S.I.,  
 RA Tanner J.A.,  
 RT "Crystal structure and mutational analysis of the human CDK2 kinase  
 RT complex with cell cycle-regulatory protein CksHsl.";  
 RL Cell 84:863-874(1996).  
 RP [15]  
 RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).  
 RX MEDLINE=96342369; PubMed=9677190;  
 RA Gray N.S., Wodicka L., Thummler A.-M.W.H., Norman T.C., Kwon S.,  
 RA Espinoza F.H., Morgan D.O., Barnes G., Leclerc S., Meijer L.,  
 RA Kim S.H., Lockhart D.J., Schultz P.G.,  
 RT "Exploiting chemical libraries, structure, and genomics in the search  
 RT for kinase inhibitors.";  
 RL Science 281:533-538(1998).  
 CC -1- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYCLE.  
 CC INTERACTS WITH CYCLINS A, D, OR E. ACTIVITY OF CDK2 IS MAXIMAL  
 CC DURING S PHASE AND G2.  
 CC -1- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES  
 CC THE ENZYME, WHILE PHOSPHORYLATION AT THR-160 ACTIVATES IT.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC CDC2/CDKX SUBFAMILY.  
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 CC -----  
 DR EMBL, X61622; CAA34807.1; -;  
 DR EMBL, X62071; CAA43985.1; -;  
 DR EMBL, M68520; AAA3567.1; -;  
 DR EMBL, AF512553; AAM34794.1; -;  
 DR EMBL, BC003065; AAH03065.1; -;  
 DR PIR, A41227; A41227.  
 DR PDB, 1FIN; 27-JAN-97.  
 DR PDB, 1HCK; 07-DEC-96.  
 DR PDB, 1HCL; 07-DEC-96.  
 DR PDB, 1A01; 12-NOV-97.  
 DR PDB, 1JST; 11-JAN-97.  
 DR PDB, 1JSU; 29-JUL-97.  
 DR PDB, 1BHU; 09-SEP-98.  
 DR PDB, 1B38; 23-DEC-98.  
 DR PDB, 1B39; 23-DEC-98.  
 DR PDB, 1B39; 23-DEC-98.  
 DR PDB, 1CKP; 13-JAN-99.  
 DR PDB, 1D18; 28-JAN-03.  
 DR PDB, 1DM2; 31-MAY-00.  
 DR PDB, 1E1V; 10-MAY-01.  
 DR PDB, 1E1X; 10-MAY-01.  
 DR PDB, 1F5Q; 27-DEC-00.  
 DR PDB, 1FQ1; 09-MAY-01.  
 DR PDB, 1FVJ; 17-JAN-01.  
 DR PDB, 1G1H; 14-NOV-01.  
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 DR PDB, 1H1Q; 19-SEP-02.  
 DR PDB, 1H1R; 19-SEP-02.

DR PDB, 1H1S; 19-SEP-02.  
 DR PDB, 1H24; 01-FEB-03.  
 DR PDB, 1H25; 01-FEB-03.  
 DR PDB, 1H26; 01-FEB-03.  
 DR PDB, 1H28; 01-FEB-03.  
 DR PDB, 1J5V; 29-AUG-01.  
 DR PDB, 1JVP; 21-DEC-01.  
 DR PDB, 1KE5; 14-MAY-02.  
 DR PDB, 1KE6; 14-MAY-02.  
 DR PDB, 1KE7; 14-MAY-02.  
 DR PDB, 1KE8; 14-MAY-02.  
 DR PDB, 1KE9; 14-MAY-02.  
 DR PDB, 1KE9; 14-MAY-02.  
 Query Match 92.3%; Score 24; DB 1; Length 298;  
 Best Local Similarity 83.3%; Pred. No. 80;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDASAL 6  
 DB 91 MDASAL 96  
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 AC Q63699; 009136;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cell division protein kinase 2 (EC 2.7.1.-).  
 GN CDK2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=thymoid;  
 RX MEDLINE=9516553; PubMed=7862443;  
 RA Kocant S., Endo T., Kitagawa M., Higashi H., Onaya T.,  
 RT "A variant form of cyclin-dependent kinase 2 (Cdk2) in a malignant  
 RT transformed rat thyroid (FRTL-Tc) cell line.";  
 RL Oncogene 10:663-669(1995).  
 RN [2]  
 RP SEQUENCE OF 19-124 FROM N.A.  
 RX MEDLINE=96113578; PubMed=8673024;  
 RA Hosokawa Y., Yang M., Kaneko S., Tanaka M., Nakashima K.,  
 RT "Synergistic gene expressions of cyclin E, cdk2, cdk5 and B2F-1  
 RT during the prolactin-induced G1/S transition in rat Nb2 pre-T  
 RT lymphoma cells.";  
 RL Biochem. Mol. Biol. Int. 37:393-399(1995).  
 CC -1- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYCLE.  
 CC INTERACTS WITH CYCLINS A, D, OR E. ACTIVITY OF CDK2 IS MAXIMAL  
 CC DURING S PHASE AND G2.  
 CC -1- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES  
 CC THE ENZYME, WHILE PHOSPHORYLATION AT THR-160 ACTIVATES IT (BY  
 CC SIMILARITY).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=alternative splicing; Named isoforms=2;  
 CC Name=CDK2-beta;  
 CC IsoId=Q63699-1; Sequence=Displayed;  
 CC IsoId=Q63699-2; Sequence=Not described;  
 CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC CDC2/CDKX SUBFAMILY.  
 CC -----  
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CC EMBL: D28753; BAA05947.1; -
CC DR EMBL: D6162; BAA09638.1; -
CC DR HSSP: P24941; 1A01
CC DR InterPro: IPR00719; Prot_kinase.
CC DR InterPro: IPR002290; Ser_thr_kinase.
CC DR Pfam: PF00069; Pkinase; 1.
CC DR ProDom: PD000001; Prot_kinase; 1.
CC DR SMART: SM00220; S_TKC; 1.
CC DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
CC DR TRANSFERASE: Serine/threonine-protein kinase; ATP-binding; Cell cycle;
CC KW Cell division; Mitosis; Phosphorylation; Alternative splicing.
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CC FT NP_BIND 10 18 ATP (BY SIMILARITY).
CC FT BINDING 33 33 BY SIMILARITY.
CC FT ACT_SITE 127 127 BY SIMILARITY.
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CC FT MOD_RES 160 160 PHOSPHORYLATION (BY CAK) (BY SIMILARITY).
CC FT CONFLICT 79 79 V -> C (IN REF. 2).
CC FT CONFLICT 99 99 L -> I (IN REF. 2).
CC FT CONFLICT 124 124 L -> C (IN REF. 2).
CC SO SEQUENCE 298 AA; 33887 MW; C8CB3ADCEB97F88 CRC64;

Query Match 92.3%; Score 24; DB 1; Length 298;
Best Local Similarity 83.3%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 91 MDASAL 96

RESULT 14
CDK2_MOUSE STANDARD; PRT; 346 AA.
ID CDK2_MOUSE
AC P97377; O55105;
DT 15-JUL-1999 (Rel. 38, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cell division protein kinase 2 (EC 2.7.1.1.-).
GN CDK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCB1_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM CDK2-ALPHA).
RC STRAIN=CS7BL/6;
RA Jun D., Lee Y.H., Park H.K., Kim Y.H.;
RT Exon-intron organization of the murine cyclin-dependent kinase-2
RT gene Cdk2-alpha and Cdk2-beta."
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RA Ellenrieder C., Bartosch B., Lee G.Y., Murphy M., Sweeney C.;
RA Hegerberg M., Hunt T., Carrington M., Jaeschke R.;
RT The 39 kDa form of CDK2 arises through alternative splicing, is
RT expressed in many but not all mammals, and is an active kinase."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLY INVOLVED IN THE CELL CYCLE.
CC INTERACTS WITH CYCLIN A, D, OR E. ACTIVITY OF CDK2 IS MAXIMAL
CC DURING S PHASE AND G2.
CC -1- ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES
CC THE ENZYME. WHILE PHOSPHORYLATION AT THR-160 ACTIVATES IT (BY
CC SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=CDK2-beta;
CC IsoId=P97377-1; Sequence=Displayed;
CC Name=CDK2-alpha;

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CC IsoId=P97377-2; Sequence=VSP_004800;
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC2/CDK2 SUBFAMILY.
CC CC
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CC -----
CC EMBL: U63337; AAB37128.1; -
CC DR EMBL: AJ223732; CA11533.1; -
CC DR EMBL: AJ223733; CA11534.1; -
CC DR EMBL: AJ223733; CA11535.1; -
CC DR HSSP: P24941; 1A01
CC DR MGD; MG1:104772; Cdk2.
CC DR InterPro: IPR000719; Prot_kinase.
CC DR InterPro: IPR002290; Ser_thr_kinase.
CC DR Pfam: PF00069; Pkinase; 1.
CC DR ProDom: PD000001; Prot_kinase; 1.
CC DR SMART: SM00220; S_TKC; 1.
CC DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
CC KW Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle;
CC Cell division; Mitosis; Phosphorylation; Alternative splicing.
CC FT DOMAIN 4 334
CC FT NP_BIND 10 18 ATP (BY SIMILARITY).
CC FT BINDING 33 33 BY SIMILARITY.
CC FT ACT_SITE 127 127 BY SIMILARITY.
CC FT MOD_RES 14 14 PHOSPHORYLATION (BY SIMILARITY).
CC FT MOD_RES 15 15 PHOSPHORYLATION (BY SIMILARITY).
CC FT MOD_RES 160 160 PHOSPHORYLATION (BY CAK) (BY SIMILARITY).
CC FT VARSPLIC 197 244 Missing (in isoform CDK2-alpha).
CC SO SEQUENCE 346 AA; 38978 MW; D806BC2F150AEDFC CRC64;

Query Match 92.3%; Score 24; DB 1; Length 346;
Best Local Similarity 83.3%; Pred. No. 94;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6
Db 91 MDASAL 96

RESULT 15
ALF_ECOLI STANDARD; PRT; 358 AA.
ID ALF_ECOLI
AC F11604;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fructose-bisphosphate aldolase class II (EC 4.1.2.13) (FBP aldolase).
DE FBA OR FBA OR FDA OR B2925 OR Z4263 OR ECS3796 OR SF2910.
GN Escherichia coli O157:H7, and
OS Escherichia coli.
OS Shigella flexneri.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCB1_TaxId=562; 83334; 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=X12 / CS520;
RX MEDLINE=89313302; PubMed=2546007;
RA Alefounder P.R., Baldwin S.A., Perham S.A., Short N.J.;
RT "Identification, molecular cloning and sequence analysis of a gene
RT cluster encoding the class II fructose 1,6-bisphosphate aldolase, 3-
RT phosphate dehydrogenase and a putative second glyceraldehyde 3-
RL Mol. Microbiol. 3:723-732(1989).

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RN [2] SEQUENCE FROM N.A., AND SEQUENCE OF 1-26.  
 RC SPECIES=E.coli;  
 RX MEDLINE=9193446; PubMed=2649077;  
 RA Alefounder P.R., Baldwin S.A., Perham R.N., Short N.J.;  
 RT "Cloning, sequence analysis and over-expression of the gene for the  
 class II fructose 1,6-bisphosphate aldolase of *Escherichia coli*.";  
 RL Biochem. J. 257:529-534(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blatterer F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 Riley M., Collado-Vides J., Glaesner J.D., Rode C.K., Mayhew G.F.,  
 Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 Mau B., Shao Y.;  
 RT "The complete genome sequence of *Escherichia coli* K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;  
 RX MEDLINE=21074935; PubMed=11206551;  
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
 Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamianos K.,  
 Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 Welch R.A., Blatterer F.R.;  
 RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7.";  
 RL Nature 409:529-533(2001).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952;  
 RX MEDLINE=21156231; PubMed=11258796;  
 RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,  
 Kihara S., Shiba T., Hattori M., Shinagawa H.;  
 RT "Complete genome sequence of enterohaemorrhagic *Escherichia coli*  
 O157:H7 and genomic comparison with a laboratory strain K-12.";  
 RL DNA Res. 8:11-22(2001).  
 RN [6]  
 RP SEQUENCE OF 1-12.  
 RC SPECIES=E.coli; STRAIN=K12 / EMG2;  
 RX MEDLINE=97443975; PubMed=9298646;  
 RA Link A.J., Robison K., Church G.M.;  
 RT "Comparing the predicted and observed properties of proteins encoded  
 in the genome of *Escherichia coli* K-12.";  
 RL Electrophoresis 18:1259-1313(1997).  
 RN [7]  
 RP SEQUENCE OF 1-4.  
 RC SPECIES=E.coli; STRAIN=K12 / W3110;  
 RX MEDLINE=98263247; PubMed=9600841;  
 RA Wilkins M.R., Gasteiger E., Tonello L., Ou K., Tyler M.,  
 Sanchez J.-C., Gooley A.A., Walsh B.J., Bairoch A., Appel R.D.,  
 Williams K.L., Hochstrasser D.F.;  
 RT "Protein identification with N and C-terminal sequence tags in  
 proteome projects.";  
 RL J. Mol. Biol. 278:599-608(1998).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;  
 RX MEDLINE=22272406; PubMed=12384590;  
 RA Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,  
 Yang J., Zhang F., Zhang J., Yang G., Wu H., Qu D., Dong J.,  
 Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,  
 Chang H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,  
 Yu J.;  
 RT "Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity  
 through comparison with *Escherichia coli* K12 and O157.";  
 RL Nucleic Acids Res. 30:4433-4441(2002).  
 RN [9]  
 RP ZINC-LIGANDS, AND MUTAGENESIS.

RC SPECIES=E.coli;  
 RX MEDLINE=93170474; PubMed=8436219;  
 RA Berry A., Marshall K.B.;  
 RT "Identification of zinc-binding ligands in the class II fructose-1,6-  
 bisphosphate aldolase of *Escherichia coli*.";  
 RL FEBS Lett. 318:11-16(1993).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS).  
 RC SPECIES=E.coli;  
 RX MEDLINE=96433074; PubMed=8836102;  
 RA Blom N.S., Tetreault S., Coulombe R., Sygusch J.;  
 RT "Novel active site in *Escherichia coli* fructose 1,6-bisphosphate  
 aldolase.";  
 RL Nat. Struct. Biol. 3:856-862(1996).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RC SPECIES=E.coli;  
 RX MEDLINE=97094986; PubMed=8939754;  
 RA Cooper S.J., Leonard G.A., McSweeney S.M., Thompson A.W.,  
 Natsmith J.H., Qamar S., Plater A., Berry A., Hunter W.N.;  
 RT "The crystal structure of a class II fructose-1,6-bisphosphate  
 aldolase shows a novel binuclear metal-binding active site embedded  
 in a familiar fold.";  
 RL Structure 4:1303-1315(1996).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RC SPECIES=E.coli;  
 RX MEDLINE=99182425; PubMed=10080900;  
 RA Hall D.R., Leonard G.A., Reed C.D., Walt C.I., Berry A., Hunter W.N.;  
 RT "The crystal structure of *Escherichia coli* class II fructose-1,  
 6-bisphosphate aldolase in complex with phosphoglycolaldehyde  
 reveals details of mechanism and specificity.";  
 RL J. Mol. Biol. 287:383-394(1999).  
 CC -1- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glyceralone  
 phosphate + D-glyceraldehyde 3-phosphate.  
 CC -1- COFACTOR: ZINC.  
 CC -1- PATHWAY: Glycolysis; sixth step.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SIMILARITY: Belongs to class II fructose-bisphosphate aldolase  
 family.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL: X1436; CAA3605.1; -;  
 DR EMBL: U28377; AAG5092.1; -;  
 DR EMBL: AE000376; AAC75862.1; -;  
 DR EMBL: AE005522; AAG58051.1; ALT INIT.  
 DR EMBL: AP002563; BAB37219.1; -;  
 DR EMBL: AE015305; AAN4392.1; ALT INIT.  
 DR PIR: D91103; D91103.  
 DR PIR: S02177; ADECA2A.  
 DR PDB: 1D0S; 07-JUL-97.  
 DR PDB: 1ZEN; 07-JUL-97.  
 DR PDB: 1B57; 07-JAN-00.  
 DR SWISS-2DPAGE; P11604; COLI.  
 DR EcoGene; EGI0282; fbaA.  
 DR InterPro; IPR006411; Fruct\_bisp\_bact.  
 DR InterPro; IPR000771; K\_bp\_aldolase.  
 DR Pfam; PF01116; F\_bp\_aldolase; 1.  
 DR ProDom; PD002376; K\_bp\_aldolase; 1.  
 DR TIGRFAMs; TIGR0167; cdbA; 1.  
 DR TIGRFAMs; TIGR01520; FruB; 1.  
 DR PROSITE; PS00602; ALDOLASE\_CLASS\_II\_1; 1.  
 DR PROSITE; PS00806; ALDOLASE\_CLASS\_II\_2; 1.  
 KW Lyase; Glycolysis; zinc; 3D-structure; Complete proteome.  
 FT INIT MET 0 0 ZINC.  
 FT METAL 107 107

	METAL	110	110	ZINC
PT MUTAGEN	107	107	H->A: LOSS OF ACTIVITY.	
PT MUTAGEN	110	110	H->A: LOSS OF ACTIVITY.	
PT MUTAGEN	111	111	C->A: PARTIAL LOSS OF ACTIVITY.	
PT HELIX	3	5		
PT TURN	6	6		
PT STRAND	10	11		
PT TURN	14	14		
PT HELIX	15	26		
PT TURN	27	28		
PT STRAND	31	35		
PT HELIX	39	52		
PT TURN	53	53		
PT STRAND	56	60		
PT HELIX	62	69		
PT TURN	71	72		
PT TURN	78	79		
PT HELIX	80	100		
PT TURN	101	101		
PT STRAND	103	108		
PT HELIX	113	115		
PT HELIX	116	133		
PT STRAND	140	143		
PT TURN	146	147		
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PT STRAND	170	174		
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PT STRAND	216	219		
PT TURN	238	238		

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Best Local Similarity 83.3%; Pred. No. 98;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
Db 190 MDASAL 195

Search completed: February 18, 2004, 14:28:03  
Job time : 5.55263 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 / Search time 16.6974 Seconds  
(without alignments)  
75.239 Million cell updates/sec

Title: US-09-643-260-3

Perfect score: 1 LDASAL 6

Sequence: BLOSUM62

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database: Listing first 45 summaries

Published Applications AA:  
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18: /cgn2\_6/ptodaca/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	6	10	US-09-847-940B-3
2	26	100.0	6	11	US-09-847-946A-3
3	26	100.0	28	10	US-09-847-940B-19
4	26	100.0	28	11	US-09-847-946A-19
5	26	100.0	191	15	US-10-156-761-8434
6	26	100.0	191	15	US-10-156-761-13332
7	26	100.0	191	15	US-10-156-761-13333
8	26	100.0	191	15	US-10-156-761-14915
9	26	100.0	240	10	US-09-738-626-4338
10	26	100.0	374	12	US-10-104-047-3578
11	26	100.0	600	11	US-09-746-660A-106
12	26	100.0	638	10	US-09-893-204-18
13	26	100.0	638	14	US-10-133-157-8
14	26	100.0	659	10	US-09-738-626-6815
15	26	100.0	704	12	US-10-104-047-3501

16	26	100.0	745	10	US-09-819-835-2	Sequence 2, Appl1
17	26	100.0	745	10	US-09-738-626-4761	Sequence 4761, Ap
18	26	100.0	745	11	US-09-746-660A-104	Sequence 104, Ap
19	26	100.0	1006	12	US-10-369-493-22729	Sequence 22729, A
20	26	92.3	14	14	US-10-038-612-107	Sequence 107, Ap
21	26	92.3	20	14	US-10-038-612-35	Sequence 35, Appl
22	26	92.3	21	14	US-10-038-612-106	Sequence 106, Ap
23	26	92.3	40	15	US-10-044-967-18	Sequence 18, Appl
24	26	92.3	157	16	US-10-080-170-565	Sequence 565, App
25	26	92.3	191	15	US-10-156-761-1181	Sequence 1181, A
26	26	92.3	259	12	US-10-369-493-9612	Sequence 9612, Ap
27	26	92.3	294	12	US-10-334-143-181	Sequence 181, App
28	26	92.3	298	10	US-09-771-161A-187	Sequence 187, App
29	26	92.3	298	12	US-10-174-794-13	Sequence 13, Appl
30	26	92.3	298	12	US-10-295-681-27	Sequence 27, Appl
31	26	92.3	298	12	US-10-295-681-29	Sequence 29, Appl
32	26	92.3	298	12	US-10-295-681-31	Sequence 31, Appl
33	26	92.3	298	12	US-10-295-681-43	Sequence 43, Appl
34	26	92.3	298	12	US-10-394-322A-7	Sequence 7, Appl1
35	26	92.3	304	10	US-09-976-059-3	Sequence 3, Appl1
36	26	92.3	346	12	US-10-295-681-33	Sequence 33, Appl1
37	26	92.3	346	12	US-10-295-681-45	Sequence 45, Appl
38	26	92.3	359	10	US-09-823-109-2	Sequence 2, Appl1
39	26	92.3	359	12	US-10-369-493-23545	Sequence 23545, A
40	26	92.3	359	15	US-10-164-204-2	Sequence 2, Appl1
41	26	92.3	405	9	US-09-815-242-10096	Sequence 10096, A
42	26	92.3	405	12	US-10-077-745-6	Sequence 6, Appl1
43	26	92.3	405	12	US-10-338-915-6	Sequence 759, App
44	26	92.3	405	12	US-10-369-493-759	Sequence 6, Appl1
45	26	92.3	405	14	US-10-078-107-6	

## ALIGNMENTS

RESULT 1  
US-09-847-940B-3  
Sequence 3, Application US/09847940B  
Parent No. US20020156000A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J.  
FILE REFERENCE: Ghosh, Sankar  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
CURRENT APPLICATION NUMBER: US/09/847, 940B  
CURRENT FILING DATE: 2001-05-02  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ. ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-3

Query Match 100.0%; Score 26; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7.1e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
DB 1 LDASAL 6

RESULT 2  
US-09-847-946A-3  
Sequence 3, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hamnig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide  
US-09-847-946A-3

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Best Local Similarity 100.0%; Pred. No. 7.1e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
DB 1 LDASAL 6

RESULT 3  
US-09-847-940B-19  
Sequence 19, Application US/09847940B  
Patent No. US20020156000A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J.  
APPLICANT: Ghosh, Sankar  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-117CP  
CURRENT APPLICATION NUMBER: US/09/847,940B  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 19  
LENGTH: 28  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NBD peptides  
US-09-847-940B-19

Query Match 100.0%; Score 26; DB 10; Length 28;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
DB 20 LDASAL 25

RESULT 4  
US-09-847-946A-19  
Sequence 19, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hamnig, Gerhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 19  
LENGTH: 28  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NBD peptide  
US-09-847-946A-19

Query Match 100.0%; Score 26; DB 11; Length 28;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
DB 20 LDASAL 25

RESULT 5  
US-10-156-761-8434  
Sequence 8434, Application US/10156761  
Publication No. US20030119018A1  
GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: ISHIKAWA, JUN  
APPLICANT: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIYUKI  
APPLICANT: HATTORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 8434  
LENGTH: 191  
TYPE: PRT  
ORGANISM: Streptomyces avermitilis  
US-10-156-761-8434

Query Match 100.0%; Score 26; DB 15; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.15e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
DB 41 LDASAL 46

RESULT 6  
US-10-156-761-13332  
Sequence 13332, Application US/10156761  
Publication No. US20030119018A1  
GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: ISHIKAWA, JUN  
APPLICANT: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIYUKI  
APPLICANT: HATTORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 13332  
LENGTH: 191  
TYPE: PRT  
ORGANISM: Streptomyces avermitilis  
US-10-156-761-13332

Query Match 100.0%; Score 26; DB 15; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6  
Db 41 LDASAL 46

RESULT 7  
US-10-156-761-13333  
Sequence 13333, Application US/10156761  
Publication No. US20030119018A1  
GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: ISHIKAWA, JUN  
APPLICANT: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIYUKI  
APPLICANT: HATTORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 13333  
LENGTH: 191  
TYPE: PRT  
ORGANISM: Streptomyces avermitilis  
US-10-156-761-13333

Query Match 100.0%; Score 26; DB 15; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6  
Db 41 LDASAL 46

RESULT 8  
US-10-156-761-14915  
Sequence 14915, Application US/10156761  
Publication No. US20030119018A1  
GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: ISHIKAWA, JUN  
APPLICANT: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: HATTORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 14915  
LENGTH: 191  
TYPE: PRT  
ORGANISM: Streptomyces avermitilis  
US-10-156-761-14915

Query Match 100.0%; Score 26; DB 15; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6  
Db 41 LDASAL 46

RESULT 9  
US-09-738-626-4338  
Sequence 4338, Application US/09738626  
Publication No. US20020197605A1  
GENERAL INFORMATION:  
APPLICANT: NAKAGAWA, SATOSHI  
APPLICANT: MIZOGUCHI, HIROSHI  
APPLICANT: ANDO, SEIKO  
APPLICANT: HAYASHI, MIKIRO  
APPLICANT: OCHIAI, KEIRO  
APPLICANT: YOKOI, HARUHIKO  
APPLICANT: YATEISHI, NAOKO  
APPLICANT: SENOH, AKIHIRO  
APPLICANT: IKEDA, MASATO  
APPLICANT: OZAKI, AKIO  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-125  
CURRENT APPLICATION NUMBER: US/09/738,626  
CURRENT FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: JP 99/377484  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: JP 00/159162  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: JP 00/280988  
PRIOR FILING DATE: 2000-08-03  
NUMBER OF SEQ ID NOS: 7059  
SOFTWARE: PatentIn ver. 3.0  
SEQ ID NO 4338  
LENGTH: 240  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-09-738-626-4338

Query Match 100.0%; Score 26; DB 10; Length 240;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6  
Db 70 LDASAL 75

RESULT 10  
US-10-104-047-3578  
Sequence 3578, Application US/10104047  
Publication No. US20030236392A1  
GENERAL INFORMATION:  
APPLICANT: HELIX RESEARCH INSTITUTE

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; TITLE OF INVENTION: NO. US20030236392A1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 3578
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3578

Query Match          100.0%; Score 26; DB 12; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASAL 6
        |||||
Db      287 LDASAL 292

RESULT 11
US-09-746-660A-106
; Sequence 106, Application US/09746660A
; Publication No. US20030049804A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Krogger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberer, Gregor
; APPLICANT: Kim, Jun-Won
; APPLICANT: Lee, Heung-Schick
; APPLICANT: Hwang, Byung-Joon
; TITLE OF INVENTION: CORINNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CP2
; CURRENT APPLICATION NUMBER: US/09/746,660A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/606740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 09/603124
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 106
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-746-660A-106

Query Match          100.0%; Score 26; DB 11; Length 600;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASAL 6
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Db      140 LDASAL 145

RESULT 12
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US-09-983-204-18
; Sequence 18, Application US/09983204
; Patent No. US20020173000A1
; GENERAL INFORMATION:
; APPLICANT: RENARD, STEPHANE
; APPLICANT: BESNARD, FRANCOIS
; APPLICANT: GRAHAM, DAVID
; TITLE OF INVENTION: SODIUM CHANNEL RECEPTOR
; FILE REFERENCE: 07586.0010
; CURRENT APPLICATION NUMBER: US/09/983,204
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 09/424,666
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/EP98/02884
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 97401196.7
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 18
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: HNACHD
US-09-983-204-18

Query Match          100.0%; Score 26; DB 10; Length 638;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASAL 6
        |||||
Db      551 LDASAL 556

RESULT 13
US-10-133-157-8
; Sequence 8, Application US/10133157
; Publication No. US20020184054A1
; GENERAL INFORMATION:
; APPLICANT: CHANG, HONG
; APPLICANT: CALAMARAS, NICHOLAS
; TITLE OF INVENTION: HIGH THROUGHPUT CELL-BASED ASSAY FOR MONITORING SODIUM
; TITLE OF INVENTION: CHANNEL ACTIVITY AND DISCOVERY OF SALTY TASTE
; FILE REFERENCE: 078003-0280790
; CURRENT APPLICATION NUMBER: US/10/133,157
; CURRENT FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: 60/287,413
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 8
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-133-157-8

Query Match          100.0%; Score 26; DB 14; Length 638;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASAL 6
        |||||
Db      551 LDASAL 556

RESULT 14
US-09-738-626-6815
; Sequence 6815, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
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; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6815
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6815

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Query Match      100.0%; Score 26; DB 10; Length 659;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 LDASAL 6
        |||||
Db      132 LDASAL 137

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RESULT 15
US-10-104-047-3501
; Sequence 3501, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3501
; LENGTH: 704
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3501

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Query Match      100.0%; Score 26; DB 12; Length 704;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 LDASAL 6
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Db      617 LDASAL 622

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Search completed: February 18, 2004, 15:41:55
Job time : 17.7529 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds  
(without alignments)  
35.929 Million cell updates/sec

Title: US-09-643-260-3

Perfect score: 26

Sequence: 1 LDASAL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310958 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	293	4	US-09-252-991A-17296
2	26	100.0	1313	3	US-08-989-299-9
3	24	92.3	20	3	US-09-140-149-9
4	24	92.3	20	4	US-09-615-917-9
5	24	92.3	40	4	US-09-480-993-18
6	24	92.3	83	1	US-08-370-225-16
7	24	92.3	83	1	US-08-461-859-16
8	24	92.3	83	5	PCT-US93-10069-16
9	24	92.3	165	4	US-09-252-991A-22877
10	24	92.3	257	4	US-09-328-352-4324
11	24	92.3	274	1	US-08-318-947A-20
12	24	92.3	274	2	US-08-795-303-20
13	24	92.3	289	4	US-09-107-532A-4402
14	24	92.3	289	2	US-08-874-347-25
15	24	92.3	288	2	US-08-869-106-2
16	24	92.3	298	3	US-09-093-522-25
17	24	92.3	298	4	US-09-457-040B-29
18	24	92.3	298	4	US-09-411-628-13
19	24	92.3	298	4	US-09-338-125-2
20	24	92.3	298	4	US-09-266-225D-14
21	24	92.3	359	4	US-09-098-219B-2
22	24	92.3	405	1	US-08-370-193A-9
23	24	92.3	544	4	US-09-417-197-113
24	24	92.3	544	4	US-09-417-197-115
25	24	92.3	723	4	US-09-434-408-2
26	24	92.3	970	4	US-09-198-452A-906
27	24	92.3	1042	4	US-09-512-250C-32

28	24	92.3	2618	3	US-09-413-814-28	Sequence 28, Appl
29	23	88.5	44	3	US-08-905-223-345	Sequence 345, App
30	23	88.5	65	1	US-08-227-536-6	Sequence 6, Appl1
31	23	88.5	65	5	PCT-US95-04682-6	Sequence 6, Appl1
32	23	88.5	159	4	US-09-252-991A-24779	Sequence 24779, A
33	23	88.5	201	1	US-08-444-083-8	Sequence 8, Appl1
34	23	88.5	201	1	US-08-266-304-8	Sequence 8, Appl1
35	23	88.5	201	1	US-08-442-745-8	Sequence 8, Appl1
36	23	88.5	201	1	US-08-443-129-8	Sequence 8, Appl1
37	23	88.5	201	1	US-08-443-952-8	Sequence 8, Appl1
38	23	88.5	201	1	US-08-443-130-8	Sequence 8, Appl1
39	23	88.5	201	1	US-08-792-019B-11	Sequence 11, Appl1
40	23	88.5	201	3	US-09-106-182-4	Sequence 4, Appl1
41	23	88.5	201	3	US-08-988-819-11	Sequence 11, Appl1
42	23	88.5	201	3	US-08-898-911-8	Sequence 8, Appl1
43	23	88.5	201	3	US-09-016-534-11	Sequence 11, Appl1
44	23	88.5	201	4	US-09-646-183-3	Sequence 3, Appl1
45	23	88.5	201	5	PCT-US95-04467-8	Sequence 8, Appl1

## ALIGNMENTS

```

RESULT 1
US-09-252-991A-17296
; Sequence 17296, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17296
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17296

Query Match          100.0%; Score 26; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 LDASAL 6
Db      91 LDASAL 96

RESULT 2
US-08-989-299-9
; Sequence 9, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSER: FOLEY, HONG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/989,299  
FILING DATE: 11-DEC-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold E., Beth  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MIA-025.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1313 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULAR TYPE: protein  
US-08-989-299-9

Query Match 100.0%; Score 26; DB 3; Length 1313;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
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DB 600 MDASAL 605

RESULT 3  
US-09-140-149-9  
Sequence 9, Application US/09140149  
Patent No. 6117680  
GENERAL INFORMATION:  
APPLICANT: Natesan, Sridaran  
APPLICANT: Gilman, Michael Z  
TITLE OF INVENTION: No. 6117680el Compositions and Methods for Regulation of  
FILE REFERENCE: 363C  
CURRENT APPLICATION NUMBER: US/09/140,149  
CURRENT FILING DATE: 1998-08-26  
EARLIER APPLICATION NUMBER: 08/918,401  
EARLIER FILING DATE: 1997-08-26  
EARLIER APPLICATION NUMBER: 08/920,610  
EARLIER FILING DATE: 1997-08-27  
EARLIER APPLICATION NUMBER: 09/126,009  
EARLIER FILING DATE: 1998-07-29  
EARLIER APPLICATION NUMBER: PCT/US97/15219  
EARLIER FILING DATE: 1997-08-27  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 9  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:synthetic  
OTHER INFORMATION: peptide  
US-09-140-149-9

Query Match 92.3%; Score 24; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 11;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
:|||||  
DB 11 MDASAL 16

RESULT 4

US-09-615-917-9  
Sequence 9, Application US/09615917  
Patent No. 6479653  
GENERAL INFORMATION:  
APPLICANT: Natesan, Sridaran  
APPLICANT: Gilman, Michael Z  
TITLE OF INVENTION: No. 6479653el Compositions and Methods for Regulation of  
FILE REFERENCE: 363C continuation  
CURRENT APPLICATION NUMBER: US/09/615,917  
CURRENT FILING DATE: 2000-07-13  
PRIOR APPLICATION NUMBER: 08/918,401  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 08/920,610  
PRIOR FILING DATE: 1997-08-27  
PRIOR APPLICATION NUMBER: 09/126,009  
PRIOR FILING DATE: 1998-07-29  
PRIOR APPLICATION NUMBER: 09/140,149  
PRIOR FILING DATE: 1998-08-26  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 9  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:synthetic  
OTHER INFORMATION: peptide  
US-09-615-917-9

Query Match 92.3%; Score 24; DB 4; Length 20;  
Best Local Similarity 83.3%; Pred. No. 11;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
:|||||  
DB 11 MDASAL 16

RESULT 5  
US-09-480-993-18  
Sequence 18, Application US/09480993  
Patent No. 6383790  
GENERAL INFORMATION:  
APPLICANT: Shokat, Kevin M.  
TITLE OF INVENTION: High Affinity Kinase Inhibitors for Target Validation  
FILE REFERENCE: 51538-5001-US  
CURRENT APPLICATION NUMBER: US/09/480,993  
CURRENT FILING DATE: 2000-01-11  
EARLIER APPLICATION NUMBER: US 60/115,340  
EARLIER FILING DATE: 1999-01-11  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 18  
LENGTH: 40  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Cdk2, cyclin-dependent kinase  
US-09-480-993-18

Query Match 92.3%; Score 24; DB 4; Length 40;  
Best Local Similarity 83.3%; Pred. No. 23;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
:|||||  
DB 33 MDASAL 38

RESULT 6  
US-08-370-225-16

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; Sequence 16, Application US/08370225
; Patent No. 5580736
; GENERAL INFORMATION:
; APPLICANT: Brent, Roger
; APPLICANT: Gyuilis, Jeno
; APPLICANT: Golemls, Erica
; TITLE OF INVENTION: Interaction Trap System for Isolating
; TITLE OF INVENTION: No. 5580736e1 Proteins
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 555X
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,225
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,038
; FILING DATE: 10/30/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/143001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 83
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-370-225-16

Query Match          92.3%; Score 24; DB 1; Length 83;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASAL 6
       :|||||
DB      18 WDASAL 23

RESULT 7
US-08-461-859-16
; Sequence 16, Application US/08461859
; Patent No. 5786169
; GENERAL INFORMATION:
; APPLICANT: Brent, Roger
; APPLICANT: Gyuilis, Jeno
; APPLICANT: Golemls, Erica
; TITLE OF INVENTION: Interaction Trap System for Isolating
; TITLE OF INVENTION: No. 5786169e1 Proteins
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

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; COMPUTER: IBM PS/2 Model 502 or 555X
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: US/08/461,859
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/370,225
; FILING DATE: January 9, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,038
; FILING DATE: October 30, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen P.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/143002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 83
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-461-859-16

Query Match          92.3%; Score 24; DB 1; Length 83;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASAL 6
       :|||||
DB      18 WDASAL 23

RESULT 8
PCT-US93-10069-16
; Sequence 16, Application PC/TUS9310069
; GENERAL INFORMATION:
; APPLICANT: Brent, Roger
; APPLICANT: Gyuilis, Jeno
; APPLICANT: Golemls, Erica
; TITLE OF INVENTION: Interaction Trap System for Isolating
; TITLE OF INVENTION: Novel Proteins
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 555X
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10069
; FILING DATE: 20-OCT-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,038
; FILING DATE: 10/30/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/143001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070

```



TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 83  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
PCT-US93-10069-16

Query Match 92.3%; Score 24; DB 5; Length 83;  
Best Local Similarity 83.3%; Pred. No. 54;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
DB 18 MDASAL 23

RESULT 9  
US-09-252-991A-23877  
Sequence 23877, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIORITY FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 23877  
LENGTH: 165  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23877

Query Match 92.3%; Score 24; DB 4; Length 165;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
DB 150 IDASAL 155

RESULT 10  
US-09-328-352-4324  
Sequence 4324, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
PRIORITY FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 4324  
LENGTH: 257  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-4324

Query Match 92.3%; Score 24; DB 4; Length 257;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6

DB :|||||  
5 IDASAL 10

RESULT 11  
US-08-318-947A-20  
Sequence 20, Application US/08318947A  
Patent No. 5798245  
GENERAL INFORMATION:  
APPLICANT: Anderson, Paul J.  
TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED  
TITLE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrie, Mion, Zimm, Macpeak & Seas  
STREET: 2100 Pennsylvania Avenue, NW Suite 800  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/318,947A  
FILING DATE: 06-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/133,530  
FILING DATE: 07-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mack, Susan J.  
REGISTRATION NUMBER: 30,951  
REFERENCE/DOCKET NUMBER: A6462  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-2820  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 274 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-318-947A-20

Query Match 92.3%; Score 24; DB 1; Length 274;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
DB 91 MDASAL 96

RESULT 12  
US-08-795-303-20  
Sequence 20, Application US/08795303  
Patent No. 5948656  
GENERAL INFORMATION:  
APPLICANT: Anderson, Paul J.  
APPLICANT: Tian, Qingsheng  
TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED  
TITLE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrie, Mion, Zimm, Macpeak & Seas  
STREET: 2100 Pennsylvania Avenue, NW Suite 800  
CITY: Washington  
STATE: DC

COUNTRY: USA  
ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,303  
FILING DATE: 04-FEB-1997  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/318,947  
FILING DATE: 06-OCT-1994  
APPLICATION NUMBER: 08/133,530  
FILING DATE: 07-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mack, Susan J.  
REGISTRATION NUMBER: 30,951  
REFERENCE/DOCKET NUMBER: A6462  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-2920  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 274 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-795-303-20

Query Match 92.3%; Score 24; DB 2; Length 274;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
DB 91 MDASAL 96

RESULT 13  
US-09-107-532A-4402  
Sequence 4402, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Arinello, Pamela Deneke  
REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 4402:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 289 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...289  
SEQUENCE DESCRIPTION: SEQ ID NO: 4402:  
US-09-107-532A-4402

Query Match 92.3%; Score 24; DB 4; Length 289;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
DB 96 MDASAL 101

RESULT 14  
US-08-874-347-25  
Sequence 25, Application US/08874347  
Patent No. 5863741  
GENERAL INFORMATION:  
APPLICANT: Limger, Andrew H.  
APPLICANT: Leaf, Edward B.  
APPLICANT: Thomas, Charles F.  
APPLICANT: Gustafson, Michael P.  
TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C., P.A.  
STREET: 60 South Sixth Street, Suite 3300  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/874,347  
FILING DATE: 13-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ellinger, Mark S.  
REGISTRATION NUMBER: 34,812  
REFERENCE/DOCKET NUMBER: 07039/055001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-335-5070  
TELEFAX: 612-288-9696  
TELEX:  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 298 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-874-347-25

Query Match 92.3%; Score 24; DB 2; Length 298;  
Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6  
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Db 91 MDASAL 96

RESULT 15  
US-08-969-106-2  
; Sequence 2, Application US/08969106  
; Patent No. 5986055  
; GENERAL INFORMATION:  
; APPLICANT: Yang, M.  
; APPLICANT: Nandabalan, K.  
; APPLICANT: Schulz, V.  
; TITLE OF INVENTION: CDK2 INTERACTIONS  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/969,106  
; FILING DATE: 13-NOV-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mastrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7934-057  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 298 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; US-08-969-106-2

Query Match 92.3%; Score 24; DB 2; Length 298;  
Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6  
:|||||  
Db 91 MDASAL 96

Search completed: February 18, 2004, 14:41:45  
Job time: 7.06579 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds

(without alignments)  
75.239 Million cell updates/sec

Title: US-09-643-260-2

Perfect score: 40

Sequence: 1 LDMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep.\*  
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6: /cgn2\_6/ptodata/1/pubppa/PCMTUS\_PUBCOMB.pep.\*  
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16: /cgn2\_6/ptodata/1/pubppa/US10C\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	10	US-09-847-940B-2
2	40	100.0	6	11	US-09-847-946A-2
3	40	100.0	6	11	US-09-847-946A-33
4	40	100.0	7	11	US-09-847-946A-37
5	40	100.0	8	11	US-09-847-946A-30
6	40	100.0	8	11	US-09-847-946A-38
7	40	100.0	9	11	US-09-847-946A-29
8	40	100.0	9	11	US-09-847-946A-32
9	40	100.0	9	11	US-09-847-946A-35
10	40	100.0	9	11	US-09-847-946A-36
11	40	100.0	10	11	US-09-847-946A-31
12	40	100.0	10	11	US-09-847-946A-34
13	40	100.0	11	11	US-09-847-946A-28
14	40	100.0	11	11	US-09-847-946A-132
15	40	100.0	11	11	US-09-847-946A-140

16	40	100.0	13	11	US-09-847-946A-143	Sequence 143, App
17	40	100.0	13	11	US-09-847-946A-144	Sequence 144, App
18	40	100.0	13	11	US-09-847-946A-145	Sequence 145, App
19	40	100.0	13	11	US-09-847-946A-148	Sequence 148, App
20	40	100.0	17	11	US-09-847-946A-141	Sequence 141, App
21	40	100.0	17	11	US-09-847-946A-142	Sequence 142, App
22	40	100.0	17	11	US-09-847-946A-146	Sequence 146, App
23	40	100.0	17	11	US-09-847-946A-147	Sequence 147, App
24	40	100.0	18	11	US-09-847-946A-135	Sequence 135, App
25	40	100.0	18	11	US-09-847-946A-131	Sequence 131, App
26	40	100.0	18	11	US-09-847-946A-136	Sequence 136, App
27	40	100.0	22	11	US-09-847-946A-133	Sequence 133, App
28	40	100.0	22	11	US-09-847-946A-134	Sequence 134, App
29	40	100.0	22	11	US-09-847-946A-137	Sequence 137, App
30	40	100.0	22	11	US-09-847-946A-138	Sequence 138, App
31	40	100.0	22	11	US-09-847-946A-139	Sequence 139, App
32	40	100.0	28	10	US-09-847-940B-18	Sequence 18, App
33	40	100.0	28	10	US-09-847-946A-18	Sequence 18, App
34	40	100.0	222	10	US-09-771-161A-141	Sequence 141, App
35	40	100.0	745	9	US-09-796-872-2	Sequence 2, App
36	40	100.0	745	10	US-09-844-908-10	Sequence 10, App
37	40	100.0	745	10	US-09-844-988-10	Sequence 10, App
38	40	100.0	745	12	US-10-408-636-3	Sequence 3, App
39	40	100.0	745	12	US-10-394-332A-32	Sequence 32, App
40	40	100.0	745	15	US-10-243-408-4	Sequence 4, App
41	40	100.0	745	15	US-10-059-585-35	Sequence 35, App
42	40	100.0	745	15	US-10-338-462-15	Sequence 15, App
43	40	100.0	756	9	US-09-796-872-15	Sequence 15, App
44	40	100.0	756	10	US-09-771-161A-232	Sequence 232, App
45	40	100.0	756	10	US-09-844-908-9	Sequence 9, App

#### ALIGNMENTS

RESULT 1  
US-09-847-940B-2  
; Sequence 2, Application US/09847940B  
; Patent No. US2002015600A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J.  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-117CP  
; CURRENT APPLICATION NUMBER: US/09/847,940B  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patent Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-2

Query Match 100.0%; Score 40; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
DB 1 LDMSWL 6

RESULT 2  
US-09-847-946A-2  
; Sequence 2, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J

```
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: NBD peptide
US-09-847-946A-2
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Query Match      100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDMSWL 6
        |||||
Db      1 LDMSWL 6
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RESULT 3
US-09-847-946A-33
; Sequence 33, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-33
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Query Match      100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDMSWL 6
        |||||
Db      1 LDMSWL 6
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RESULT 4
US-09-847-946A-37
; Sequence 37, Application US/09847946A
; Publication No. US20030054999A1
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GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: NEMO binding
US-09-847-946A-37
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Query Match      100.0%; Score 40; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 LDMSWL 6
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Db      1 LDMSWL 6
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RESULT 5
US-09-847-946A-30
; Sequence 30, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findels, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-30
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Query Match      100.0%; Score 40; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 LDMSWL 6
        |||||
Db      3 LDMSWL 8
```

```
RESULT 6
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US-09-847-946A-38  
; Sequence 38, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Pindels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 38  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-38

Query Match 100.0%; Score 40; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
DB 1 LDMSWL 6

RESULT 7  
US-09-847-946A-29  
; Sequence 29, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Pindels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-29

Query Match 100.0%; Score 40; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
DB 1 LDMSWL 6

RESULT 8  
US-09-847-946A-32  
; Sequence 32, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Pindels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-32

Query Match 100.0%; Score 40; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
DB 1 LDMSWL 6

RESULT 9  
US-09-847-946A-35  
; Sequence 35, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Pindels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 35  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:MEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-35

Query Match 100.0%; Score 40; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMWSL 6  
|||  
Db 3 LDMWSL 8

## RESULT 10

US-09-847-946A-36  
; Sequence 36, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hamig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 36  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-36

Query Match 100.0%; Score 40; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMWSL 6  
|||  
Db 2 LDMWSL 7

## RESULT 11

US-09-847-946A-31  
; Sequence 31, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hamig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-31

Query Match 100.0%; Score 40; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 19;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LDMWSL 6  
|||  
Db 2 LDMWSL 7

## RESULT 12

US-09-847-946A-34  
; Sequence 34, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hamig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-34

Query Match 100.0%; Score 40; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMWSL 6  
|||  
Db 3 LDMWSL 8

## RESULT 13

US-09-847-946A-28  
; Sequence 28, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hamig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-28

US-09-847-946A-28

Query Match 100.0%; Score 40; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6  
Db 3 LDMSWL 8

RESULT 14

US-09-847-946A-132  
; Sequence 132, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PFI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 132  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial  
; OTHER INFORMATION: Sequence:anti-inflammatory compound  
US-09-847-946A-132

Query Match 100.0%; Score 40; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6  
Db 3 LDMSWL 8

RESULT 15

US-09-847-946A-140  
; Sequence 140, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findeis, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PFI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 140  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

FEATURE:  
; OTHER INFORMATION: Description of Artificial  
; OTHER INFORMATION: Sequence:anti-inflammatory compound  
US-09-847-946A-140

Query Match 100.0%; Score 40; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6  
Db 3 LDMSWL 8

Search completed: February 18, 2004, 15:41:54  
Job time : 16.7529 secs



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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds  
(without alignments)  
35.929 Million cell updates/sec

Title: US-09-643-260-2  
Perfect score: 40  
Sequence: 1 LDMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/prodata/1/aa/5B\_COMB.pep.\*  
3: /cgn2\_6/prodata/1/aa/6A\_COMB.pep.\*  
4: /cgn2\_6/prodata/1/aa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/aa/PCUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/aa/backfilee1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	745	2	US-08-887-518-3
2	40	100.0	745	2	US-09-023-321-3
3	40	100.0	745	2	US-08-890-853-4
4	40	100.0	745	2	US-09-032-475-3
5	40	100.0	745	2	US-09-099-124A-4
6	40	100.0	745	2	US-09-099-124A-4
7	40	100.0	745	3	US-09-032-476-4
8	40	100.0	745	3	US-08-890-854-4
9	40	100.0	745	3	US-09-023-324-4
10	40	100.0	745	3	US-09-168-629-2
11	40	100.0	745	3	US-08-910-820-10
12	40	100.0	745	3	US-08-810-131A-2
13	40	100.0	745	4	US-09-109-986-4
14	40	100.0	745	4	US-09-844-908-10
15	40	100.0	745	4	US-09-868-758-3
16	40	100.0	745	2	US-08-887-518-4
17	40	100.0	745	2	US-09-023-321-4
18	40	100.0	745	2	US-08-890-853-2
19	40	100.0	745	2	US-09-032-475-4
20	40	100.0	745	2	US-09-099-124A-2
21	40	100.0	745	2	US-09-099-124A-2
22	40	100.0	745	3	US-09-032-476-2
23	40	100.0	745	3	US-08-890-854-2
24	40	100.0	745	3	US-09-023-324-2
25	40	100.0	745	3	US-09-168-629-15
26	40	100.0	745	3	US-08-910-820-9
27	40	100.0	745	4	US-09-109-986-2

28	40	100.0	756	4	US-09-844-908-9	Sequence 9, Appl1
29	40	100.0	756	4	US-09-868-758-4	Sequence 4, Appl1
30	40	100.0	996	4	US-09-417-197-123	Sequence 123, App
31	40	100.0	997	4	US-09-417-197-121	Sequence 28, App1
32	36	90.0	100	1	US-08-241-853-28	Sequence 29, App1
33	36	90.0	100	1	US-08-241-853-28	Sequence 28, App1
34	36	90.0	100	2	US-08-850-917-28	Sequence 28, App1
35	36	90.0	100	2	US-08-850-917-28	Sequence 28, App1
36	36	90.0	242	4	US-09-345-236B-3	Sequence 3, Appl1
37	36	90.0	334	4	US-09-252-991A-22395	Sequence 22395, A
38	36	90.0	454	4	US-09-252-991A-28780	Sequence 28780, A
39	36	90.0	616	3	US-09-136-574A-47	Sequence 47, Appl1
40	36	90.0	982	2	US-08-673-789-4	Sequence 4, Appl1
41	36	90.0	983	1	US-08-162-809-16	Sequence 16, Appl1
42	36	90.0	983	1	US-08-167-919A-10	Sequence 10, Appl1
43	36	90.0	983	2	US-08-449-645A-21	Sequence 21, Appl1
44	36	90.0	983	2	US-08-702-367A-21	Sequence 21, Appl1
45	36	90.0	983	3	US-08-715-106-10	Sequence 10, Appl1

## ALIGNMENTS

RESULT 1  
US-08-887-518-3  
Sequence 3, Application US/08887518  
Patent No. 5843721  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Wu, Lin  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887, 518  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A.  
REGISTRATION NUMBER: 36,627  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-887-518-3

Query Match 100.0%, Score 40, DB 2, Length 745,  
Best Local Similarity 100.0%, Pred. No. 1.4e+02,  
Matches 6, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 1 LDMSWL 6  
DB 738 LDMSWL 743

RESULT 2  
US-09-023-321-3  
Sequence 3, Application US/09023321  
Patent No. 5844073  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Wu, Lin  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,321  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-321-3

Query Match 100.0%; Score 40; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
DB 738 LDMSWL 743

RESULT 3  
US-08-890-853-4  
Sequence 4, Application US/08890853  
Patent No. 5851812  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Moronitz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-853-4

Query Match 100.0%; Score 40; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
DB 738 LDMSWL 743

RESULT 4  
US-09-032-475-3  
Sequence 3, Application US/09032475  
Patent No. 5854003  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Wu, Lin  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,475  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/887,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-032-475-3

Query Match 100.0%; Score 40; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6  
Db 738 LDMSWL 743

RESULT 5  
US-09-099-125A-4  
Sequence 4, Application US/09099125A  
Patent No. 5916760

GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099.125A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890.853

ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ. ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-099-125A-4

Query Match 100.0%; Score 40; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6  
Db 738 LDMSWL 743

RESULT 6  
US-09-099-124A-4  
Sequence 4, Application US/09099124A  
Patent No. 5939502

GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099.124A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890.853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ. ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-099-124A-4

Query Match 100.0%; Score 40; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6  
Db 738 LDMSWL 743

RESULT 7  
US-09-032-476-4  
Sequence 4, Application US/09032476  
Patent No. 6235492

GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
APPLICANT: Cao, Zhaoan  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032.476  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/890.854  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-032-476-4

Query Match 100.0%; Score 40; DB 3; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
DB 738 LDMSWL 743

RESULT 8  
US-08-890-854-4  
Sequence 4, Application US/08890854  
GENERAL INFORMATION:  
PATENT No. 6235512  
APPLICANT: Roche, Mike  
APPLICANT: Cao, Zhaodan  
APPLICANT: R. gnter, Catherine  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
ZIP: 94104  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,854  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-854-4

Query Match 100.0%; Score 40; DB 3; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
DB 738 LDMSWL 743

RESULT 9  
US-09-023-324-4  
Sequence 4, Application US/09023324  
PATENT No. 6235513  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
APPLICANT: Cao, Zhaodan  
APPLICANT: R. gnter, Catherine  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,324  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/890,854  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-324-4

Query Match 100.0%; Score 40; DB 3; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
DB 738 LDMSWL 743

RESULT 10  
US-09-168-629-2  
Sequence 2, Application US/09168629  
PATENT No. 6242253  
GENERAL INFORMATION:  
APPLICANT: Karin, Michael  
APPLICANT: Didonato, Joseph A.  
APPLICANT: Rothwarf, David M.  
APPLICANT: Hayakawa, Makio  
APPLICANT: Zandi, Ebrahim  
TITLE OF INVENTION: IKK Kinase, Subunits Thereof, and Methods of Using Same  
FILE REFERENCE: P-UD 3295  
CURRENT APPLICATION NUMBER: US/09/168,629  
CURRENT FILING DATE: 1998-10-08  
EARLIER APPLICATION NUMBER: 60/061,470  
EARLIER FILING DATE: 1997-10-09  
NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 745  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-168-629-2

Query Match  
Best Local Similarity 100.0%; Score 40; DB 3; Length 745;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
Db 738 LDMSWL 743

RESULT 11  
US-08-910-820-10  
Sequence 10, Application US/08910820  
Patent No. 6258579

GENERAL INFORMATION:  
APPLICANT: Mercurio, Frank  
APPLICANT: Zhu, Henry  
APPLICANT: Barbosa, Miguel  
APPLICANT: Li, Gian  
APPLICANT: Murray, Brian W.  
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE  
TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910, 820  
FILING DATE: 12-AUG-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 860098.413C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear

US-08-910-820-10

Query Match  
Best Local Similarity 100.0%; Score 40; DB 3; Length 745;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
Db 738 LDMSWL 743

RESULT 12  
US-08-810-131A-2  
Sequence 2, Application US/08810131A  
Patent No. 6268194

GENERAL INFORMATION:  
APPLICANT: Karin, Michael  
APPLICANT: Didonato, Joseph A.  
APPLICANT: Rothwarf, David M.  
APPLICANT: Hayakawa, Makio  
APPLICANT: Zandi, Ebrahim  
TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using  
TITLE OF INVENTION: Same  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/810,131A  
FILING DATE: 25-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 2408  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

Query Match  
Best Local Similarity 100.0%; Score 40; DB 3; Length 745;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
Db 738 LDMSWL 743

RESULT 13  
US-09-109-986-4  
Sequence 4, Application US/09109986  
Patent No. 6479266  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Cao, Zhaodan  
APPLICANT: R gnier, Catherine  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/109,986

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/890,854  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-109-986-4

Query Match  
Best Local Similarity 100.0%; Score 40; DB 4; Length 745;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6  
Db 738 LDMSWL 743

RESULT 14  
US-09-844-908-10  
Sequence 10, Application US/09844908  
Patent No. 6576437  
GENERAL INFORMATION:  
APPLICANT: Mercurio, Frank  
Zhu, Hengyi  
Barbosa, Miguel  
Li, Gian  
Murray, Brian W.  
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE  
COMPLEX AND METHODS OF USE THEREFOR  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/844,908  
FILING DATE: 27-Apr-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,820  
FILING DATE: 12-AUG-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 860098.413C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid

STRANDEDNESS: <unknown>  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-844-908-10

Query Match  
Best Local Similarity 100.0%; Score 40; DB 4; Length 745;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6  
Db 738 LDMSWL 743

RESULT 15  
US-09-868-758-3  
Sequence 3, Application US/09868758  
Patent No. 6576439  
GENERAL INFORMATION:  
APPLICANT: Glaxo Wellcome KK  
APPLICANT: Takemoto, Yoshihiro  
APPLICANT: Sakai, Yutaka  
APPLICANT: Hashimoto, Yasuhiro  
TITLE OF INVENTION: IKK3  
FILE REFERENCE: 9950986P  
CURRENT APPLICATION NUMBER: US/09/868,758  
CURRENT FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: GB 9826704.8  
PRIOR FILING DATE: 1998-12-24  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 745  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-868-758-3

Query Match  
Best Local Similarity 100.0%; Score 40; DB 4; Length 745;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6  
Db 738 LDMSWL 743

Search completed: February 18, 2004, 14:41:45  
Job time : 8.06579 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds  
(without alignments)  
87.531 Million cell updates/sec

Title: US-09-643-260-2

Perfect score: 40

Sequence: 1 LDMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR\_76:\*

2: PIR1:\*

3: PIR2:\*

4: PIR3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	745	1	149101 conserved helix-10
2	38	95.0	1139	2	A10379 probable potassium
3	37	92.5	1322	2	A13395 NADH2 dehydrogenas
4	36	90.0	122	2	S69909 Ig V-D-J region (M
5	36	90.0	132	2	S65785 mel-13a protein -
6	36	90.0	277	1	JC5900 bo-type ubiquinol
7	36	90.0	296	2	A84985 cytochrome o ubiqn
8	36	90.0	307	1	A36885 bo-type ubiquinol
9	36	90.0	318	2	AD0384 cytochrome o ubiqn
10	36	90.0	321	2	D83480 cytochrome o ubiqn
11	36	90.0	344	2	AG3489 cytochrome o ubiqn
12	36	90.0	353	2	A87469 ubiquinol oxidase
13	36	90.0	362	2	S23471 uroporphyrinogen d
14	36	90.0	386	2	C96006 probable cytochrom
15	36	90.0	409	2	T47298 probable replicati
16	36	90.0	747	2	D70802 hypochemical prote
17	36	90.0	803	2	P90485 hypochemical prote
18	36	90.0	915	2	A43802 cellulae (EC 3.2.
19	36	90.0	983	2	B45583 receptor tyrosine
20	36	90.0	983	2	A38224 protein-tyrosine k
21	36	90.0	983	2	A45583 receptor tyrosine
22	36	90.0	1039	2	S02711 cellulae (EC 3.2.
23	36	90.0	1329	2	D87226 conserved hypoche
24	35	87.5	162	2	C70829 hypochemical prote
25	35	87.5	348	2	AE2733 NADH ubiquinone ox
26	35	87.5	348	2	G97514 NADH dehydrogenase
27	35	87.5	443	2	AE0309 probable sugar tra
28	34	85.0	82	2	C69013 hypochemical prote
29	34	85.0	116	2	T03472 conserved hypoche

30	34	85.0	214	2	G83692 hypochemical prote
31	34	85.0	282	1	D86CMA DNA-3-methyladenin
32	34	85.0	282	2	E90988 3-methyl-adenine D
33	34	85.0	282	2	G85833 DNA-3-methyl-adenin
34	34	85.0	289	2	A10770 DNA-3-methyladenin
35	34	85.0	299	2	B83243 hypochemical prote
36	34	85.0	332	2	AH2593 cytochrome o ubiqn
37	34	85.0	377	2	B97376 cytochrome ba(3) (
38	34	85.0	394	2	C85064 hypochemical prote
39	34	85.0	411	2	E84949 tetrahydrofolylipo
40	34	85.0	414	2	B82408 hypochemical prote
41	34	85.0	418	2	D85064 hypochemical prote
42	34	85.0	420	2	A54759 cytochrome ba(3) c
43	34	85.0	501	2	S45914 probable glucan 1,
44	34	85.0	764	2	AD3144 formate dehydrogen
45	34	85.0	764	2	H98143 cbbBc protein (U60

#### ALIGNMENTS

RESULT 1  
149101  
Conserved helix-loop-helix ubiquitons kinase (EC 2.7.1.-) CHUK - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C/Accession: I49101  
R/Mock, B.A.; Connolly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.  
Genomics 27, 348-351, 1995  
A/Title: CHUK, a conserved helix-loop-helix ubiquitons kinase, maps to human chromosome  
A/Reference number: I49101; M01D:96044444; PMID:7558004  
A/Accession: I49101  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-745 <RES>  
A/Cross-references: EMBL:U12473; NID:G1079492; P1DN:JACS2589.1; PID:G1079493  
C/Genetics:  
A/Gene: CHUK  
C/Superfamily: mouse conserved helix-loop-helix ubiquitons kinase; protein kinase homo  
C/Keywords: ATP; phosphotransferase  
F/13-283/Domain: protein kinase homology <KIN>

Query Match 100.0%; Score 40; DB 1; Length 745;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
Db 738 LDMSWL 743

RESULT 2  
A10379  
Probable potassium efflux system YPO3129 [imported] - Yersinia pestis (strain CO92)  
C/Species: Yersinia pestis  
C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C/Accession: A10379  
R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibbail, R.W.; Holden, M.T.G.; Prentice, M.  
demo-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.  
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell  
Nature 413, 523-527, 2001  
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A/Reference number: AB0001; M01D:21470413; PMID:11586360  
A/Accession: A10379  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1139 <KUR>  
A/Cross-references: GB:AL590842; P1DN:CA092364.1; PID:G15981067; GSPDB:GN00175  
C/Genetics:  
A/Gene: YPO3129

Query Match 95.0%; Score 36; DB 2; Length 1139;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSWL 6  
 |||||  
 Db 480 MDMSWL 485

## RESULT 3

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) [imported] - Brucella melitensis (strain 1  
 C/Species: Brucella melitensis  
 C/Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 03-May-2002  
 C/Accession: A13395  
 R/DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,  
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
 A/Reference number: AD3252; PMID:1175688  
 A/Accession: A13395  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-322 <KIR>  
 A/Cross-references: GB:AE008917; PIDN:AAU52332.1; PID:G17983126; GSPDB:GN00190  
 A/Experimental source: strain 16M  
 C/Genetics:  
 A/Gene: BME1151  
 A/Map position: 1  
 C/Superfamily: NADH dehydrogenase (ubiquinone) chain 1  
 C/Keywords: oxidoreductase

Query Match 92.5%; Score 37; DB 2; Length 322;  
 Best Local Similarity 83.3%; Pred. No. 67;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
 |||||  
 Db 174 LDMSWL 179

## RESULT 4

Ig V-D-J region (MS) - human  
 C/Species: Homo sapiens (man)  
 C/Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
 C/Accession: S69909  
 R/Shora, S.; Hamblin, T.; Oester, D.G.; Stevenson, F.K.  
 Leukemia 8, 1285-1289, 1994  
 A/Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi  
 A/Reference number: S69909; MUID:94335315; PMID:8057663  
 A/Accession: S69909  
 A/Status: preliminary; nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-122 <SAH>  
 A/Cross-references: EMBL:Z33399; NID:9871348; PIDN:CAA83850.1; PID:9871349  
 A/Note: the sequence of residues 112-122 and the corresponding nucleic acid sequence are  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 F/15-97/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 36; DB 2; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6  
 |||||  
 Db 33 DMSWL 37

## RESULT 5

S65785  
 mel-13a protein - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 26-Aug-1999  
 C/Accession: S65785

R/Tetsu, O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.  
 Biochim. Biophys. Acta 1305, 109-112, 1996  
 A/Title: Cloning and characterization of two transcripts generated from the mel-13 gen  
 A/Reference number: S65785; MUID:96180310; PMID:8597592

A/Accession: S65785  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-132 <TET>  
 A/Cross-references: EMBL:U35309  
 C/Genetics:  
 A/Gene: mel-13  
 C/Superfamily: mouse mel-13a protein  
 C/Keywords: alternative splicing

Query Match 90.0%; Score 36; DB 2; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6  
 |||||  
 Db 58 DMSWL 62

## RESULT 6

bo-c-type ubiquinol oxidase (EC 1.10.3.-) chain II - Bradyrhizobium japonicum  
 C/Species: Bradyrhizobium japonicum  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C/Accession: JCS900  
 R/Surpin, M.A.; Lueden, M.; Water, R.J.  
 Gene 183, 201-206, 1996  
 A/Title: The Bradyrhizobium japonicum coxwxyz gene cluster encodes a bb3-c-type ubiquinol  
 A/Reference number: JCS900; MUID:97149299; PMID:8996107  
 A/Accession: JCS900  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: DNA  
 A/Residues: 1-277 <SUR>  
 C/Genetics:  
 A/Gene: coxw  
 C/Superfamily: bo-c-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain  
 C/Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; re

Query Match 90.0%; Score 36; DB 1; Length 277;  
 Best Local Similarity 83.3%; Pred. No. 83;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
 |||||  
 Db 108 LDMSWL 113

## RESULT 7

cytochrome o ubiquinol oxidase subunit II [imported] - Buchnera sp. (strain APS)  
 C/Species: Buchnera sp.  
 C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 02-Apr-2001  
 C/Accession: A84985  
 R/Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.  
 Nature 407, 81-86, 2000  
 A/Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.  
 A/Reference number: A84930; MUID:20445173; PMID:10993077  
 A/Accession: A84985  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-296 <STO>  
 A/Cross-references: GB:AP000398; GSPDB:GN00144  
 A/Experimental source: strain APS  
 C/Genetics:

A/Gene: cyoA; B0472

C/Superfamily: bo-c-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain  
 C/Keywords: copper; electron transfer; membrane-associated complex; respiratory chain  
 Query Match 90.0%; Score 36; DB 2; Length 296;



Best Local Similarity 83.3%; Pred. No. 88;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
|||  
|||  
Db 125 LDMSWL 130

## RESULT 8

A36885  
bo-type ubiquinol oxidase (EC 1.10.3.-) chain II precursor - Acetobacter aceti  
N/Alternate names: cytochrome a1 chain II  
C/Species: Acetobacter aceti  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
C/Accession: A36885  
R/Pukaya, M.; Tayama, K.; Tamaki, T.; Ebisuya, H.; Okumura, H.; Kawamura, Y.; Horiouchi, J.; Bacteriol. 175, 4307-4314, 1993  
A/Title: Characterization of a cytochrome a-1 that functions as a ubiquinol oxidase in *A. acetii*  
A/Reference number: A36885; PMID:93322308; PMID:8392509  
A/Accession: A36885  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-307 <RUK>  
A/Cross-references: GB:D13185; NID:9409064; PIDN:BA02480.1; PID:9433186  
A/Experimental source: isolate 1023  
C/Genetics:  
A/Gene: cyb  
C/Complex: heterotetramer; chains I, II, III and IV  
C/Function:  
A/Description: terminal oxidase for ethanol oxidation  
C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain  
C/Keywords: copper; electron transfer; heterotetramer; membrane-associated complex; oxid  
F/1-23/Domain: signal sequence #status predicted <Sig>  
F/1-24-307/Product: bo-type ubiquinol oxidase chain II #status predicted <MAT>  
F/48-64/Domain: transmembrane #status predicted <TM1>  
F/89-105/Domain: transmembrane #status predicted <TM2>

Query Match 90.0%; Score 36; DB 1; Length 307;  
Best Local Similarity 83.3%; Pred. No. 92;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
|||  
|||  
Db 135 LDMSWL 140

## RESULT 9

AD0384  
cytochrome o ubiquinol oxidase chain II (EC 1.10.3.-) [imported] - Yersinia pestis (str  
C/Species: Yersinia pestis  
C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 27-Nov-2001  
C/Accession: AD0384  
R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlhalil, R.W.; Holden, M.T.G.; Prentice, M.B.  
demo-Tarrega, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;  
11. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,  
Nature 413, 523-527, 2001  
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A/Reference number: AB0001; NCID:21470413; PMID:11586360  
A/Accession: AD0384  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-318 <KUR>  
A/Cross-references: GB:AL590842; PIDN:CAC92399.1; PID:915981102; GSPDB:GN00175  
C/Genetics:  
A/Gene: cyoA  
C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain  
C/Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; resp

Query Match 90.0%; Score 36; DB 2; Length 318;  
Best Local Similarity 83.3%; Pred. No. 95;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSWL 6

Db 135 LDMSWL 140  
|||  
|||

## RESULT 10

D83480  
cytochrome o ubiquinol oxidase subunit II P1317 [imported] - Pseudomonas aeruginosa (C  
C/Species: Pseudomonas aeruginosa  
C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C/Accession: D83480  
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;  
adman, S.; Yvan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Larbig, K.; Lin  
; Loy, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat  
A/Reference number: A82950; NCID:20437337; PMID:10984043  
A/Accession: D83480  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-331 <STO>  
A/Cross-references: GB:AE004561; GB:AE004091; NID:99947253; PIDN:AA04706.1; GSPDB:GN0  
A/Experimental source: strain PA01  
C/Genetics:  
A/Gene: cyoA; P1317  
C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain  
C/Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match 90.0%; Score 36; DB 2; Length 331;  
Best Local Similarity 83.3%; Pred. No. 99;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
|||  
|||  
Db 133 LDMSWL 138

## RESULT 11

AG3489  
cytochrome o ubiquinol oxidase chain II (EC 1.10.3.-) [imported] - Brucella melitensis  
C/Species: Brucella melitensis  
C/Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 22-Mar-2002  
C/Accession: AG3489  
R/DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Muir, C.; Lo, T.; Ivanova,  
.; Mazur, M.; Goldstein, B.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Lete  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A/Title: The genome sequence of the facultative intracellular pathogen Brucella melite  
A/Reference number: AD3252; PMID:11756688  
A/Accession: AG3489  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-344 <KUR>  
A/Cross-references: GB:AE008917; PIDN:AL53082.1; PID:917983945; GSPDB:GN00190  
A/Experimental source: strain 16M  
C/Genetics:  
A/Gene: BME11901  
A/Map position: I  
C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain  
C/Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; res

Query Match 90.0%; Score 36; DB 2; Length 344;  
Best Local Similarity 83.3%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
|||  
|||  
Db 141 LDMSWL 146

## RESULT 12

A87469  
ubiquinol oxidase subunit II [imported] - Caulobacter crescentus  
C/Species: Caulobacter crescentus  
C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 24-May-2001

C/Accession: A87469  
 R/Nerman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
 B.; Labib, M.T.; DeBey, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A/Title: Complete Genome Sequence of *Caioibacter crescentus*.  
 A/Reference number: A87469; MUID:21173696; PMID:11259647  
 A/Accession: A87469  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-353 <STO>  
 A/Cross-references: GB:AE005673; NID:G13423199; PIDN:AAK3749.1; GSPDB:GN00148  
 C/Genetics:  
 A/Gene: CCL773  
 C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain  
 C/Keywords: copper; electron transfer; membrane-associated complex; respiratory chain

Query Match 90.0%; Score 36; DB 2; Length 353;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMSW 5  
 |||||  
 Db 146 LDMSW 151

RESULT 13  
 S23471  
 uroporphyrinogen decarboxylase (EC 4.1.1.37) - Yeast (*Saccharomyces cerevisiae*)  
 N/Alternate names: protein YD9609.03; protein YDR047W  
 C/Species: *Saccharomyces cerevisiae*  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 22-Jun-1999  
 C/Accession: S23471; S33965; S54033; S20190; S21348; S31312  
 R/Garey, J.R.; Labbe-Bois, R.; Chelstowska, A.; Rycka, J.; Harrison, L.; Kushner, J.; La  
 eur, J. Biochem. 205, 1011-1016, 1992  
 A/Title: Uroporphyrinogen decarboxylase in *Saccharomyces cerevisiae*. HEM12 gene sequence  
 A/Reference number: S23471; MUID:92249304; PMID:11576986  
 A/Accession: S23471  
 A/Molecule type: DNA  
 A/Residues: 1-362 <GAR>  
 A/Cross-references: EMBL:X63721; NID:G3766; PIDN:CAA45253.1; PID:G3767  
 R/Hunt, S.; Bowman, S.; Harris, D.  
 submitted to the EMBL Data Library, May 1995  
 A/Reference number: S54031  
 A/Accession: S33965  
 A/Molecule type: DNA  
 A/Residues: 1-362 <DIF>  
 A/Cross-references: EMBL:Z19089; NID:G4775; PIDN:CAA79514.1; PID:G4776  
 R/Hunt, S.; Bowman, S.; Harris, D.  
 submitted to the EMBL Data Library, May 1995  
 A/Reference number: S54031  
 A/Accession: S54033  
 A/Molecule type: DNA  
 A/Residues: 1-362 <HIN>  
 A/Cross-references: EMBL:Z49209; NID:G798897; PIDN:CAA89078.1; PID:G798900; MIPS:YDR047W  
 C/Genetics:  
 A/Gene: HEM12; HEM6; POB3  
 A/Cross-references: MIPS:YDR047W; SGD:S0002454  
 A/Map position: 4R  
 C/Superfamily: uroporphyrinogen decarboxylase  
 C/Keywords: carbon-carbon lyase; carboxy-lyase; porphyrin biosynthesis

Query Match 90.0%; Score 36; DB 2; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSW 5  
 |||||  
 Db 279 LDMSW 283

RESULT 14

C96006  
 Probable cytochrome o ubiquinol oxidase chain II protein (EC 1.10.3.-) [Imported] - Si  
 C/Species: *Sinorhizobium meliloti*  
 C/Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
 C/Accession: C96006  
 R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hern  
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
 A/Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing en  
 A/Reference number: A95842; MUID:21396508; PMID:11481431  
 A/Accession: C96006  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-386 <KUR>  
 A/Cross-references: GB:AL591985; PIDN:CA49715.1; PID:G15141202; GSPDB:GN00167  
 A/Experimental source: strain 1021, megaplasmid pSymB  
 R/Galber, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Huble  
 pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federpohl, N.A.; Fisher, R.F.  
 L.; Hyman, R.W.; Jones, T.  
 Science 293, 668-672, 2001  
 A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kise, E.; Komp, C.; Leleur  
 heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Weiler, D.H.; Wong, K.; Yeh,  
 A/Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.  
 A/Reference number: A96039; MUID:21368234; PMID:11474104  
 A/Cross-references: annotation  
 C/Genetics:  
 A/Gene: cyoA; SMD21487  
 A/Genome: plasmid  
 C/Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain  
 C/Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; re

Query Match 90.0%; Score 36; DB 2; Length 386;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMSW 6  
 |||||  
 Db 141 LDMSW 146

RESULT 15  
 T47298  
 Probable replication protein - *Arabidopsis thaliana*  
 N/Alternate names: protein T14K23.110  
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 C/Accession: T47298  
 R/Wakutara, G.; Fartmann, B.; Danner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.  
 Mayer, K.F.X.  
 submitted to the Protein Sequence Database, April 2000  
 A/Reference number: Z24458  
 A/Accession: T47298  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-409 <NYA>  
 A/Cross-references: EMBL:AL132909  
 A/Experimental source: cultivar Columbia; BAC clone T14K23  
 C/Genetics:  
 A/Map position: 3  
 A/Intons: 47/3; 95/3; 131/2; 175/3; 240/2; 261/3; 304/1; 336/3  
 A/Note: T14K23.110

Query Match 90.0%; Score 36; DB 2; Length 409;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSW 5  
 |||||  
 Db 190 LDMSW 194

Search completed: February 18, 2004, 14:38:33  
 Job time: 7.5921 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2004, 13:39:39, Search time 3.55263 Seconds  
(without alignments)  
79.423 Million cell updates/sec

Title: US-09-643-260-2  
Perfect score: 40  
Sequence: 1 LDMSWL 6

Scoring table: BLOSUM62  
Gap 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	745	1 IKKA_HUMAN	O15111 h inhibitor
2	40	100.0	745	1 IKKA_MOUSE	O60680 m inhibitor
3	40	100.0	756	1 IKKB_HUMAN	O14920 homo sapien
4	40	100.0	757	1 IKKB_MOUSE	O88351 mus musculu
5	40	100.0	757	1 IKKB_RAT	O9QV78 rattus norv
6	36	90.0	296	1 CYO4_BUCAL	P57544 buchnera ap
7	36	90.0	307	1 COX2_ACEAC	P50653 acetobacter
8	36	90.0	314	1 CYO4_PSEPU	O9WWT1 pseudomonas
9	36	90.0	362	1 DCUP_YEAST	P23347 saccharomyc
10	36	90.0	983	1 EPB3_CHICK	P29330 gallus gall
11	36	90.0	983	1 EPB3_HUMAN	P29330 mus sapien
12	36	90.0	983	1 EPB3_MOUSE	P29330 mus musculu
13	36	90.0	984	1 EPB3_RAT	O08680 rattus norv
14	36	90.0	1039	1 GUNB_CALSA	P10474 c endogluca
15	36	90.0	1039	1 GUNB_PSEPU	O8K993 buchnera ap
16	36	90.0	1039	1 GUNB_YEAST	O8K993 buchnera ap
17	36	90.0	1039	1 GUNB_MOUSE	O8K993 buchnera ap
18	36	90.0	1039	1 GUNB_HUMAN	O8K993 buchnera ap
19	36	90.0	1039	1 GUNB_MOUSE	O8K993 buchnera ap
20	36	90.0	1039	1 GUNB_HUMAN	O8K993 buchnera ap
21	36	90.0	1039	1 GUNB_MOUSE	O8K993 buchnera ap
22	36	90.0	1039	1 GUNB_HUMAN	O8K993 buchnera ap
23	36	90.0	1039	1 GUNB_MOUSE	O8K993 buchnera ap
24	36	90.0	1039	1 GUNB_HUMAN	O8K993 buchnera ap
25	36	90.0	1039	1 GUNB_MOUSE	O8K993 buchnera ap
26	36	90.0	1039	1 GUNB_HUMAN	O8K993 buchnera ap
27	36	90.0	1039	1 GUNB_MOUSE	O8K993 buchnera ap
28	36	90.0	1039	1 GUNB_HUMAN	O8K993 buchnera ap
29	36	90.0	1039	1 GUNB_MOUSE	O8K993 buchnera ap
30	36	90.0	1039	1 GUNB_HUMAN	O8K993 buchnera ap
31	36	90.0	1039	1 GUNB_MOUSE	O8K993 buchnera ap
32	36	90.0	1039	1 GUNB_HUMAN	O8K993 buchnera ap
33	36	90.0	1039	1 GUNB_MOUSE	O8K993 buchnera ap

34	32	80.0	360	1 WNT2_CABEL	P34889 caenorhabdi
35	32	80.0	376	1 PGR_PENGR	O93883 penicillium
36	32	80.0	387	1 INTD_ECOLI	P24218 escherichia
37	32	80.0	400	1 HOCF_ECOLI	P36646 escherichia
38	32	80.0	470	1 NOS2_ONCMY	O92091 oncorhynch
39	32	80.0	470	1 NRAM_IADBU	O07570 influenza a
40	32	80.0	470	1 NRAM_IADCH	O07571 influenza a
41	32	80.0	470	1 NRAM_IADH2	O07572 influenza a
42	32	80.0	470	1 NRAM_IADH2	O07573 influenza a
43	32	80.0	470	1 NRAM_IADU3	O07599 influenza a
44	32	80.0	470	1 NRAM_IAGFN	O07574 influenza a
45	32	80.0	470	1 NRAM_IAGHD	O07577 influenza a

## ALIGNMENTS

RESULT 1  
IKKA\_HUMAN STANDARD; PRT; 745 AA.  
AC O15111; 014666; Q11312; Q92467;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 15-SEP-2003 (Rel. 42, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (BC 2.7.1.-)  
DE (I kappa-B kinase alpha) (IKK-alpha) (IKK-A) (IkappaB kinase)  
DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous  
DE kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKB1KA).  
GN CHUK OR IKKA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.  
RC TISSUE=T-cell;  
RX MEDLINE=97386461; PubMed=92443310;  
RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;  
RT "Identification and characterization of an IkappaB kinase.";  
RL Cell 90:373-383(1997).  
RN [2]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=97394468; PubMed=9252186;  
RA Didonato J.A., Hayakawa M., Roehrs D.M., Zandi E., Karin M.;  
RT "A cytokine-responsive IkappaB kinase that activates the transcription  
RT factor NF-kappaB.";  
RL Nature 388:548-554(1997).  
RN [3]  
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND  
RP SER-176.  
RX TISSUE=Cervical carcinoma;  
RC MEDLINE=98008813; PubMed=9346484;  
RA Mercutio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,  
RT Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;  
RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for  
RT NF-kappaB activation.";  
RL Science 278:860-866(1997).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RX MEDLINE=99032998; PubMed=9813230;  
RA Hu M.C.-T., Wang Y.-P.;  
RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and  
RT embryonic tissues but localized to different human chromosomes.";  
RL Gene 222:31-40(1998).  
RN [5]  
RP SEQUENCE OF 32-745 FROM N.A.  
RC TISSUE=Cervical carcinoma;  
RX MEDLINE=96258427; PubMed=8777433;  
RA Connolly M.A., Marcu K.B.;  
RT "CHUK, a new member of the helix-loop-helix and leucine zipper  
RT families of interacting proteins, contains a serine-threonine kinase  
RT catalytic domain.";

RL Cell. Mol. Biol. Res. 41:537-549(1995).

RP [6] PHOSPHORYLATION BY MAPK14/NIK, AND MUTAGENESIS OF SRR-176; THR-179

RP AND SER-180.

RA MEDLINE=98188283; PubMed=9520446;

RA Ling L., Cao Z., Goeddel D.V.;

RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of Ser-176.";

RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).

RP [7] PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.

RP MEDLINE=99413720; PubMed=10485710;

RA Ozeo O.N., Mayo L.D., Guetin J.A., Pfeiffer S.R., Pfeiffer L.M.,

RA Donner D.B.;

RT "NF-kappaB activation by tumour necrosis factor requires the Akt serine-threonine kinase.";

RL Nature 401:82-85(1999).

RP [8] IKKA-IKKB BINDING.

RP MEDLINE=99212141; PubMed=10195894;

RA Delhase M., Hayakawa M., Chen Y., Karin M.;

RT "Positive and negative regulation of IkappaB kinase activity through IKKbeta subunit phosphorylation.";

RL Science 284:309-313(1999).

RP [9] IKK PHOSPHORYLATION.

RP MEDLINE=99038238; PubMed=9819420;

RA Nemoto S., DiDonato J.A., Lin A.;

RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappaB-inducing kinase.";

RL Mol. Cell. Biol. 18:7336-7343(1998).

RP [10] REVIEW.

RP MEDLINE=20178139; PubMed=10712233;

RA Jobin C., Sartor R.B.;

RT "The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";

RL Am. J. Physiol. 278:C451-C462(2000).

RP [11] SUBUNIT OF A COMPLEX CONTAINING CREBBP, NCOA2, NCOA3, IKKB AND IKKG.

RP MEDLINE=21968797; PubMed=11971985;

RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J., O'Malley B.W.;

RT "Regulation of SRC-3 (PCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator activity by I kappa B kinase.";

RL Mol. Cell. Biol. 22:3549-3561(2002).

CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates NCOA3.

CC -1- ENZYME REGULATION: Activated when phosphorylated and inactivated when dephosphorylated.

CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but also as an homodimer. Directly interacts with IKK-GAMMA/NEMO. Heterodimers form the active complex. The trimeric complex can also bind to MAPK14/NIK, MEK1, IKAP and IKB-alpha-P65-P50 complex. A weak interaction with TRAF2 cannot be excluded. Part of a complex composed of NCOA2, NCOA3, IKKB, IKKG and CREBBP.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- TISSUE SPECIFICITY: Widely expressed.

CC -1- PTM: Phosphorylated by MAPK14/NIK, AKT and to a lesser extent by MEK1, and dephosphorylated by PP2A. Autophosphorylated.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. IKAPAB KINASE SUBFAMILY.

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DR EMBL: AF012890; AAC5162.1; -

DR EMBL: AF009225; AAC5167.1; -

DR EMBL: AF080157; AAC08996.1; -

DR EMBL: U22512; AAC50713.1; -

DR HSPF: 063450; 1A06.

DR Genem: HGNC:1974; CHUK.

DR MIM: 600664; -

DR GO: GO:0005737; C:cytoplasm; TAS.

DR GO: GO:0008384; P:IkappaB kinase activity; TAS.

DR GO: GO:0007345; P:embryogenesis and morphogenesis; TAS.

DR GO: GO:0007252; P:I-kappaB phosphorylation; TAS.

DR GO: GO:0006955; P:immune response; TAS.

DR InterPro: IPR000719; Prot\_Kinase.

DR InterPro: IPR002290; Ser\_Thr\_Kinase.

DR InterPro: IPR001245; Tyr\_Kinase.

DR Pfam: PF00069; pkinase; 1.

DR PRINTS: PR00109; TYRKINASE.

DR ProDom: PD000001; Prot\_kinase; 1.

DR SMART: SM00220; S\_TKc\_1.

DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.

DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.

DR Transfaser: Serine/threonine-protein kinase; ATP-binding; phosphorylation.

KW TRANSFERASE; Serine/threonine-protein kinase; ATP-binding; phosphorylation.

FT DOMAIN 15 302 PROTEIN KINASE.

FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).

FT DOMAIN 738 743 NEMO-BINDING.

FT NP\_BIND 21 29 ATP (BY SIMILARITY).

FT BINDING 44 44 ATP (BY SIMILARITY).

FT ACT\_SITE 144 144 BY SIMILARITY.

FT MOD\_RES 23 23 PHOSPHORYLATION (BY PKA/AKT1).

FT MOD\_RES 176 176 PHOSPHORYLATION (BY MAPK14).

FT MUTAGEN 23 23 T->A: LOSS OF PHOSPHORYLATION AND DECREASE OF KINASE ACTIVITY.

FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.

FT MUTAGEN 44 44 K->M: LOSS OF AUTOPHOSPHORYLATION.

FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF ACTIVITY.

FT MUTAGEN 176 176 S->B: FULL ACTIVATION.

FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.

FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.

FT CONFLICT 543 543 E->G (IN REF. 2).

FT CONFLICT 604 604 L->R (IN REF. 5).

FT CONFLICT 679 680 TS->AY (IN REF. 5).

FT CONFLICT 684 684 P->A (IN REF. 3 AND 5).

FT CONFLICT 686 687 TS->DL (IN REF. 5).

SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;

Query Match 100.0%; Score 40; DB 1; Length 745;

Best Local Similarity 100.0%; Pred. No. 32;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6

Db 738 LDMSWL 743

RESULT 2

ID IKKA\_MOUSE STANDARD; PRT; 745 AA.

AC 060680; Q9D2X3;

DT 16-OCT-2001 (Rel. 40, Created)

DT 15-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (BC 2.7.1.1-)

DE (I kappa-B kinase alpha) (IKK-A) (IKK-alpha) (IkappaB kinase)

DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKB1A).

GN CHUK OR IKKA.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxId=10090;



FT VARSPLIC 452 471 MSLRYNANLTMKNTLIS -> IFRKAVSMERNKKGH  
 FT SLP (in isoform 2).  
 FT VARSPLIC 472 745 /Frid=VSP 004866.  
 FT Missing (in isoform 2).  
 FT VARSPLIC 577 584 /Frid=VSP 004867.  
 FT DHTSDST -> GKTQSQY (in isoform 3).  
 FT VARSPLIC 585 745 Missing (in isoform 3).  
 FT /Frid=VSP 004869.  
 FT K -> E (IN REF. 3).  
 FT CONFLICT 236 236 S -> Y (IN REF. 3).  
 FT CONFLICT 400 400  
 SQ SEQUENCE 745 AA; 84728 MW; 3FEF5582AF92233 CRC64;  
 Query Match 100.0%; Score 40; DB 1; Length 745;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LDMSWL 6  
 Db 738 LDMSWL 743  
 RESULT 3  
 IKKB HUMAN STANDARD; PRT; 756 AA.  
 AC 014920; 075327;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase subunit (EC 2.7.1.1-)  
 DE (1-kappa-B kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase  
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).  
 GN IKKB OR IKK2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.  
 RC TISSUE=Cervical carcinoma;  
 RA MEDLINE=98008813; PubMed=9346484;  
 RA Mercutio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,  
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;  
 RA "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for  
 RA NF-kappaB activation.";  
 RL Science 278:860-866(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.  
 RC MEDLINE=98008814; PubMed=9346485;  
 RA Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;  
 RA "IkappaB kinase-beta: NF-kappaB activation and complex formation with  
 RA IkappaB kinase-alpha and NIK.";  
 RL Science 278:866-869(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RA MEDLINE=99032998; PubMed=9812230;  
 RA Hu M.C.-T., Wang Y.-P.;  
 RA "IkappaB kinase-alpha and -beta genes are coexpressed in adult and  
 RA embryonic tissues but localized to different human chromosomes.";  
 RL Gene 222:31-40(1998).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND GENE MAPPING.  
 RC MEDLINE=98438415; PubMed=9763654;  
 RA Shindo M., Nakano H., Sakon S., Yasgita H., Mihara M., Okumura K.;  
 RA "Assignment of IkappaB kinase beta (IKKB) to human chromosome band  
 RA 8p12--p11 by in situ hybridization.";  
 RL Cytogenet. Cell Genet. 82:32-33(1998).  
 RN [5]  
 RP SEQUENCE OF 1-256 FROM N.A.  
 RC TISSUE=Lung;  
 RA MEDLINE=22388257; PubMed=12477932;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Pang C.,  
 RA Raha S.S., Loughran N.A., Peters G.J., Abraham R.D., Millaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnarra P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schenker A., Schein J.E., Jones S.J.W., Meitz M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length  
 RA human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]  
 RP IKK PHOSPHORYLATION.  
 RA MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., Didonato J.A., Lin A.;  
 RA "Coordinate regulation of IkappaB kinases by mitogen-activated protein  
 RA kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [7]  
 RP REVIEW.  
 RA MEDLINE=20178139; PubMed=10712233;  
 RA Tobin C., Sartor R.B.;  
 RA "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 RA inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 RN [8]  
 RP IDENTIFICATION IN A COMPLEX WITH CREBBP; NCOA2; NCOA3; IKKA AND IKKB.  
 RA MEDLINE=21968797; PubMed=11971985;  
 RA Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,  
 RA O'Malley B.W.;  
 RA "Regulation of SRC-3 (pCTP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator  
 RA activity by I kappa B kinase.";  
 RL Mol. Cell. Biol. 22:3549-3561(2002).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 CC the dissociation of the inhibitor/NF-kappa-B complex and  
 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3 (By similarity).  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MEK1, MAP3K14/NIK, IKAP and IKK-alpha-P65-P50  
 CC complex. Phosphorylated IKK-alpha is further released from the  
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKB  
 CC and CREBBP.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal  
 CC muscle, kidney, pancreas, spleen, thymus, prostate, testis and  
 CC peripheral blood.  
 CC -1- PTM: Phosphorylated by MEK1 and probably also by MAP3K14/NIK.  
 CC Weakly autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPB KINASE SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 CC EMBL; AF029684; AAC51860.1; -  
 CC EMBL; AF080158; AAD08997.1; -  
 CC EMBL; AF031416; AAC64675.1; -  
 CC EMBL; BC006231; AA06231.1; -

DR HSSE; Q63450; 1A06.  
 DR Genew; HGNC:5960; IKKB.  
 DR MIM; 603258; -.  
 DR CO; GO:0005523; C:cytoplasm; NAS.  
 DR CO; GO:0005524; F:ATP binding activity; NAS.  
 DR CO; GO:0004674; F:protein serine/threonine kinase activity; NAS.  
 DR CO; GO:0016563; F:transcriptional activator activity; NAS.  
 DR CO; GO:0006468; P:protein amino acid phosphorylation; NAS.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser Thr kinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00240; Ubiquitin; 1.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE\_NEG.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding; phosphorylation.  
 FT DOMAIN 15 300 PROTEIN KINASE.  
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 FT NP\_BIND 737 742 NEMO-BINDING.  
 FT BINDING 21 29 ATP (BY SIMILARITY).  
 FT ACT\_SITE 44 44 ATP (BY SIMILARITY).  
 FT MOD\_RES 145 145 BY SIMILARITY.  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 177 177 PHOSPHORYLATION.  
 FT MOD\_RES 181 181 PHOSPHORYLATION.  
 FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO EFFECT ON BINDING TO NIK.  
 FT MUTAGEN 177 177 S->A: DECREASE OF ACTIVITY.  
 FT MUTAGEN 177 177 S->E: FULL ACTIVATION.  
 FT MUTAGEN 181 181 S->A: DECREASE OF ACTIVITY.  
 FT MUTAGEN 181 181 S->E: FULL ACTIVATION.  
 FT CONFLICT 231 255 WMSKXQKSEVDIVSDNLQTVWF -> CWRMPQTVVHS  
 FT CONFLICT 425 425 Q -> H (IN REF. 1).  
 FT SEQUENCE 756 AA; 86563 MW; P9CADP671AE9E14E CRC64;  
 SO QUERY MATCH 100.0%; Score 40; DB 1; Length 756;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSML 6  
 Db 737 LDMSML 742  
 RESULT 4  
 ID IKKB MOUSE STANDARD; PRT; 757 AA.  
 AC 088351; Q9R1J6;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-EBR-2003 (Rel. 41, Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)  
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (I-kappa-B kinase  
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1X).  
 GN IKKB OR IKKB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEKK1.  
 RC STRAIN=C57BL/6; TISSUE=Spleen;  
 RX MEDLINE=98188239; Pubmed=9520401;  
 RA Nakano H., Shindo M., Sakon S., Mitsuoka S., Mihara M., Yagita H.,  
 RA Okumura K.;  
 RT "Differential regulation of Ikkapab kinase alpha and beta by two  
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated  
 RT protein kinase/SRK kinase kinase-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;  
 RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that  
 RT constitutively phosphorylates serine residues of Ikb.";  
 RL Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP DEVELOPMENTAL STAGE.  
 RX MEDLINE=99455228; Pubmed=10523828;  
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;  
 RT Hematopoietic progenitor kinase-1 (HPK1) stress response signaling  
 RT pathway activates Ikkapab kinases (IKK-alpha/beta) and IKK-beta is a  
 RT developmentally regulated protein kinase.";  
 RL Oncogene 18:5514-5524(1999).  
 RN [4]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; Pubmed=9819420;  
 RA Nemoto S., Didonato J.A., Lin A.;  
 RT "Coordinate regulation of Ikkapab kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [5]  
 RP REVIEW.  
 RX MEDLINE=20178139; Pubmed=10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 RT inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC -I- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 CC the dissociation of the inhibitor/NF-kappa-B complex and  
 CC ultimately the degradation of the inhibitor. Also phosphorylates  
 CC NCOA3.  
 CC -I- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 CC also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 CC also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-ALPHA-P5-P50  
 CC complex. Phosphorylated IKK-alpha is further released from the  
 CC complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG  
 CC and CREBBP (by similarity).  
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -I- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.  
 CC -I- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout  
 CC the mouse embryo, at E9.5 day its expression begins to be  
 CC localized to the brain, neural ganglia, neural tube, and in liver  
 CC at E12.5 day. At E15.5 day, the expression is further restricted  
 CC to specific tissues of the embryo.  
 CC -I- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.  
 CC Weakly autophosphorylated.  
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPAB KINASE SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; AF026524; AAC23557.1; -;  
 CC EMBL; AF088910; AAD52095.1; -;  
 CC HSSE; Q63450; 1A06.  
 CC MGD; MGI:1338071; Ikbb.  
 CC InterPro; IPR000719; Prot kinase.  
 CC InterPro; IPR002290; Ser Thr kinase.  
 CC InterPro; IPR001245; Tyr\_Pkinase.  
 CC Pfam; PF00069; Pkinase; 1.  
 CC PRINTS; PR00109; TYRKINASE.  
 CC ProDom; PD000001; Prot kinase; 1.  
 CC PROSITE; PS00107; PROTEIN KINASE ATP; FALSE\_NEG.  
 CC PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 CC PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding; phosphorylation.

FT DOMAIN 15 300 PROTEIN KINASE.  
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 FT NP\_BIND 737 742 NEMO-BINDING.  
 FT BINDING 21 29 ATP (BY SIMILARITY).  
 FT ACT\_SITE 44 44 ATP (BY SIMILARITY).  
 FT MOD\_RES 145 145 BY SIMILARITY.  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).  
 FT CONFLICT 56 56 N -> D (IN REF. 2).  
 FT CONFLICT 343 343 N -> E (IN REF. 2).  
 FT CONFLICT 356 356 L -> F (IN REF. 2).  
 FT CONFLICT 390 390 P -> Q (IN REF. 2).  
 FT CONFLICT 406 406 K -> R (IN REF. 2).  
 FT CONFLICT 573 573 TLDMSLOWMEDERCSLEQACD -> VTA (IN REF. 2).  
 FT CONFLICT 736 757  
 SQ SEQUENCE 757 AA; 86690 MW; FED962P095449CSE CRC64;  
 Query Match 100.0%; Score 40; DB 1; Length 757;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSWL 6  
 ID IKKB\_RAT STANDARD; PRT; 757 AA.  
 AC Q90Y78;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)  
 DE (I-kappa-B-kinase beta) (IKBK) (IKK-B) (I-kappa-B kinase  
 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).  
 GN IKBKX OR IKKB.  
 OC Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang Y., Sun S., Ravid K.;  
 RT "IKK beta in megakaryocyte differentiation."  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., DiDonato J.A., Lin A.;  
 RT "Coordinate regulation of I-kappaB kinases by mitogen-activated protein  
 kinase kinase kinase 1 and NF-kappaB-inducing kinase."  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [3]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Jodin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 inflammation and protection."  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC -1- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to  
 the dissociation of the inhibitor/NF-kappa-B complex and  
 ultimately the degradation of the inhibitor. Also phosphorylates  
 NCOA3.  
 CC -1- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but  
 also as a homodimer. Directly interacts with IKK-gamma/NEMO.  
 CC Heterodimers form the active complex. The tripartite complex can  
 also bind to MEKK1, MAP3K14/NIK, IKAP and IKK-alpha-P65-P50  
 complex. Phosphorylated IKK-alpha is further released from the  
 complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKKBG  
 and CREBBP (by similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.  
 CC Weakly autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPAB KINASE SUBFAMILY.  
 CC -----  
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 or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 CC EMBL; AF115282; AAF21978.1; --  
 CC HSSP; Q63450; 1A06.  
 DR InterPro; IPR000719; Prot. Kinase.  
 DR InterPro; IPR002290; Ser. Thr. kinase.  
 DR InterPro; IPR001245; Tyr. kinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PRODOM; PD000001; Prot. kinase; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP, PALSE\_NRG.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation.  
 FT DOMAIN 15 300 PROTEIN KINASE.  
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 FT NP\_BIND 737 742 NEMO-BINDING.  
 FT BINDING 21 29 ATP (BY SIMILARITY).  
 FT ACT\_SITE 44 44 ATP (BY SIMILARITY).  
 FT MOD\_RES 145 145 BY SIMILARITY.  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 757 AA; 86866 MW; 3AFB6A7D931FPC CRC64;  
 Query Match 100.0%; Score 40; DB 1; Length 757;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSWL 6  
 ID CVOA\_BUCAL STANDARD; PRT; 296 AA.  
 AC P57544;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O  
 subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase  
 subunit 2).  
 GN CVOA OR BU472.  
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum  
 symbiotic bacterium).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Buchnera.  
 OX NCBI\_TaxID=118099;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=Tokyo 1998;  
 RA MEDLINE=20445173; PubMed=10993077;  
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;  
 RT "Genome sequence of the endocellular bacterial symbiont of aphids  
 Buchnera sp. Aps."  
 RL Nature 407:81-86(2000).  
 CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT  
 OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE



```

CC GROWN AT HIGH AERATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(1/2) = Ubiquinone-8 + H(2)O.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
CC BUT LACK HEME-BINDING DOMAIN.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL: AP001119; BAB13169.1; -.
CC HSSP: P18400; ICYW.
CC InterPro: IPR001505; Copper_Cua.
CC InterPro: IPR006333; CytoA_II.
CC InterPro: IPR002429; Cyt_Cox_2.
CC InterPro: IPR000437; Prok_LipoProt.
CC Pfam: PF00116; COX2; 1.
CC ProDom: PD000131; Copper_Cua; 1.
CC TIGRfam: TIGR01433; CytoA; 1.
CC PROSITE: PS00013; PROKAR_LIPOPROTEIN; FALSE_NEG.
CC Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
CC Signal; Lipoprotein; Complete proteome.
CC FT SIGNAL 1 15 POTENTIAL.
CC FT CHAIN 16 296 UBIQUINOL OXIDASE POLYPEPTIDE II.
CC FT LIPID 16 16 N-ACYL DIGLYCERIDE (POTENTIAL).
CC FT DOMAIN 34 33 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 34 34 POTENTIAL.
CC FT DOMAIN 55 78 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 79 99 POTENTIAL.
CC FT DOMAIN 100 296 EXTRACELLULAR (POTENTIAL).
CC SQ SEQUENCE 296 AA; 34180 MW; 1AB2B4F0408FB64;

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Query Match 90.0%; Score 36; DB 1; Length 296;  
 Best Local Similarity 83.3%; Pred. No. 54;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 LDMSWL 6
Db 125 LDMSWL 130

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RESULT 7  
 ID QOX2 ACEAC STANDARD; PRT; 307 AA.  
 AC P50653;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome  
 DE A1 subunit 2) (Oxidase BA(3) subunit 2).  
 GN CYAB.  
 OS Acetobacter aceti.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;  
 OC Acetobacteraceae; Acetobacter.  
 ON NCB1\_Taxid=435;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1023;  
 RX MEDLINE=93322308; PubMed=8392509;  
 RA Fukaya M., Tayama K., Tamaki T., Ebisuya H., Okumura H.,  
 RA Kawamura Y., Horinouchi S., Bepko T.;  
 RT "Characterization of a cytochrome at that functions as a ubiquinol  
 RT oxidase in Acetobacter aceti."  
 RL J. Bacteriol. 175:4307-4314 (1993).  
 CC -1- PATHWAY: TERMINAL OXIDASE FOR ETHANOL OXIDATION.  
 CC -1- SUBUNIT: HETEROTETRAMER OF THE SUBUNITS 1, 2, 3 AND 4.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.  
 CC BUT LACK HEME-BINDING DOMAIN.

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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL: D13185; BAA02480.1; -.
CC PIR: A56885; A56885.
CC HSSP: P18400; ICYW.
CC InterPro: IPR001505; Copper_Cua.
CC InterPro: IPR006333; CytoA_II.
CC InterPro: IPR002429; Cyt_Cox_2.
CC Pfam: PF00116; COX2; 1.
CC PRINTS: PR01166; CYTOXIDASEII.
CC ProDom: PD000131; Copper_Cua; 1.
CC TIGRfam: TIGR01433; CytoA; 1.
CC PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
CC Oxidoreductase; Transmembrane; Respiratory chain; Signal;
CC Lipoprotein.
CC FT SIGNAL 1 23 POTENTIAL.
CC FT CHAIN 24 307 UBIQUINOL OXIDASE POLYPEPTIDE II.
CC FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).
CC FT TRANSMEM 46 66 POTENTIAL.
CC FT TRANSMEM 87 107 POTENTIAL.
CC SQ SEQUENCE 307 AA; 33921 MW; E66734B8441096D CRC64;

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Query Match 90.0%; Score 36; DB 1; Length 307;  
 Best Local Similarity 83.3%; Pred. No. 56;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 LDMSWL 6
Db 135 LDMSWL 140

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RESULT 8  
 ID CYOA PSEPU STANDARD; PRT; 314 AA.  
 AC Q9MWR1;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O  
 DE subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase  
 DE subunit 2).  
 GN CYOA.  
 OS Pseudomonas putida.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 ON NCB1\_Taxid=303;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IH-2000;  
 RX MEDLINE=99085656; PubMed=9868765;  
 RA Hirayama H., Takami H., Inoue A., Horikoshi K.;  
 RT "Isolation and characterization of toluene-sensitive mutants from  
 RT Pseudomonas putida IH-2000."  
 RL FEMS Microbiol. Lett. 169:219-225 (1998).  
 CC -1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT  
 CC OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE  
 CC GROWN AT HIGH AERATION (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(1/2) = Ubiquinone-8 + H(2)O.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.  
 CC BUT LACK HEME-BINDING DOMAIN.  
 CC -----
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 CC -----  
 DR EMBL; AB016787; BAA76356.1; -  
 DR HSBP; P18400; ICM.  
 DR InterPro; IPR001505; Copper CUA.  
 DR InterPro; IPR006333; Cyto\_II.  
 DR InterPro; IPR002429; Cyt\_cox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR ProDom; PD000131; Copper CUA; 1.  
 DR TIGRPFAMs; TIGR01433; CytoA; 1.  
 DR PROSITE; PS00013; PROKAR\_LIPROTEIN; 1.  
 DR Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;  
 KM Inner membrane; Signal; Lipoprotein.  
 FT SIGNAL 1 23 POTENTIAL.  
 FT CHAIN 1 23 UBIQUINOL OXIDASE POLYPEPTIDE II.  
 FT LIPID 24 314 N-ACYL DIGLYCERIDE (POTENTIAL).  
 FT DOMAIN 24 42 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 43 63 POTENTIAL.  
 FT DOMAIN 64 86 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 87 107 POTENTIAL.  
 FT DOMAIN 108 314 PERIPLASMIC (POTENTIAL).  
 SQ SEQUENCE 314 AA; 34702 MW; 96EB04FC3AA7F07 CRC64;  
 Query Match 90.0%; Score 36; DB 1; Length 314;  
 Best Local Similarity 83.3%; Pred. No. 57;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 LDMSWL 6  
 Db 133 LDMSWL 138  
 RESULT 9  
 DCPUP\_YEAST STANDARD; PRT; 362 AA.  
 AC P32347;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD).  
 DE HEM12 OR HEME OR POP3 OR YD9609.03.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 CC NCBI\_TaxID=4932;  
 CC [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=92249304; PubMed=1576986;  
 RA Garey J.R., Labbe-Bois R., Chelstowska A., Rytka J., Harrison L.,  
 RA Kushner J., Labbe P.;  
 RA "Uroporphyrinogen decarboxylase in Saccharomyces cerevisiae. HEM12  
 RT gene sequence and evidence for two conserved glycines essential for  
 RT enzymatic activity";  
 RL Eur. J. Biochem. 205:1011-1016(1992).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=93348774; PubMed=8346678;  
 RX Dileumert C., Laroque R., Keng T.;  
 RA "Molecular analysis of HEME (HEM12) in Saccharomyces cerevisiae, the  
 RT gene for uroporphyrinogen decarboxylase";  
 RL Yeast 9:613-623(1993).  
 RL [3]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=8288C / AB972;  
 RA Hunt S., Bowman S., Harris D., Barrell B.G., Rajandream M.A.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 RL [4]  
 RP MUTANTS.  
 RA MEDLINE=93111946; PubMed=1471989;  
 RX Chelstowska A., Zosdek T., Garey J.R., Kushner J., Rytka J.,  
 RA Labbe-Bois R.;

RT "Identification of amino acid changes affecting yeast  
 RT uroporphyrinogen decarboxylase activity by sequence analysis of hem12  
 RT mutant alleles";  
 RL Biochem. J. 288:753-757(1992).  
 CC -1- CATALYTIC ACTIVITY: Uroporphyrinogen-III = coproporphyrinogen + 4  
 CC CO(2).  
 CC -1- PATHWAY: Porphyrin and heme biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE UROPORPHYRINOGEN DECARBOXYLASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; X63721; CAA45253.1; -  
 DR EMBL; Z19089; CAA79514.1; -  
 DR EMBL; Z49209; CAA89078.1; -  
 DR PIR; S23471; S23471.  
 DR HSBP; P06132; URO.  
 DR SGD; S0002454; HEM12.  
 DR GO; GO:0004853; F:uroporphyrinogen decarboxylase activity; IMP.  
 DR GO; GO:006783; F:heme biosynthesis; IMP.  
 DR InterPro; IPR006361; Heme.  
 DR InterPro; IPR00257; Uro\_decarboxyls.  
 DR Pfam; PF01208; URO-D; 1.  
 DR ProDom; PD003225; Uro decarboxyls; 1.  
 DR TIGRPFAMs; TIGR01464; heme; 1.  
 DR PROSITE; PS00906; UROD\_1; 1.  
 DR PROSITE; PS00907; UROD\_2; 1.  
 KM Lyase; Decarboxylase; Porphyrin biosynthesis; Heme biosynthesis.  
 FT VARIANT 59 59 S -> P (IN HEM12-6 AND HEM12-12).  
 FT VARIANT 62 62 T -> I (IN HEM12-14).  
 FT VARIANT 107 107 L -> S (IN HEM12-3 AND HEM12-13).  
 FT VARIANT 215 215 S -> N (IN HEM12-2 AND HEM12-11).  
 FT MUTAGEN 33 33 G->D: INACTIVATION.  
 FT NOTAGEN 300 300 G->D: INACTIVATION.  
 SQ SEQUENCE 362 AA; 41349 MW; B9CB3AA8B62BC277 CRC64;  
 Query Match 90.0%; Score 36; DB 1; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 65;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LDMSW 5  
 Db 279 LDMSW 283  
 RESULT 10  
 EPPA\_CHICK STANDARD; PRT; 983 AA.  
 AC P29318;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Eppin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein  
 DE kinase receptor ETK1) (CEK4).  
 GN EPPA3 OR ETK1 OR CEK4.  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eucelostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phaethonidae; Phaethoninae;  
 CC Gallus.  
 CC NCBI\_TaxID=9031;  
 CC [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92031278; PubMed=1657122;  
 RA Sajjadi F.G., Paaguale R.B., Subraman S.;  
 RT "Identification of a new eph-related receptor tyrosine kinase gene  
 RT from mouse and chicken that is developmentally regulated and encodes  
 RT at least two forms of the receptor.";

RL New Biol. 3:769-778 (1991).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO  
 CC EPHRIN-A2, -A3, -A4 AND -A5.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING BRAIN AND  
 CC EMBRYONIC TISSUES. IN ADULT, THE GREATEST LEVELS OF EXPRESSION  
 CC OCCURS IN THE BRAIN. IT IS EXPRESSED IN A GRADDED MANNER ACROSS THE  
 CC RETINA WITH THE HIGHEST EXPRESSION AT ITS TEMPORAL POLE.  
 CC DETECTABLE IN ALL OTHER ADULT TISSUES EXAMINED, EXCEPT THE LIVER.  
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.  
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC RECEPTOR SUBFAMILY.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; M68514; AAA48666.1; -  
 CC PIR; B45583; B45583.  
 CC HSSP; P00523; 2PTK.  
 CC InterPro: IPR006209; EGF like.  
 CC InterPro: IPR001090; Ephrin\_receptor.  
 CC InterPro: IPR003961; FNIII\_subd.  
 CC InterPro: IPR003962; FNIII\_subd.  
 CC InterPro: IPR000719; Proc\_Kinase.  
 CC InterPro: IPR001650; SAM.  
 CC InterPro: IPR001245; Tyr\_kinase.  
 CC InterPro: IPR001426; YKase\_receptorV.  
 CC Pfam; PF01404; EPH\_Lbd; 1.  
 CC Pfam; PF00041; Fn3; 2.  
 CC Pfam; PF00069; pkinase; 1.  
 CC Pfam; PF00536; SAM; 1.  
 CC PRINTS; PR00014; FNTYPEIII.  
 CC PRINTS; PR00109; TYRKINASE.  
 CC ProDom; PD001495; Ephrin\_receptor; 1.  
 CC ProDom; PD000001; Proc\_Kinase; 1.  
 CC SMART; SM00615; EPH\_Lbd; 1.  
 CC SMART; SM00650; FN3; 2.  
 CC SMART; SM00454; SAM; 1.  
 CC SMART; SM00219; TYRK; 1.  
 CC PROSITE; PS01166; EGF\_2; UNKNOWN 1.  
 CC PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 CC PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 CC PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 CC PROSITE; PS50105; SAM\_DOMAIN; 1.  
 CC Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 CC SIGNAL 1  
 CC CHAIN 19  
 CC EPHRIN TYPE-A RECEPTOR 3.  
 CC TRANSMEM 20 540  
 CC TRANSMEM 541 564  
 CC DOMAIN 565 583  
 CC DOMAIN 188 321  
 CC DOMAIN 322 431  
 CC DOMAIN 432 529  
 CC DOMAIN 621 882  
 CC DOMAIN 911 975  
 CC SITE 981 983  
 CC NP\_BIND 627 635  
 CC BINDING 653 653  
 CC ACT\_SITE 746 746  
 CC MOD\_RES 596 596  
 CC MOD\_RES 602 602  
 CC MOD\_RES 779 779  
 CC MOD\_RES 779 779

FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 492 492 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 983 AA; 109910 MW; B8895F0BDP77651E CRC64;  
 Query Match 90.0%; Score 36; DB 1; Length 983;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSM 5  
 DB 342 LDMSM 346  
 RESULT 11  
 ID EPI3 HUMAN STANDARD; PRT; 983 AA.  
 AC P29320; O9H2V3; O9H2V4;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein  
 DE kinase receptor ETK) (HEK) (HEK4).  
 GN EPI3 OR ETK1 OR ETK OR HEK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=92179233; PubMed=1311845;  
 RA Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.;  
 RT "Molecular cloning of HEK, the gene encoding a receptor tyrosine  
 RT kinase expressed by human lymphoid tumor cell lines."  
 RT Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).  
 RL (2)  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE=Melanoma;  
 RA Chialdi R., Hames G., Strobant V., Maille B., Textier C., Mach B.,  
 RA Boon T., Coulle P.G.;  
 RT "Identification of a tumor specific shared antigen derived from an  
 RT Eph-receptor and presented to CD4 T cells on HLA class II  
 RT molecules."  
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION.  
 RX MEDLINE=92147681; PubMed=1737782;  
 RA Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wicks A.,  
 RA Welch K., Loudovaris M., Rockman S., Buemante I.;  
 RT "Isolation and characterization of a novel receptor-type protein  
 RT tyrosine kinase (hek) from a human pre-B cell line."  
 RL J. Biol. Chem. 267:3262-3267(1992).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO  
 CC EPHRIN-A2, -A3, -A4 AND -A5. COULD PLAY A ROLE IN LYMPHOID  
 CC FUNCTION.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1);  
 CC SECRETED (ISOFORM 2).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=P29320-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=P29320-2; Sequence=VSP 002995, VSP 002996;  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST LEVEL IN PLACENTA.  
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.  
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC RECEPTOR SUBFAMILY.

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DR EMBL: M68151; AAA35521.1; -  
 DR EMBL: AF213459; AAG43576.1; -  
 DR EMBL: AF213460; AAG43577.1; -  
 DR EMBL: A28003; CAA01906.1; -  
 DR PIR: A38224; A38224.  
 DR HSSP: P00523; 2PTK.  
 DR GeneW: HGNC:3387; EPHA3.  
 DR MIM: 176111; -  
 DR GO: GO:000587; C: integral to plasma membrane; TAS.  
 DR GO: GO:0007165; P: signal transduction; TAS.  
 DR InterPro: IPR006209; EGF\_1like.  
 DR InterPro: IPR001090; Ephrin\_receptor.  
 DR InterPro: IPR003961; FN\_III-  
 DR InterPro: IPR000719; FNIII\_subd.  
 DR InterPro: IPR001600; Proc\_Kinase.  
 DR InterPro: IPR001245; Tyr\_kinase.  
 DR InterPro: IPR001426; YKase\_receptor.  
 DR Pfam: PF01404; EPH\_1bd; 1.  
 DR Pfam: PF00041; FN3\_2.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Pfam: PF00536; SAM; 1.  
 DR PRINTS: PR00014; FNTPEP11.  
 DR PRINTS: PR00109; TYRKINSE.  
 DR ProDom: PD001495; Ephrin\_receptor; 1.  
 DR ProDom: PD000001; Proc\_kinase; 1.  
 DR SMART: SM00615; EPH\_1bd; 1.  
 DR SMART: SM00060; FN3\_2.  
 DR SMART: SM00454; SAM; 1.  
 DR SMART: SM00219; Tyrc; 1.  
 DR PROSITE: PS01186; EGF\_21\_UNKNOWN; 1.  
 DR PROSITE: PS01107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V1; 1.  
 DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V2; 1.  
 DR PROSITE: PS50105; SAM\_DOMAIN; 1.  
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
 KW Alternative splicing.

FT CHAIN 1 983 EPHRIN TYPE-A RECEPTOR 3.  
 FT DOMAIN 21 541 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 542 565 POTENTIAL.  
 FT DOMAIN 566 983 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 189 983 CYS-RICH.  
 FT DOMAIN 323 432 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 433 530 FIBRONECTIN TYPE-III 2.  
 FT DOMAIN 621 882 PROTEIN KINASE.  
 FT DOMAIN 911 975 SAM.  
 FT SITE 981 983 PDZ-BINDING MOTIF (POTENTIAL).  
 FT NE\_BIND 627 635 ATP (BY SIMILARITY).  
 FT BINDING 653 653 ATP (BY SIMILARITY).  
 FT ACT\_SITE 746 746 BY SIMILARITY.  
 FT MOD\_RES 596 596 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT MOD\_RES 602 602 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT MOD\_RES 779 779 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT CARBOHYD 232 232 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 337 337 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 391 391 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 404 404 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 493 493 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT VARSPPLIC 532 539 SEGISGS -> CMYENAV (in isoform 2).  
 FT VARSPPLIC 540 983 /FTID=VSP\_002995.  
 FT VARSPPLIC 540 983 Missing (in isoform 2).

FT CONFLICT 507 507 /FTID=VSP\_002996.  
 FT CONFLICT 724 724 F -> L (IN REF. 1; CAA01906).  
 FT CONFLICT 911 911 V -> L (IN REF. 1; CAA01906).  
 FT CONFLICT 924 924 S -> T (IN REF. 2).  
 FT CONFLICT 924 924 R -> W (IN REF. 2).  
 SQ SEQUENCE 983 AA; 110086 MW; B8D900FA80FF5121 CRC64;

Query Match  
 Best Local Similarity 90.0%; Score 36; DB 1; Length 983;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LDMSW 5  
 Db 343 LDMSW 347

RESULT 12  
 ID EPHA3\_MOUSE STANDARD; PRT; 983 AA.  
 AC P23119;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein  
 GN kinase receptor ETK1) (MEK4).  
 GN EPHA3 OR ETK1 OR MEK4 OR TYR04.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).  
 RP STRAIN=ICR X Swiss Webster; TISSUE=Embryo;  
 RX MEDLINE=92031278; PubMed=1657122;  
 RA Sajjadi F.G., Pasquale E.B., Subramani S.,  
 RT "Identification of a new eph-related receptor tyrosine kinase gene  
 RT from mouse and chicken that is developmentally regulated and encodes  
 RT at least two forms of the receptor."  
 RL New Biol. 3:769-778 (1991).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO  
 CC EPHRIN-A2, -A3, -A4 AND -A5.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE SHORT ISOFORM  
 CC IS SECRETED.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Long;  
 CC IsoId=P23119-1; Sequence=Displayed;  
 CC Name=Short;  
 CC IsoId=P23119-2; Sequence=VSP\_002997;  
 CC -1- TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN THE  
 CC BRAIN, ALSO DETECTED IN TESTIS.  
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.  
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
 CC RECEPTOR SUBFAMILY.

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DR EMBL: M68151; AAA35521.1; -  
 DR EMBL: M68151; AAA35522.1; ALT\_SEQ.  
 DR PIR: A45583; A45583.  
 DR HSSP: P00523; 2PTK.  
 DR MGD: MGI:99612; Epha3.  
 DR InterPro: IPR006209; EGF\_1like.  
 DR InterPro: IPR001090; Ephrin\_receptor.

Qy	DB	1	LDMSW	5	342	LDMSW	346
Query Match				90.0%;	Score 36;	DB 1;	Length 983;
Best Local Similarity				100.0%;	Pred. No. 1.7e+02;		
Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0
RESULT 13							
EP43_RAT		STANDARD;		PRT;		984 AA.	
AC	008680;						
DT	01-NOV-1997	(Rel. 35, Created)					
DT	01-NOV-1997	(Rel. 35, Last sequence update)					
DT	16-OCT-2001	(Rel. 40, Last annotation update)					
DE	Ephrin type-A receptor 3 precursor (BC 2.7.1.112)	(Tyrosine-protein kinase receptor REK4) (TYRO-4).					
GN	EPHA3 OR REK4 OR TYRO4.						

[illegible]

FT DOMAIN 912 976 SAM.  
 FT SITE 982 984 PDB-BINDING MOTIF (POTENTIAL).  
 FT NP BIND 628 636 ATP (BY SIMILARITY).  
 FT BINDING 654 654 ATP (BY SIMILARITY).  
 FT ACT SITE 747 747 BY SIMILARITY.  
 FT MOD RES 597 597 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT MOD RES 603 603 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT MOD RES 780 780 PHOSPHORYLATION (AUTO-) (POTENTIAL).  
 FT CARBOHYD 232 232 N-LINKED (GLUCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 337 337 N-LINKED (GLUCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 391 391 N-LINKED (GLUCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 404 404 N-LINKED (GLUCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 493 493 N-LINKED (GLUCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 493 493 N-LINKED (GLUCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 984 AA; 110227 MW; F170C49312F7A0AB CRC64;

Query Match 90.0%; Score 36; DB 1; Length 984;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 343 LDMSM 347  
 1 LDMSM 5  
 |||||

RESULT 14  
 GUNB\_CALSA STANDARD; PRT; 1039 AA.  
 ID GUNB\_CALSA  
 AC P10474;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endoglucanase/exoglucanase B precursor [includes: Endoglucanase  
 DE (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (cellulase)  
 DE (Cellulohydrolase); Exoglucanase (EC 3.2.1.91) (Exocellulohydrolase)  
 DE (1,4-beta-cellulohydrolase)].  
 GN CELB.  
 OS Caldicellum saccharolyticum (Caldicellulosiraptor saccharolyticus).  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;  
 OC Caldicellulosiraptor.  
 NCBI TaxId=44001;

RA [1]  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE=89098398; PubMed=2789517;  
 RA Saul D.J., Williams L.C., Love D.R., Chanley I.W., Bergquist P.I.;  
 RT "Nucleotide sequence of a gene from Caldicellum saccharolyticum  
 RT encoding for exoglucanase and endocellulase activity.";  
 RL Nucleic Acids Res. 17:439-439(1989).  
 CC -1- FUNCTION: THIS PROTEIN IS MADE UP OF TWO DOMAINS: THE N-TERMINAL  
 CC DOMAIN HAS EXOGLUCANASE ACTIVITY WHILE THE C-TERMINAL DOMAIN IS  
 CC AN ENDOGLUCANASE.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolase of 1,4-beta-D-glucosidic  
 CC linkages in cellulose, lichenin and cereal beta-D-glucans;  
 CC -1- CATALYTIC ACTIVITY: Hydrolase of 1,4-beta-D-glucosidic linkages  
 CC in cellulose and cellobiose, releasing cellobiose from the non-  
 CC reducing ends of the chains.  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO CELLULASE FAMILY  
 CC F (FAMILY 10 OF GLYCOSYL HYDROLASES).  
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO CELLULASE FAMILY  
 CC A (FAMILY 5 OF GLYCOSYL HYDROLASES).  
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DR EMBL: X13602; CAA1936.1; -  
 DR PIR: S02711; S02711.  
 DR HSRF: Q06851; INSC.  
 DR InterPro: IPR001956; CBD\_3.  
 DR InterPro: IPR001000; Glyco\_hydro\_10.

DR InterPro: IPR001547; Glyco\_hydro\_5.  
 DR Pfam: PF00942; CBM\_3; 1.  
 DR Pfam: PF00150; cellulase; 1.  
 DR Pfam: PF00331; Glyco\_hydro\_10; 1.  
 DR PRINTS: PR00134; GLHYDLASE10.  
 DR ProDom: PDD01947; CBD\_3; 1.  
 DR SMART: SM00633; Glyco\_10; 1.  
 DR PROSITE: PS00591; GLYCOSYL\_HYDROL\_F10; 1.  
 DR PROSITE: PS00659; GLYCOSYL\_HYDROL\_F5; 1.  
 KW Cellulose degradation; Hydrolase; Glycosidase; Repeat;  
 KW Multifunctional enzyme; Signal.  
 FT SIGNAL 1 28  
 FT CHAIN 29 1039  
 FT DOMAIN 376 416 THR/PRO-RICH, TANDM REPEATS OF T-P.  
 FT DOMAIN 417 570 CELLULOSE-BINDING (BY SIMILARITY).  
 FT DOMAIN 571 618 THR/PRO-RICH, TANDM REPEATS OF T-P.  
 FT ACT SITE 177 177 PROTON DONOR (POTENTIAL).  
 FT ACT SITE 285 285 NUCLEOPHILE (BY SIMILARITY).  
 FT ACT SITE 792 792 BY SIMILARITY.  
 SQ SEQUENCE 1039 AA; 117641 MW; 080378171594DDAE CRC64;

Query Match 90.0%; Score 36; DB 1; Length 1039;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 540 DMSWL 544  
 2 DMSWL 6  
 |||||

RESULT 15  
 CYOA\_BUCUP STANDARD; PRT; 290 AA.  
 ID CYOA\_BUCUP  
 AC 08X93;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O  
 DE subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase  
 DE subunit 2).  
 GN CYOA OR BUSG456.  
 OS Buchnera aphidicola (subsp. Schizaphis graminum).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Buchnera.  
 NCBI TaxId=98794;

RA [1]  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE=22084549; PubMed=12089438;  
 RA Tamas I., Klaesson L., Canback B., Naeelund A.K., Eriksson A.-S.,  
 RA Wernegreen J.J., Sandstrom J.P., Moran N.A., Andersson S.G.E.;  
 RT "50 million years of genomic stasis in endosymbiotic bacteria.";  
 RL Science 296:2376-2379(2002).  
 CC -1- FUNCTION: Cytochrome O terminal oxidase complex is the component  
 CC of the aerobic respiratory chain that predominates when cells are  
 CC grown at high aeration (by similarity).  
 CC -1- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).  
 CC -1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.  
 CC BUT LACK HEME-BINDING DOMAIN.

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DR EMBL: AE014121; AAM67999.1; -  
 DR InterPro: IPR001505; Copper\_Gua.  
 DR InterPro: IPR006333; CYOA\_II.  
 DR InterPro: IPR002429; Cyf\_cox\_2.  
 DR InterPro: IPR000437; Prok\_Iipoprot.

DR Pfam: PF00116; COX2; 1.  
DR PRINTS: PR01166; CYCOXIDASE1.  
DR ProDom: PD000131; Copper\_Gua; 1.  
DR TIGRFAMs: TIGR01433; CydA; 1.  
DR PROSITE: PS00013; PROKAR\_LIPOPROTEIN; FALSE\_NEG.  
KW Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;  
KW Signal; Lipoprotein; Complete proteome.  
FT SIGNAL 1 24 POTENTIAL.  
FT CHAIN 25 290 UBIQUINOL OXIDASE POLYPEPTIDE II.  
FT LIPID 25 25 N-ACYL DIGLYCERIDE (POTENTIAL).  
FT DOMAIN 25 42 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 43 63 POTENTIAL.  
FT DOMAIN 64 87 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 88 108 POTENTIAL.  
FT DOMAIN 109 290 EXTRACELLULAR (POTENTIAL).  
SQ SEQUENCE 290 AA; 33730 MW; 3D80A02A64732963 CRC64;

Query Match 87.5%; Score 35; DB 1; Length 290;  
Best Local Similarity 83.3%; Pred. No. 75;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDMSWL 6  
Db 134 LDMSWL 139

Search completed: February 18, 2004, 14:28:01  
Job time : 5.55263 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 / Search time 17.3684 Seconds  
(without alignments)  
89.145 Million cell updates/sec

Title: US-09-643-260-2

Sequence: 1 LDMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mmc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_prokaryote:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	740	6 Q95KVL	Q95KVL bos taurus
2	40	100.0	745	11 Q8CBT3	Q8CBT3 mus musculus
3	40	100.0	756	6 Q95KV0	Q95KV0 bos taurus
4	38	95.0	1139	16 Q8KC91	Q8KC91 yersinia pe
5	37	92.5	173	16 Q8ESU2	Q8ESU2 streptococ
6	37	92.5	173	16 Q8E065	Q8E065 streptococ
7	37	92.5	310	2 Q9XBS7	Q9XBS7 zymomonas m
8	37	92.5	322	16 Q8YKX7	Q8YKX7 brucella me
9	37	92.5	347	16 Q8G1B0	Q8G1B0 brucella su
10	37	92.5	361	16 Q8P955	Q8P955 xanthomonas
11	37	92.5	645	2 Q9X6C6	Q9X6C6 thermus bro
12	37	92.5	85	16 Q8PBL8	Q8PBL8 escherichia
13	36	90.0	205	16 Q9ACRS	Q9ACRS streptomyc
14	36	90.0	227	4 Q8IXK8	Q8IXK8 homo sapien
15	36	90.0	242	12 Q919K8	Q919K8 culex nigri
16	36	90.0			

17	36	90.0	261	2 Q9ACG7	Q9ACG7 caldicellul
18	36	90.0	282	16 Q8D354	Q8D354 wigglewort
19	36	90.0	288	2 Q8VTT4	Q8VTT4 pseudomonas
20	36	90.0	308	2 Q8KX52	Q8KX52 acetobacter
21	36	90.0	313	2 Q8YU06	Q8YU06 pseudomonas
22	36	90.0	318	16 Q8ZC58	Q8ZC58 yersinia pe
23	36	90.0	329	16 Q8XVB4	Q8XVB4 raietonia s
24	36	90.0	331	16 Q914Z7	Q914Z7 pseudomonas
25	36	90.0	341	16 Q8G3A8	Q8G3A8 brucella su
26	36	90.0	344	16 Q8YEH7	Q8YEH7 brucella me
27	36	90.0	353	16 Q9AF00	Q9AF00 callobacter
28	36	90.0	355	11 Q8B1T9	Q8B1T9 mus musculu
29	36	90.0	366	16 Q92U27	Q92U27 rhizobium m
30	36	90.0	393	16 Q8B7Z1	Q8B7Z1 rhizobium 1
31	36	90.0	409	10 Q9M3F6	Q9M3F6 arabidopsis
32	36	90.0	452	4 Q96AB7	Q96AB7 homo sapien
33	36	90.0	477	11 Q8CYU6	Q8CYU6 mus musculu
34	36	90.0	484	4 Q9BTU6	Q9BTU6 homo sapien
35	36	90.0	538	11 Q8C9K6	Q8C9K6 mus musculu
36	36	90.0	703	10 Q9F1S0	Q9F1S0 arabidopsis
37	36	90.0	747	16 Q8YXG3	Q8YXG3 arabidopsis
38	36	90.0	803	17 Q97UH8	Q97UH8 mycobacteri
39	36	90.0	803	17 Q97UH8	Q97UH8 sulfobolus
40	36	90.0	984	11 Q8C3U1	Q8C3U1 mus musculu
41	36	90.0	984	11 Q8B8B1	Q8B8B1 mus musculu
42	36	90.0	996	2 Q9ACD0	Q9ACD0 caldicellul
43	36	90.0	1329	16 Q9CD30	Q9CD30 mycobacteri
44	36	90.0	1426	2 Q9X3P6	Q9X3P6 caldicellul
45	36	90.0	1751	2 Q9A0G4	Q9A0G4 caldicellul

## ALIGNMENTS

RESULT 1  
ID Q95KVL PRELIMINARY; PRT; 740 AA.  
AC Q95KVL;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE IKB kinase-alpha.  
GN BIKKALPHA.  
OS Bos taurus (bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rottenberg S., Dobbelaere D.A.B., Heussler V.T.;  
RT "Identification and characterisation of the bovine IKB kinases (IKKs)  
RT alpha, beta and gamma.";  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ41555; CAC93686.1; -  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR002290; Ser Thr kinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR ProDom; PD000001; Prot kinase; 1.  
DR SMART; SM00220; S\_TKc\_1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS50108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 740 AA; 84343 MW; 01903BE11F44D176 CRC64;

Query Match 100.0%; Score 40; DB 6; Length 740;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; LDMSWL 6  
|||||||



Db 733 LDMSWL 738

## RESULT 2

ID 08CBT3 PRELIMINARY; PRT; 745 AA.

AC 08CBT3; 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DE Conserved helix-loop-helix ubiquitous kinase.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;  
 RX MEDLINE=22354683; PubMed=1246851;  
 RA The FANTOM Consortium,  
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;  
 "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK035326; BAC29034.1; -.  
 SQ SEQUENCE 745 AA; 84770 MW; 48C9B01C17A61184 CRC64;

Query Match 100.0%; Score 40; DB 11; Length 745;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6

Db 738 LDMSWL 743

RESULT 3  
 ID 09SKV0 PRELIMINARY; PRT; 756 AA.

AC 09SKV0; 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE 1kB kinase-beta.  
 GN BIKBETA.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovine; Bos.  
 NCBI\_TaxId=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Rottberg S., Dobbelaere D.A.B., Heuseler V.T.;  
 RT "Identification and characterisation of the bovine 1kB kinases (IKKs)  
 alpha, beta and gamma.";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; AJ144556; CAC93687.1; -.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_Thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PRODOM; PD000001; Prot\_kinase; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR ATP-binding; KINASE; Serine/threonine-protein kinase; Transferase.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 756 AA; 86647 MW; A072D15614A17655 CRC64;

Query Match 100.0%; Score 40; DB 6; Length 756;

Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
 Db 737 LDMSWL 742

## RESULT 4

ID 08ZC91 PRELIMINARY; PRT; 1139 AA.

AC 08ZC91; 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DE Putative potassium efflux system (Putative alpha helix protein).  
 GN YPO3129 OR AEPF A Y1054.  
 OS Yersinia pestis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.  
 NCBI\_TaxId=632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CO-92 / Biovar Orientalis;  
 RX MEDLINE=21470413; PubMed=11586360;  
 RA Parhill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,  
 RA Prentice M.B., Sebald M., James K.D., Churcher C., Mungall K.L.,  
 RA Baker S., Basham D., Bentley S.D., Brooke K., Cerdano-Tarraga A.M.,  
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
 RA Felwell T., Hamlin N., Holtroyd S., Jagels K., Karlyshev A.V.,  
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,  
 RA Stimpson M., Skelton J., Stevens K., Whitehead S., Barrett B.G.,  
 RT "Genome sequence of Yersinia pestis, the causative agent of plague.";  
 RL Nature 413:523-527(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KIMS / Biovar Mediaevalis;  
 RX MEDLINE=22137863; PubMed=12142430;  
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liao P.,  
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,  
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,  
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,  
 RA Perry R.D.;  
 RT "Genome sequence of Yersinia pestis KIM.";  
 RL J. Bacteriol. 184:4601-4611(2002).  
 DR EMBL; AJ141155; CAC92364.1; -.  
 DR EMBL; AE013709; AAM84635.1; -.  
 DR InterPro; IPR006685; MSion\_channel.  
 DR InterPro; IPR006686; MS\_channel\_dom.  
 DR Pfam; PF00924; MS\_channel; 1.  
 DR PROSITE; PS01246; UPR0003; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 1139 AA; 128409 MW; 7B5410BFC39A6B1 CRC64;

Query Match 95.0%; Score 38; DB 16; Length 1139;

Best Local Similarity 83.3%; Pred. No. 6.5e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6

Db 480 LDMSWL 485

## RESULT 5

ID 08ESU2 PRELIMINARY; PRT; 173 AA.

AC 08ESU2; 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DE Hypothetical protein.  
 GN GBS0887.  
 OS Streptococcus agalactiae (serotype III).  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 NCBI\_TaxId=216495;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MEM316 / Serotype III;  
 RX MEDLINE=2242508; PubMed=12354221;  
 RA Glaeser P., Rusniok C., Buchrieser C., Chevallier F., Frangoul L.,  
 RA Madak T., Zouine M., Couve E., Lalloui L., Poyart C., Tlieu-Cuot P.,  
 RA Kunst F.;  
 RT "Genome sequence of *Streptococcus agalactiae*, a pathogen causing  
 RT invasive neonatal disease.";   
 RL Mol. Microbiol. 45:1499-1513 (2002).  
 DR EMBL; AL766847; CAD46531.1; -.  
 DR Sagsalisc; SPS0887; -.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 173 AA; 20135 MW; F5F34044F0224CD1 CRC64;

Qy Query Match 92.5%; Score 37; DB 16; Length 173;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6  
 Db 125 LDMAWL 130

RESULT 6  
 Q8E065 PRELIMINARY; PRT; 173 AA.  
 AC Q8E065;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Acetyltransferase, GNAT family.  
 OS *Streptococcus agalactiae* (serotype V).  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 CC Streptococcus.  
 OX NCBI\_TaxID=216466;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=2603 V/R / Serotype V;  
 RX MEDLINE=2222988; PubMed=12200547;  
 RA Tettelin H., Maignan V., Cieslewicz M.J., Eissen J.A., Peterson S.,  
 RA Wessels M.R., Paulsen I.T., Nelson K.E., Margalit I., Read T.D.,  
 RA Madoff L.C., Wolf A.M., Beaman M.J., Brinkac L.M., Daugherty S.C.,  
 RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,  
 RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,  
 RA Carey H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,  
 RA Jacobini E.T., Bretoni C., Galli G., Mariani M., Vegni F., Malone D.,  
 RA Rinaldo D., Rappunli R., Telford J.L., Kasper D.L., Grandi G.,  
 RA Fraser C.M.;  
 RT "Complete genome sequence and comparative genomic analysis of an  
 RT emerging human pathogen, serotype V *Streptococcus agalactiae*.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).  
 DR EMBL; AE014231; AAM99756.1; -.  
 DR TIGR; SAG0870; -.  
 KW Transferase; Complete proteome.  
 SQ SEQUENCE 173 AA; 20135 MW; 0081677125975921 CRC64;

Qy Query Match 92.5%; Score 37; DB 16; Length 173;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6  
 Db 125 LDMAWL 130

RESULT 7  
 Q9XB57 PRELIMINARY; PRT; 310 AA.  
 AC Q9XB57;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Putative carboxymethylglutaminylase.  
 GN DLH.  
 OS *Zymomonas mobilis*.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;  
 OC Sphingomonadaceae; Zymomonas.  
 OX NCBI\_TaxID=542;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ZM4;  
 RA Um H.W., Kang H.S.;  
 RT "The sequence analysis of 42D7 fosmid clone of *Zymomonas mobilis*  
 RT ZM4";  
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF157493; AAD42398.1; -.  
 DR InterPro; IPR002925; DLH.  
 DR InterPro; IPR000379; Ser\_estra\_site.  
 DR Pfam; PF01738; DLH; 1.  
 SQ SEQUENCE 310 AA; 34092 MW; 34AC821E1F91259D CRC64;

Qy Query Match 92.5%; Score 37; DB 2; Length 310;  
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6  
 Db 153 VDMSWL 158

RESULT 8  
 Q8YK7 PRELIMINARY; PRT; 322 AA.  
 AC Q8YK7;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE NADH-quinone oxidoreductase chain H (EC 1.6.5.3).  
 GN BMR1151.  
 GN *Brucella melitensis*.  
 OS Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bacteria; Proteobacteria; Brucella.  
 OX NCBI\_TaxID=29459;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=16W / Biotype 1;  
 RX MEDLINE=20020109; PubMed=11756588;  
 RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mijer C., Los T.,  
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,  
 RA Jablonaki L., Larsen N., D'Souza M., Bernal A., Mazur M., Coleman E.,  
 RA Selkov E., Bizer P.H., Hagius S., O'Callaghan D., Lelsson J.-J.,  
 RA Haaseltorn R., Kyriades N., Overbeek R.;  
 RT "The genome sequence of the facultative intracellular pathogen  
 RT *Brucella melitensis*.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).  
 DR EMBL; AE009554; AAL52332.1; -.  
 DR InterPro; IPR001694; Resp\_NADH\_dhl.  
 DR Pfam; PF00146; NADHdh; 1.  
 DR PROSITE; PS00668; COMPLEX1\_ND1\_2; 1.  
 KW Oxidoreductase; Complete proteome.  
 SQ SEQUENCE 322 AA; 35966 MW; D5B5B123AB2C13B7 CRC64;

Qy Query Match 92.5%; Score 37; DB 16; Length 322;  
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6  
 Db 174 LDMAWL 179

RESULT 9  
 Q9BK3 PRELIMINARY; PRT; 347 AA.  
 ID Q9BK3

AC Q98KR3;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE NADH-ubiquinone dehydrogenase chain 8.  
 GN ML1361.  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 OC NCBI\_TaxID=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAFF303099;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneke T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Maenabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 RT Mesorhizobium loti."  
 RL DNA Ref. 7:331-338(2000).  
 DR EMBL; AP002997; BAB48751.1;  
 DR InterPro; IPR001694; Resp\_NADH\_dh1.  
 DR Pfam; PF00146; NADHdh; 1.  
 DR PROSITE; PS00668; COMPLEX1\_ND1\_2; 1.  
 DR UniProt; Complete proteome.  
 KW Ubiquinone; Complete proteome.  
 SQ SEQUENCE 347 AA; 38370 MW; 1092F351BD97EC57 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 347;  
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6  
 Db 199 LDMSWL 204

## RESULT 10

Q981B0 PRELIMINARY; PRT; 347 AA.  
 AC Q981B0;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE NADH dehydrogenase I, H subunit.  
 GN NUOH OR BR0809.  
 OS Brucella suis.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Brucellaceae; Brucella.  
 OC NCBI\_TaxID=29461;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1330 / Biovar 1;  
 RX MEDLINE=22247741; PubMed=12271122;  
 RA Paulsen I.T., Seeshadri R., Nelson K.B., Eisen J.A., Heidelberg J.F.,  
 RA Read T.D., Dodson R.J., Umeyam L., Brinkac L.M., Beaman M.J.,  
 RA Daugherty S.C., Debey R.T., Durkin A.S., Kolonay J.F., Madupu R.,  
 RA Nelson W.C., Ayodeji B., Krahl M., Shetty J., Malek J., Van Aken S.E.,  
 RA Riedmuller S., Tectelin H., Gill S.R., White O., Salzberg S.L.,  
 RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;  
 RT "The Brucella suis genome reveals fundamental similarities between  
 RT animal and plant pathogens and symbionts."  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).  
 GN EMBL; AB014385; AAN29738.1;  
 DR TIGR; BR0809;  
 KW Complete proteome.  
 SQ SEQUENCE 347 AA; 38428 MW; DA7F7471PD34D127 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 347;  
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6  
 Db 199 LDMSWL 204

## RESULT 11

Q9P955 PRELIMINARY; PRT; 361 AA.  
 AC Q9P955;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Exopolysaccharide biosynthesis protein.  
 GN XCC2011.  
 OS Xanthomonas campestris (pv. campestris).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 OC Xanthomonadaceae; Xanthomonas.  
 OC NCBI\_TaxID=340;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 33913 / NCPPB 528;  
 RX MEDLINE=22022145; PubMed=12024217;  
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,  
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,  
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,  
 RA Camarotte G., Camarvan P., Cardoso J., Chambergo P., Clapina L.P.,  
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,  
 RA Faria J.B., Ferreira A.U.S., Ferreira R.C.C., Ferro M.I.T.,  
 RA Fornighieri E.F., Franco M.C., Greggio C.C., Gruber A.,  
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,  
 RA Locali E.C., Machado M.A., Madalra A.M.B.N., Martinez-Rossi N.M.,  
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,  
 RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,  
 RA Trindade dos Santos M., Truffi D., Teal S.M., White F.F.,  
 RA Setubal J.C., Kitajima J.P.;  
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing  
 RT host specificities."  
 RL Nature 417:459-463(2002).  
 DR EMBL; AB012305; AAM41300.1;  
 DR InterPro; IPR002656; Acyl\_transf\_3.  
 DR Pfam; PF01757; Acyl\_transf\_3; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 361 AA; 39147 MW; 37AB21791BE0393F CRC64;

## Query Match

92.5%; Score 37; DB 16; Length 361;  
 Best Local Similarity 83.3%; Pred. No. 3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDMSWL 6  
 Db 117 LDMSWL 122

## RESULT 12

Q9X6C6 PRELIMINARY; PRT; 645 AA.  
 AC Q9X6C6;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Beta-galactosidase.  
 GN BGLT.  
 OS Thermus brockianus.  
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;  
 OC Thermus.  
 OC NCBI\_TaxID=56956;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IT1360;  
 RX MEDLINE=99402735; PubMed=10473401;  
 RA Fridjerson O., Matzilewicz H., Genweiller A., Rohrlirsch T., Matces R.,

RT "Cloning of the gene encoding a novel thermostable alpha-galactosidase  
 RT from *Thermus brockianus* IT1360."  
 RL Appl. Environ. Microbiol. 65:3955-3963(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IT1360;  
 RX MEDLINE=20203878; PubMed=10741834;  
 RA Fridlonsen O., Matzlawick H., Mattes R.;  
 RT "The structure of the alpha-galactosidase gene loci in *Thermus*  
 RT *brockianus* IT1360 and *Thermus thermophilus* IT125.";  
 RL Extremophiles 4:23-33(2000).  
 DR EMBL: AF135398; AAD33667.1; -  
 DR Interpro: IPR001584; Glyco\_hydro\_14.  
 DR Interpro: IPR003476; Glyco\_hydro\_42.  
 DR Pfam: PF01373; Glyco\_hydro\_14; 1.  
 DR Pfam: PF02449; Glyco\_hydro\_42; 1.  
 SQ SEQUENCE 645 AA; 73420 MW; C79A9E1C0020EC40 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 645;  
 Best Local Similarity 83.3%; Pred. No. 5.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
 Db 48 LDMAWL 53

RESULT 13  
 ID 08FBL8 PRELIMINARY; PRT; 85 AA.  
 AC 08FBL8;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 GN C4754.  
 OS *Escherichia coli* O6.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=217992;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O6.H1 / CFT073 / ATCC 700928;  
 RX MEDLINE=22388234; PubMed=12471157;  
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,  
 RA Rasko D., Buckles E.L., Lou S.-R., Boutin A., Hackett J., Stroud D.,  
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;  
 RT "Extensive mosaic structure revealed by the complete genome sequence  
 RT of uropathogenic *Escherichia coli*."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).  
 DR EMBL: AE016769; AAN83187.1; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 85 AA; 9675 MW; 47DADB502F570A8B CRC64;

Query Match 90.0%; Score 36; DB 16; Length 85;  
 Best Local Similarity 66.7%; Pred. No. 1e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
 Db 19 LDMSWL 24

RESULT 14  
 ID 09ACR5 PRELIMINARY; PRT; 205 AA.  
 AC 09ACR5;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Hypothetical protein SCPL.253.  
 GN SCPL.253.

OS Streptomyces coelicolor.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycinae; Streptomyces; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RX MEDLINE=21996410; PubMed=12000953;  
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kiese H.,  
 RA Harper D., Baileman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 RA Huang C.-H., Kiese T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabinowitsch B., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wietzorek A., Woodward J., Barrall B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete *Streptomyces*  
 RT *coelicolor* A3(2)."  
 RL Nature 417:141-147(2002).  
 DR EMBL: AL590464; CAC36779.1; -  
 DR KW Hypothetical protein; Plasmid; Complete proteome.  
 SQ SEQUENCE 205 AA; 23051 MW; 6602396CF93F2D9 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 205;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6  
 Db 11 DMSWL 15

RESULT 15  
 ID 08IXK8 PRELIMINARY; PRT; 227 AA.  
 AC 08IXK8;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Similar to hypothetical protein BC017335.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC040173; AAH40173.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 227 AA; 25487 MW; F1A71EA57062A05 CRC64;

Query Match 90.0%; Score 36; DB 4; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWL 6  
 Db 114 DMSWL 118

Search completed: February 18, 2004, 14:35:34  
 Job time : 19.3684 secs